Dense time-course gene expression profiling of the *Drosophila melanogaster* innate immune response

Florencia Schlamp[1], Sofie Y. N. Delbare[2], Angela M. Early[1], Martin T. Wells[2], Sumanta Basu[2], Andrew G. Clark[1,2]

[1] Molecular Biology and Genetics, Cornell University, Ithaca NY, United States
[2] Statistics and Data Science, Cornell University, Ithaca NY, United States

Corresponding authors: Florencia Schlamp (mfs97@cornell.edu), Andrew G. Clark (ac347@cornell.edu), Sumanta Basu (sb2457@cornell.edu).

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ABSTRACT

Immune responses need to be initiated rapidly, and maintained as needed, to prevent establishment and growth of infections. Still, immune genes differ in both initiation kinetics and shutdown dynamics. Here, we performed an RNA-seq time course on *D. melanogaster* with 20 time points post-LPS injection. A combination of methods, including spline fitting, cluster analysis, and Granger Causality inference, allowed detailed dissection of expression profiles and functional annotation of genes through guilt-by-association. We identified antimicrobial peptides as immediate-early response genes with a sustained up-regulation up to five days after stimulation, and genes in the IM family as having early and transient responses. We further observed a strong trade-off with metabolic genes, which strikingly recovered to pre-infection levels before the immune response was fully resolved. This high-dimensional dataset enables the comprehensive study of immune response dynamics through the parallel application of multiple temporal data analysis methods.

INTRODUCTION

Upon microbial infection, *Drosophila* launch rapid and efficient immune responses that are crucial to survival. However, immune responses are energetically costly (Lazzaro and Galac 2006) because they draw resources from other physiological processes (Zerofsky *et al.* 2005, DiAngelo *et al.* 2009) such as metabolism, reproduction, and environmental stress responses. An excessive or overly prolonged immune response can lead to metabolic dysregulation, causing wasting in mammals and flies (Fitzpatrick and Young 2013). Furthermore, it has been shown that allocating resources to the immune system reduces resources for mating (McKean *et al.* 2008, Howick and Lazzaro 2014), and the opposite is also true, where mating reduces survivorship after infection and decreases resistance to infection (Fedorka *et al.* 2007, Short and Lazzaro 2010, Short *et al.* 2012). This represents a trade-off where limited resources need to be allocated to either the immune response or reproduction (Schwenke *et al.* 2016). Therefore, we

expect that natural selection will act to tune the immune response to strike a balance between the advantage of a rapid and robust ability to fight infection, and the costly side-effects of an over-prolonged immune response. This tuning is likely to be mediated through a series of regulatory and feedback properties of the immune system of the fly.

While gene expression has been examined at several time points after infection in *Drosophila* (De Gregorio *et al.* 2001, Boutros *et al.* 2002, Sackton *et al.* 2010), the dynamics of this immune response have not yet been studied with high temporal resolution. A high-resolution time-course analysis can help profile with more certainty the types of expression dynamics that different genes and pathways undergo after infection. Dense and extended time-course sampling of gene expression of the immune response can allow us to distinguish between transient and sustained expression patterns, where expression of genes with a transient response to perturbation will return back to normal after a certain period of time, while expression of genes with a sustained response will remain at a different level of expression compared to pre-perturbation levels. This kind of temporal profiling of the immune response, coupled with computational modeling of gene regulatory networks (GRN), can also suggest candidates to examine for possible interactions and trade-offs between the immune response and other physiological processes.

Statistical analysis of such high-dimensional longitudinal time-course omics data is not straightforward. While the problems of detecting differentially expressed (DE) genes and learning GRN from gene expression data are common in genomics, computational methods have focused primarily on cross-section rather than time-course data. Most popular methods to analyze static RNA-seq data — such as edgeR (Robison *et al.* 2010) or DESeq2 (Love *et al.* 2014) — are not ideal for dealing with time-course RNA-seq data since they do not directly model the correlation of genes between successive time points (Bar-Joseph *et al.* 2012, Spies and Ciaudo 2015). Smooth polynomial or spline based models of temporal dependence in gene expression, such as those employed in Limma-Voom (Law *et al.* 2014) and maSigPro (Conesa *et al.* 2006; Nueda, Tarazona, and Conesa 2014), can fail to capture early impulses in stress response situations, as we highlight in this paper. Also, joint GRN modeling of temporal associations among many genes requires tackling high-dimensionality, an aspect that has not received much attention in the literature. Because there is not one consensus method for the analysis of time-course RNA-seq data, it is important to ensure robustness of findings across different types of computational modeling techniques.

In this study, we performed a dense time-course RNA-seq analysis of the *Drosophila* transcriptional response to commercial lipopolysaccharide (LPS) exposure, which poses a full immune challenge, to better understand the dynamics of activation and resolution of the innate immune response. Flies were sampled over 5 days generating a total of 20 time points post-LPS injection with an additional time point pre-injection as a control. We analyzed the resulting longitudinal RNA-seq dataset using a broad range of statistical methods, including a cross-sectional and a dynamic method for differential expression (DE), clustering, and multivariate Granger causality (Granger 1969), a method to investigate lead-lag relationships among DE genes. We found that commercial LPS exposure has a major impact on the expression of not only immune genes, but also genes involved in metabolism and replication stress. Clustering analysis showed that both the onset and persistence of expression changes

varied across these DE genes. Clustering analysis further suggested a role in the immune response and circadian rhythm for several previously uncharacterized genes. Finally, throughout our analyses we observed a theme of interplay and trade-off between the immune response and metabolism.

RESULTS

High-resolution profiling of gene expression after immune challenge

To generate a full transcriptional profile of gene expression dynamics in *Drosophila melanogaster* after immune challenge, we injected adult male flies with commercial lipopolysaccharide (LPS), a known non-pathogenic elicitor that stimulates a full yet transient immune response (Imler *et al.* 2000; Leulier *et al.* 2003), while avoiding the confounding effects from a growing and changing population of pathogens. Flies were sampled in duplicate for a total of 21 time points throughout the course of five days, which includes an uninfected un-injected sample as control at time zero, and 20 time points after injection. Since this is a perturbation-response experiment, denser sampling occurred at early time points (Bar-Joseph *et al.* 2012), with the first 13 time points taken within the first 24 hr (1, 2, 3, 4, 5, 6, 8, 10, 12, 14, 16, 20, and 24 hr). Sampling is also essential at later time points to know how long it takes to return to 'normality', and to differentiate between transient and sustained responses (Bar-Joseph *et al.* 2012). For this reason, sampling continued until day 5 after LPS injection, although more sparsely (30, 36, 42, 48, 72, 96, 120 h) (**Figure 1A**). For this dataset we obtained 41 high-quality libraries with an average of 23.5 million mapped reads per sample. After normalization of libraries, only genes with more than 5 counts in at least 2 samples were kept, leaving 12,657 genes for further analysis.

Principal components analysis (PCA) on the 500 top genes with highest row variance across all time points revealed a horseshoe temporal trend, with the control samples clustering in the middle, and the post-injection time points following a horseshoe-shaped track, consistent with a pattern of many genes displaying a coordinated change over the five-day interval (**Figure 1B**). This type of "horse-shoe" or arch temporal trend in PCA has been seen in other time-series experiments (Deng *et al.* 2014; Law *et al.* 2014; Bendjilali *et al.* 2017; White *et al.* 2017), and is commonly seen in spatial population genetic variation (Novembre and Stephens 2008) and in ecological gradient data that varies in a non-linear manner (Podani and Miklós 2002). PC1, PC2, and PC3 captured 35, 15, and 14.5% of the variance in gene expression respectively, and the first six PCs account for over 80% of the total variance in the data.

Proper normalization of the data was assessed by confirming the behavior of known *Drosophila* housekeeping genes across time (Qiagen Housekeeping Genes RT^2 Profiler PCR Array and (Lü *et al.* 2018)). As expected, housekeeping genes showed little change across time (**Figure S1A**). The success of the immune challenge was confirmed by the immediate up-regulation of known immune response genes within the first time points (**Figure S1B**).

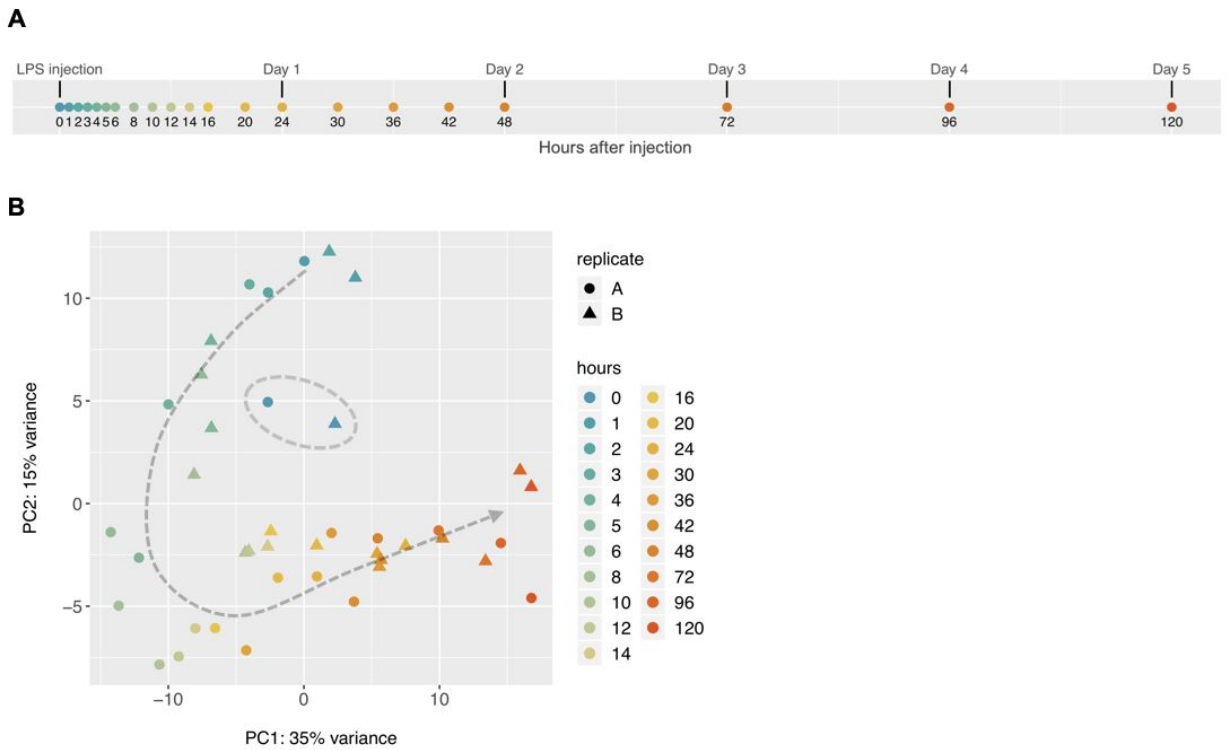

Figure 1. **Transcriptional profiling of *Drosophila* immune response.** (**A**) Timeline of 21 time points, including un-infected un-injected sample as control at time 0. Sampling was denser in the first 24 hr and continued — although more sparsely — until day 5 (120 h). (**B**) Principal component analysis (PCA) of the top 500 genes with highest row variance across all time points shows a coordinated change of gene expression over five days. Both replicates are shown for all samples except for the time point at 3 h, where one replicate was excluded from the analysis during RNA-seq data processing. The two samples in blue clustering in the middle (marked with grey dashed circle) correspond to the control time point (0 h). All other time points from 1 to 120 h show a horseshoe temporal pattern around the controls.

Spline modeling and pairwise comparisons identify 951 genes that are differentially expressed over time following commercial LPS exposure

To identify genes whose expression levels were significantly altered across the time course, we employed two methods. First, we used gene-wise linear models to fit cubic splines with time, on both the first 8 hr and first 48 hr after commercial LPS exposure. Second, because we noticed that certain expression patterns were not adequately described using cubic splines (as discussed below), we also characterized the temporal patterns of expression by estimating the differential expression of every gene at each time point, from 1 to 48 hr, compared to the un-infected un-injected control samples at time zero.

Cubic spline fits identified a total of 411 DE genes, based on a 5% False Discovery Rate (FDR) using the Benjamini-Hochberg method (Benjamini and Hochberg 1995). Of these 411 genes, 31 genes were detected only using short spline fits on the first 8 hr post-injection. Long spline fits on the first 48 hr post-injection identified 363 genes, and 17 genes were identified using both short and long spline fits **(Figure 2A**). Long spline fits excelled at identifying gradual changes and global patterns, such as the ones shown by genes *Gale* and *Galk* (**Figure 2B**). However, long spline fits failed to detect early impulse patterns, such as those observed in the

known immune response genes *AttA* and *DptB* (**Figure 2C**), which were better captured by short spline fits on the first 8 hr post-injection. Still, even short spline fits failed to identify additional known immune genes with early impulse patterns, such as *CecC and CecB*. We also fit third degree polynomials using the R package maSigPro (Conesa *et al.* 2006; Nueda, Tarazona, and Conesa 2014). This approach identified many DE genes that had been selected using spline modeling (**Figure S2**), but similarly failed to adequately describe early impulse patterns. Based on these observations, we also used pairwise comparisons to identify additional DE genes whose trajectories were not well described using cubic splines. Pairwise comparisons identified 729 DE genes that were significantly (FDR < 0.05) up- or down-regulated by an absolute fold change of at least 2 in at least one time point throughout the first 48 hr after injections. Within this gene set, there were 214 genes that were up- or down-regulated at least 4-fold, in at least one time interval after injection (**Figure S3**). Of these 214 genes, 91 "core" DE genes underwent at least a 4-fold change in expression in at least two time intervals after injection, with an FDR < 0.01 (**Figure 3A**). Among the most strongly induced genes were known immune genes *DptB, AttC, Mtk, Dro, DptA* and *edin* (bottom of **Figure 3A** and **Figure S4A**). These genes underwent an expression change of approximately 32-fold and remained elevated up until 48 hr after commercial LPS injection. Further investigation of the 91 core genes showed that the number of up-regulated genes was much higher than the number of downregulated genes across all time points (**Figure 3B**). Eleven of the upregulated genes at each time point were known immune genes, as identified by a list of immune genes curated in (Early *et al.* 2017a). Within these 91 core DE genes, we also found circadian rhythm genes *period* (*per*), *timeless* (*tim*), *takeout* (*to*), and *vrille* (*vri*), which when plotted against time exhibit the classic 24 hr periodic expression of the circadian rhythm (**Figure S4B**).

Of a total of 951 DE genes, 189 genes were identified as differentially expressed using both pairwise methods and spline modeling, but 762 out of 951 genes were identified using only one of these methods, indicating the importance of using complementary methods for the analysis of time course RNA-seq data (**Figure 2D)**.

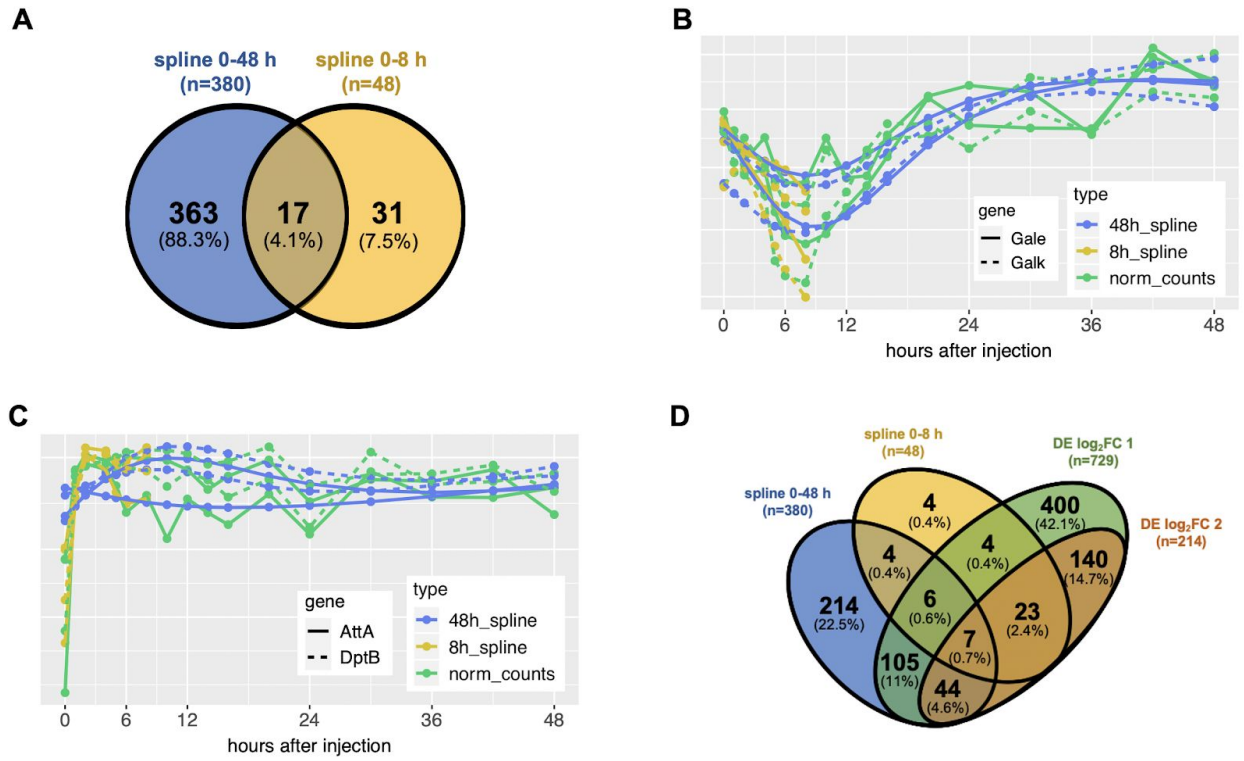

Figure 2. Identification of time-dependent genes. (**A**) Genes that significantly change in expression across time according to spline analysis in the first 8 hr (yellow) vs 48 hr (blue). (**B**) Spline modeling of genes *Galk* and *Gale* when using first 48 hr (blue) and first 8 hr (yellow) compared to the pattern of normalized counts (green), spline modeling over 8 hr misses the main change in pattern. (**C**) Spline modeling of two immune genes (*AttA* and *DptB*) when using first 48 hr (blue) and first 8 hr (yellow) compared to the pattern of normalized counts (green), spline modeling over 48 hr smooths out the early impulse signal. (**D**) Comparing results from spline analysis (over 48 hr in blue and over 8 hr in yellow) vs. results from differential expression analysis (2-fold change in green and 4-fold change in orange) at FDR < 0.05.

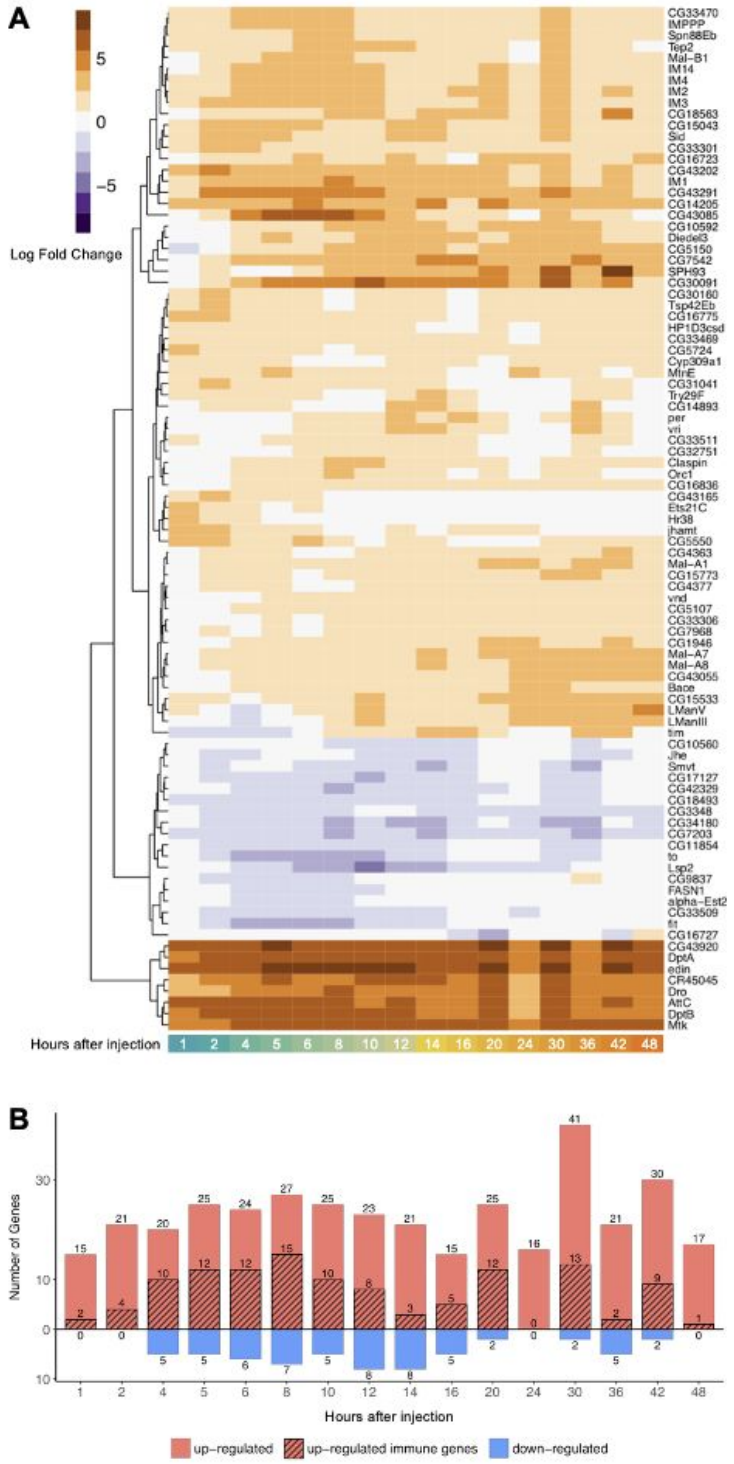

Figure 3. **Dynamics and functions of genes with changing expression patterns over time.** (**A**) Heatmap of gene expression changes. Up-regulated genes in orange, down-regulated genes in purple. FDR correction of 0.01, 2-fold or higher change in expression in at least two time points. 91 genes total, across 48 hr. Genes ordered using Euclidean distance. (**B**) Number of significantly up- and down-regulated genes, from the core 91 DE genes, at each timepoint (in red and blue, correspondingly). Known immune genes are shaded over red. No down-regulated immune genes were observed.

Gene Ontology and Gene Set Analysis demonstrate a divergence in expression between immune and metabolic processes after commercial LPS injection

To understand the biological functions of genes whose expression is influenced by commercial LPS, we performed both a Gene Ontology (GO) and Gene Set Analysis. GO analysis is a useful tool to illustrate the functions of genes with significant differential expression over time, in this case 951 DE genes selected using spline fitting and/or pairwise contrasts. However, focusing only on the top-scoring genes can lead to missing biologically significant signals from genes with modest expression changes. Furthermore, GO analysis does not take into account expression changes over time. Both of these limitations are addressed by Gene Set Analysis, which searches for enriched pathways (Gene Sets) across all 12,657 genes in the dataset, guided by their fold changes for all available time points.

GO analysis of the 951 DE genes using PANTHER identified a significant (FDR < 0.05) overrepresentation of GO terms related to the immune and stress response, carbohydrate, carboxylic acid and lipid metabolism, and proteolysis. Immune response related genes included Attacins (*AttA*, *AttB*, *AttC*), Diptericins (*DptA*, *DptB*), Cecropins (*CecB*, *CecC*), Immune-induced peptides (*IM1*, *IM2*, *IM3*, *IM4*, *IM14*, *IM23*, *IMPPP*), *Drosocin* (*Dro*), *Drosomycin* and Drosomycin-like genes (*Drs*, *Drsl1*, *Drsl2*, *Drsl3*), *Metchnikowin* (*Mtk*), Peptidoglycan Recognition Proteins (*PGRP-SB1*, *PGRP-SD*), *Diedel*, *Relish* (*Rel*) and *elevated during infection* (*edin*), among others. DE genes related to stress response pathways included Turandots (*TotA*, *TotC*, *TotM*) and Heat Shock proteins (*Hsp70Aa*, *Hsp70Ab*, *Hsp70Ba*, *Hsp70Bb*, *Hsp70Bbb*, *Hsp70Bc*).

Of the 951 DE genes, we identified 20 genes that encode known or putative transcription factors, based on the FlyTF database (**Table S1**). Seven of these twenty genes have a fast impulse of up-regulation, reaching their maximum expression in the first two hours following injection (*Rel*, *Dif*, *CrebA*, *luna*, *Ets21C*, *Hr38* and *stripe;* **Figure 4A**). *Rel* and *Dif* encode downstream components of the imd and Toll pathways respectively, both involved in the activation of the immune response (Meng, Khanuja, and Ip 1999; Manfruelli *et al.* 1999; Myllymäki *et al.* 2014; Mundorf *et al.* 2019). *Ets21C* encodes a stress-inducible transcription factor, and *Hr38* and *stripe* are the two most robust activity-regulated genes (ARGs, defined as genes that are rapidly induced upon stimulation of neurons, mostly within an hour) in *Drosophila* (Chen *et al.* 2016). Three genes encoding transcription factors had oscillating expression patterns over time and are involved in the regulation of the circadian clock (*vri*, *clk*, *Pdp1;* **Figure S5A**; Cyran *et al.* 2003; Collins *et al.* 2006). One gene of interest, *p53*, involved in the response to genotoxic stress (**Figure S5B**; Brodsky et al. 2004), reached its maximum up-regulation later, at 6 hr after injection.

Overall, the GO analysis indicates that the flies manifest a robust immune response to the commercial LPS injections, as the gene expression changes are consistent with known expression profiles of immune response deployment in *Drosophila* (De Gregorio *et al.* 2001; Boutros *et al.* 2002). In addition, the GO analysis demonstrates that the response to commercial LPS also affects metabolic homeostasis.

Supporting these results, Gene Set analysis across all 12,657 genes and all time points showed that the top up-regulated pathways were all related to immune response, defense response to bacteria, and peptidoglycan functions (**Figure 4B**). Within these we found pathways related to defense response against both Gram-negative and Gram-positive bacteria. While the commercial LPS used for injections is derived from the outer membrane of Gram-negative bacteria, the injections themselves also result in septic injury, which is known to activate both Gram-positive and Gram-negative immune pathways (Toll and Imd pathways correspondingly) (Hoffmann and Reichhart 2002). Among down-regulated pathways we found many metabolism-related functions. Three of these pathways (glycogen metabolic process, triglyceride biosynthetic process, and gluconeogenesis) are highlighted in **Figure 4C-D** and **S5**. The glycogen pathway down-regulation pattern was driven by genes *Fatty acid synthase 1* (*FASN1*), and *UGP*, which encodes a UTP--glucose-1-phosphate (**Figure 4C**). Down-regulation of the triglyceride pathway was driven by *FASN1* and *minotaur* (*mino*), a glycerol-3-phosphate 1-O-acyltransferase (**Figure 4D**). Finally, the gluconeogenesis pathway down-regulation was driven by *fructose-1,6-bisphosphatase* (*fbp*), a rate limiting enzyme for gluconeogenesis (Miyamoto and Amrein 2017) (**Figure S6**). These metabolic genes reached their lowest expression within the first 6 hr after injections, and mostly recovered to pre-injection levels by hours 12-24.

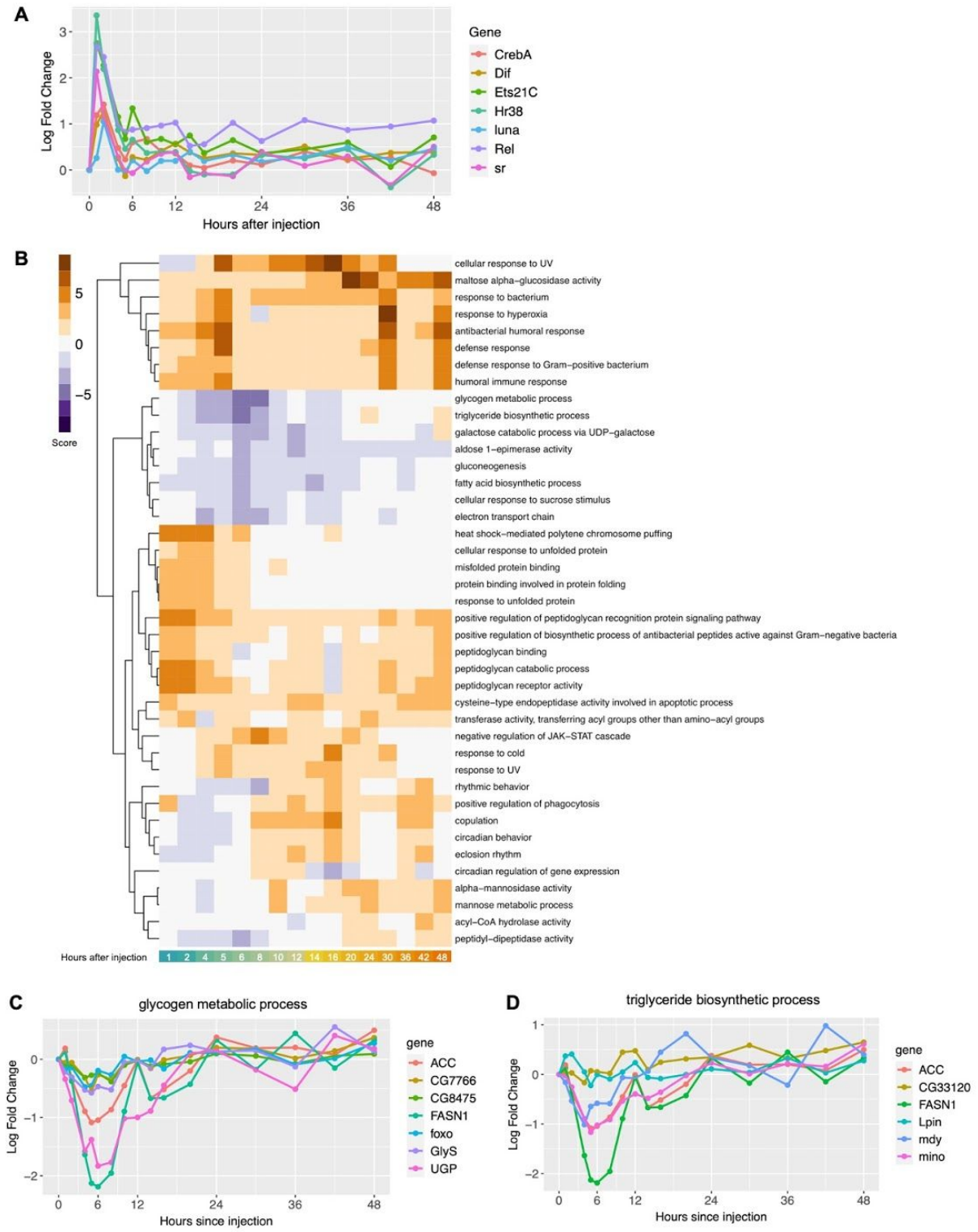

Figure 4. **Dynamics and functions of genes with changing expression patterns over time.** (**A**) Temporal dynamics of Differentially Expressed Transcription Factors: Immediately early (*Ets21C*, *Hr38*, *Rel*, and *sr*) and late (*Orc1*) up-regulation after immune challenge. **(B)** Heatmap showing most up- and down-regulated pathways (orange and purple respectively) through the first 48 h post-injections (absolute score > 2.5 and *P*-value < 0.05 in at least one time point). (**C-D**) **Gene Set Analysis identifies up- and down-regulated pathways.** Selected significantly down-regulated metabolic pathways with corresponding gene memberships.

Clustering of temporal profiles highlights differences in the initiation and shutdown of immune and metabolic genes and demonstrates a regular rhythm of circadian clock genes

GO and Gene Set Analysis illuminated functions of genes that respond to commercial LPS, and indicated a trade-off between immune and metabolic processes. However, both GO and Gene Set Analysis are based on prior knowledge of gene function. Clustering of genes based on their expression profiles is not influenced by prior annotations. Such an unbiased approach can thus identify responses of poorly annotated genes. In addition, clustering can illustrate how gene expression trajectories differ over time. We performed three analyses to characterize temporal profiles. First, we performed hierarchical clustering based on Pearson correlation on a set of 551 predominant time-dependent genes to identify major expression patterns over time. These 551 genes included the 411 genes identified using spline modeling, and 214 genes with at least a 4-fold change in expression as identified using pairwise comparisons. Second, we performed clustering based on autocorrelation on these 551 genes. As opposed to Pearson or Euclidean correlation, an autocorrelation function takes the ordering of time points into account, allowing us to identify more detailed characteristics of gene expression profiles in time series. Third, because circadian rhythm genes were not apparent in the clusters identified using the previous methods, but were expected to be present in our dataset, we used the R package *JTK_Cycle* (Hughes *et al.* 2010) to identify genes with 24 hr cycling patterns among all genes in the dataset. We were interested in these patterns since the circadian clock is known to regulate the expression of immune genes (Cirelli, LaVaute, and Tononi 2005), and in turn, infections are known to influence the flies' circadian rhythm (Shirasu-Hiza *et al.* 2007).

First, expression profiles of the 551 predominant time-dependent genes fell into four main hierarchical clusters (**Figure 5A**). Clusters 1 and 2 both had a strong increase in expression after injection (**Figure 5B**). Cluster 1 had a more immediate increase in expression following injection, reaching a maximum within the first 2 hr. Cluster 2, on the other hand, reached a maximum expression later, at around 9 h. Cluster 1 showed significant enrichment of GO terms for immune and stress response related processes, and contained Attacins and Cecropins, as well as Heat Shock protein family genes. Cluster 2 was enriched for GO terms for abiotic stimulus response, and contained the Immune-induced peptide family and other immune response related genes, as well as genes from the Turandot family (**Figure 5C)**. Clusters 3 and 4 were characterized by an initial decrease in expression followed by an increase in expression after 3 hr and 6 hr respectively (**Figure 5B**), with cluster 4 showing a stronger decrease in expression in the early hours after injection. These clusters had a significant enrichment of GO terms for biosynthetic, catabolic, and metabolic processes (**Figure 5C**), and their down-regulation again indicates a trade-off between metabolism and the initiation of an immune response.

Our second clustering analysis based on autocorrelation revealed additional differences regarding the initiation and resolution of gene expression after commercial LPS injection. First, we identified a cluster of genes with an immediate and sustained up-regulation. This cluster was

characterized by a strong early induction with a ~6 to 64 fold change within the first hour, reaching a maximum of 64 to 362 fold change, and maintaining persistent up-regulation of 6 to 32 fold change throughout 5 days (**Figure 6A**). This cluster contained canonical immune response genes such as *AttA*, *AttB*, *AttC*, *DptA*, *DptB*, *Dro*, *edin*, *Mtk*, *PGRP-SB1*, *PGRP-SD.* The cluster further contained *CR44404* or *IBIN* (*Induced by Infection*), whose exact mode of action is unknown, but whose up-regulation stimulates starch catabolism as part of an immune-induced metabolic switch, likely to make free glucose available to circulating immune cells (Valanne *et al.* 2019). Finally, this immediate-response cluster also contained *CG43236, CG43920* and *CR45045*, which are uncharacterized transcripts known to be up-regulated after bacterial infection (Troha *et al.* 2018).

Autocorrelation-based analysis also identified clusters of genes with transient responses to infection. One of these clusters was composed of a putative class of immune induced peptides: *IM1*, *IM14*, *IM2*, *IM23*, *IM3*, *IM4*, *IMPPP*, and *CG33470*. These IM genes are located in the 55C4 region of chromosome 2R and have been recently labeled as “Bomanins” (Clemmons *et al.* 2015). *CG33470* is an uncharacterized transcript located 3.3 kb downstream of *IMPPP* and might belong to the same open reading frame, as both are sometimes referred to as *IM10* (Kenmoku *et al.* 2017), and show nearly identical gene counts in our dataset. This cluster of immune-induced molecules was characterized by an early induction (but not as immediate as the AMP cluster) of ~6 to 11 fold changes within the first two hours, reaching a max of 6 to 32 fold changes, and returning to a steady state after 3-5 days (**Figure 6B**). Thus, clustering analysis identified effector immune genes segregating by function: AMPs showed an immediate early sustained up-regulation even after 5 days (**Figure 6A**), while the IM family had an early up-regulation that eventually returned to steady state levels (**Figure 6B**).

A final cluster illustrated a more complex expression pattern: many genes in this cluster were down-regulated immediately, 1-2 hr after injection, after which they were up-regulated, reaching their maximum fold change after 8-12 hr, followed by a return to baseline after 2-3 days (**Figure 6C**). This cluster was composed of genes from the stress-induced Turandot family (Ekengren *et al.* 2001) and included *Diedel*, *Grik*, *lectin-24A*, *NimB3*, *CG11459*, *CG16836*, and *CG30287*. *Diedel* encodes an immunomodulatory cytokine known to down-regulate the imd pathway. *Grik* encodes a glutamate receptor, and *Lectin-24A* encodes a pattern recognition receptor that mediates pathogen encapsulation by hemocytes (Ao *et al.* 2007). *Lectin-24A* has been shown to be down-regulated in the first 2 hr following septic injury and then up-regulated 9 hr after (Keebaugh and Schlenke 2012), consistent with the pattern we see in our data. *NimB3* is part of the Nimrod gene family, which is involved in phagocytosis (Zsámboki *et al.* 2013). *CG11459* encodes a predicted cathepsin-like peptidase induced by bacterial infection and injury (Katzenberger *et al.* 2016). *CG16836* is located near IM genes *IM1*, *IM2*, *IM3* and *IM23* (expressed in the previous cluster, **Figure 6B**), which could explain the similar transient expression pattern. *CG30287* encodes a predicted serine protease, a class of proteins that plays roles in immune response proteolytic cascades (Buchon *et al.* 2009).

Finally, using JTK_cycle, we identified 22 periodic genes with a 24 hr cycle, using a cutoff of BH *Q*-value < 0.05 and amplitude > 0.5 (**Figure 7**). Among them were four well characterized circadian genes, suggesting that their periodicity was not affected by commercial LPS-injection: *period* (*per*), *takeout* (*to*), *vrille* (*vri*), and *PAR-domain protein 1* (*Pdp1*), as well as eight genes

which do not have assigned circadian functions but have evidence of cyclic behavior in previous literature (**Table 1**), and 10 genes, of which 8 are uncharacterized, that have not yet been reported to have cyclic expression outside this study (**Table 1**; *CG10560*, Sgroppino, *CG15253*, *CG15254*, *CG18493*, *CG31321*, *CG33511*, *CG34134*, *CG42329, salt*).

Overall, the combination of clustering methods combined with GO analysis allowed us to identify strong temporal patterns that correspond to early and late induction of immune processes, as well as both transient and sustained responses to infection, which point to a trade-off between the immune response and metabolism. We found that genes that share functions often have similar temporal expression patterns, suggesting co-regulation. This observation further allowed us to assign putative functions to previously uncharacterized genes that cluster together with well-studied genes.

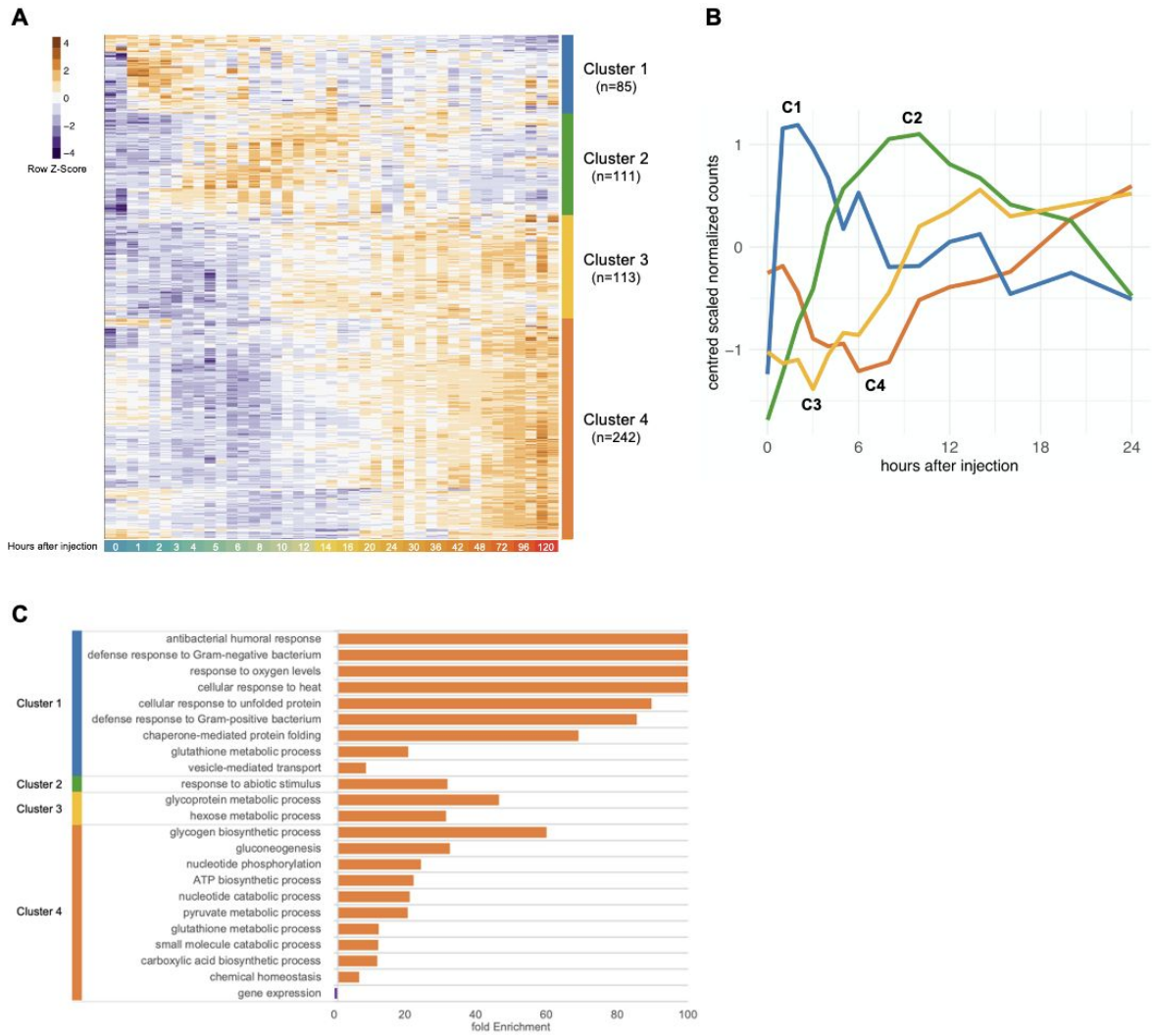

Figure 5. Global dynamics of time-dependent genes show divergent patterns of expression. (**A**) Heatmap of the 551 most predominant time-dependent genes, identified by spline modeling over 48 and 8 hr (FDR < 0.05) and pairwise differential expression (with at least a 2-fold change in expression and FDR < 0.05). Hierarchical clustering of the genes shows four main clusters characterized by time points in which the genes reach maximum and minimum expression across time. Z-score values of each gene are shown from dark purple (minimum expression across time) to dark orange (maximum expression across time). (**B**) Mean patterns of expression across time for genes within

each of the four main clusters during the first 24 hr, displayed by their centered and scaled normalized counts. (**C**) Significant Gene Ontology terms (FDR < 0.05) for over-represented Biological Processes at each cluster.

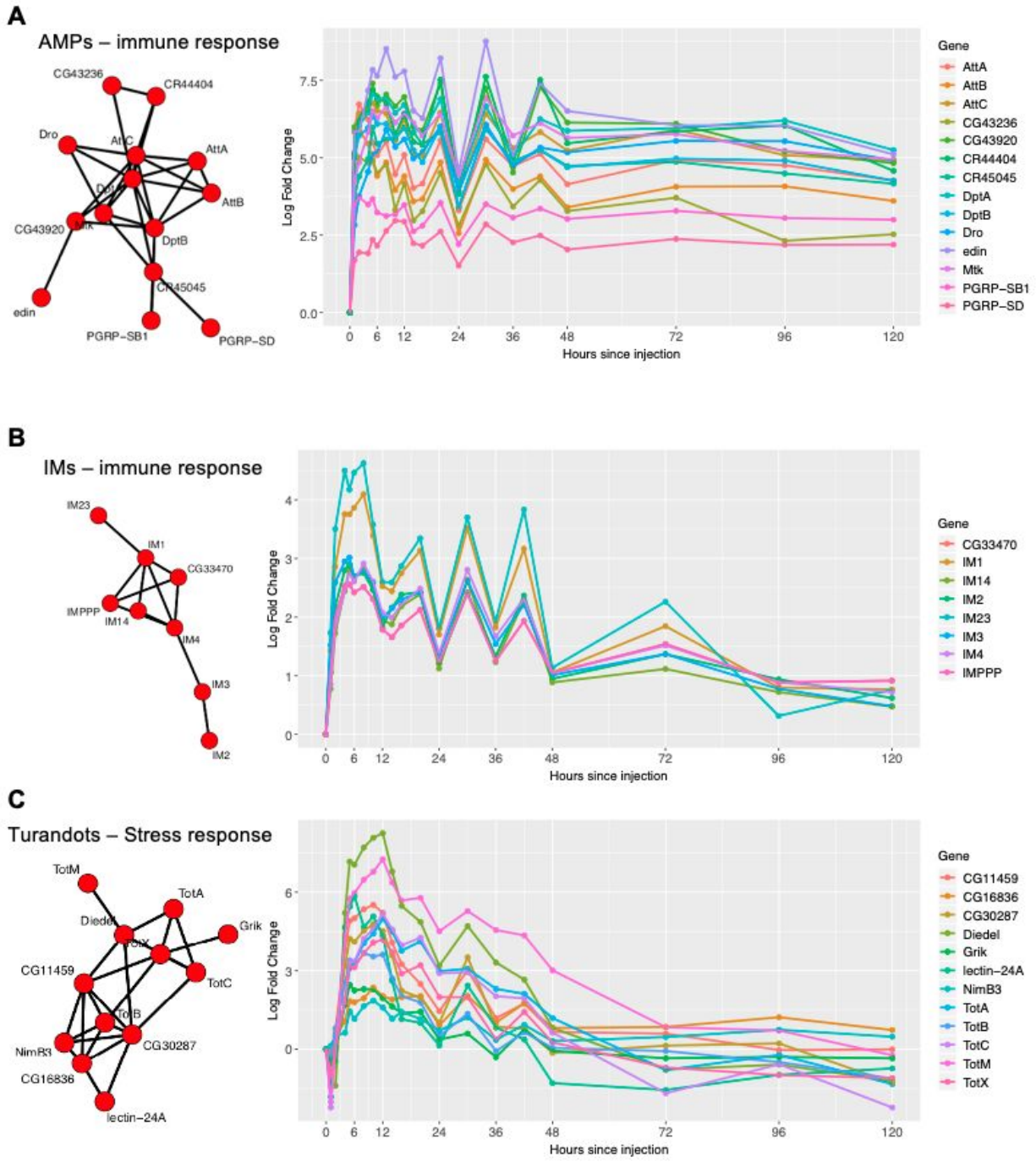

Figure 6. Clusters of genes identified using autocorrelation. Network nodes represent genes; network edges represent the distance between gene autocorrelations, based on ACF analysis using TSclust. (**A**) AMPs show sustained expression after immune inducement throughout 5 days (120 h). (**B**) Putative effector immune genes show a transient response to commercial LPS. (**C**) Turandots (humoral stress response) return to steady state by day 5 (120 h) post immune inducement.

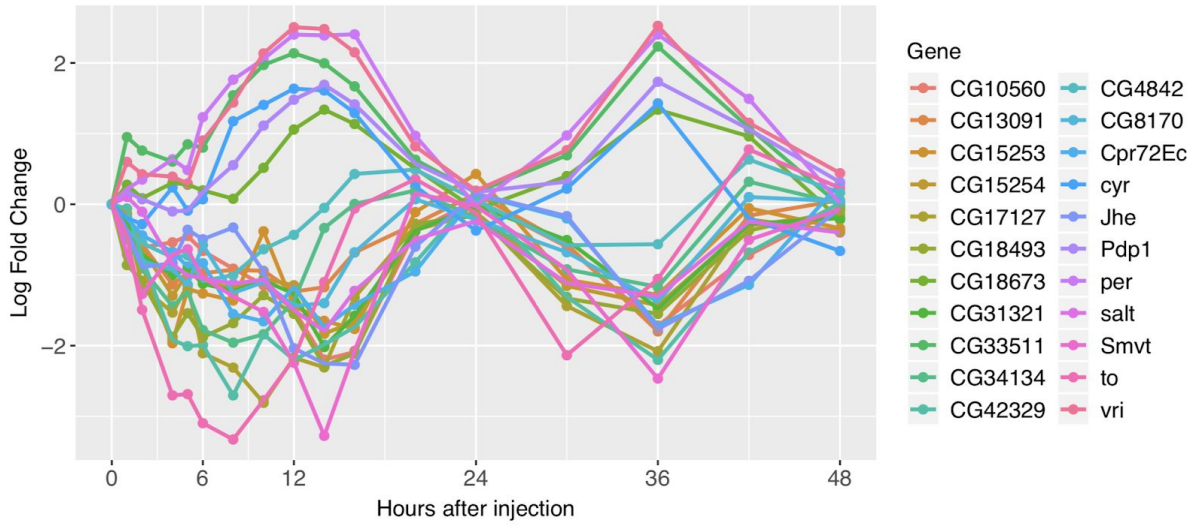

Figure 7. Top 22 genes identified by JTK_Cycle show 24 hr temporal cycling.

Table 1. Evidence of cyclic behavior for top genes identified by JTK_Cycle.

Gene	Evidence of cyclic behavior	Source
CG18673 (*CAH5*, *carbonic anhydrase 5*)	upregulated DE gene in response to light stimulation	Adewoye *et al.* 2015
cypher (*cyr*)	dowregulated DE gene in response to light stimulation	
CG17127	photoperiodic	Pegogaro and Tauber 2018
	rhythmically expressed in constant dark conditions	Ueda *et al.* 2002
Alcohol dehydrogenase *CG4842 and Cuticular protein 72Ec (Cpr72Ec)*	downregulated in the retina after *heme oxygenase* (*ho*) silencing in photoreceptor cells	Damulewicz *et al.* 2019
CG8170	cycling mRNA	Huang *et al.* 2013
Juvenile hormone esterase (*Jhe*)	cyclic hemolymph activity	Zhao and Zera 2004
Sodium-dependent multivitamin transporter (*Smvt*)	modulated by the circadian rhythm in mice	He *et al.* 2016
CG10560, *CG13091* (*Sgroppino*), *CG15253*, *CG15254*, *CG18493*, *CG31321*, *CG33511*, *CG34134*, *CG42329*, and sodium/solute symporter *salty dog* (*salt*)	none reported	

Sources: (Ueda *et al.* 2002; Zhao and Zera 2004; Huang *et al.* 2013; Adewoye *et al.* 2015; He *et al.* 2016; Damulewicz *et al.* 2018; Pegoraro and Tauber 2018)

Gene interaction modeling of lead-lag patterns using Granger causality

Clustering methods based on single gene's autocorrelation or cyclicity patterns can detect genes with similar expression profiles. However, these methods are not suitable for seeking causal relationships between genes that manifest in a lead-lag relationship, for instance when high expression of gene A results in a high expression of gene B shortly afterwards. Detecting such lead-lag patterns (**Figure 8A**) is a unique advantage of dense time-course experiments. Granger causality (GC), a statistical method popular in analysis of macroeconomic time series,

provides an ideal framework for modeling such patterns and building directed networks among genes. The concept of GC is based on predictability. If the knowledge of the past of one time series improves the prediction of a second one, the first is said to be Granger causal (GC) for the second. *Bivariate* GC analysis between two genes A and B, as described above, does not account for possible confounding effects of other genes C, D, E which can also influence genes A and B (**Figure 8B**). *Multivariate* GC analysis alleviates this problem by explicitly accounting for the effects of the confounding genes by a joint modeling (Fujita *et al.* 2012; Finkle, Wu, and Bagheri 2018), but does not account for high-dimensionality and consequently cannot jointly model hundreds of genes based on tens of data points. We used modern high-dimensional methods (viz LASSO (Tibshirani 1996) and de-biased LASSO (Javanmard and Montanari 2014, Dezeure *et al.* 2015)) to address this problem and build lead-lag network models among 258 genes.

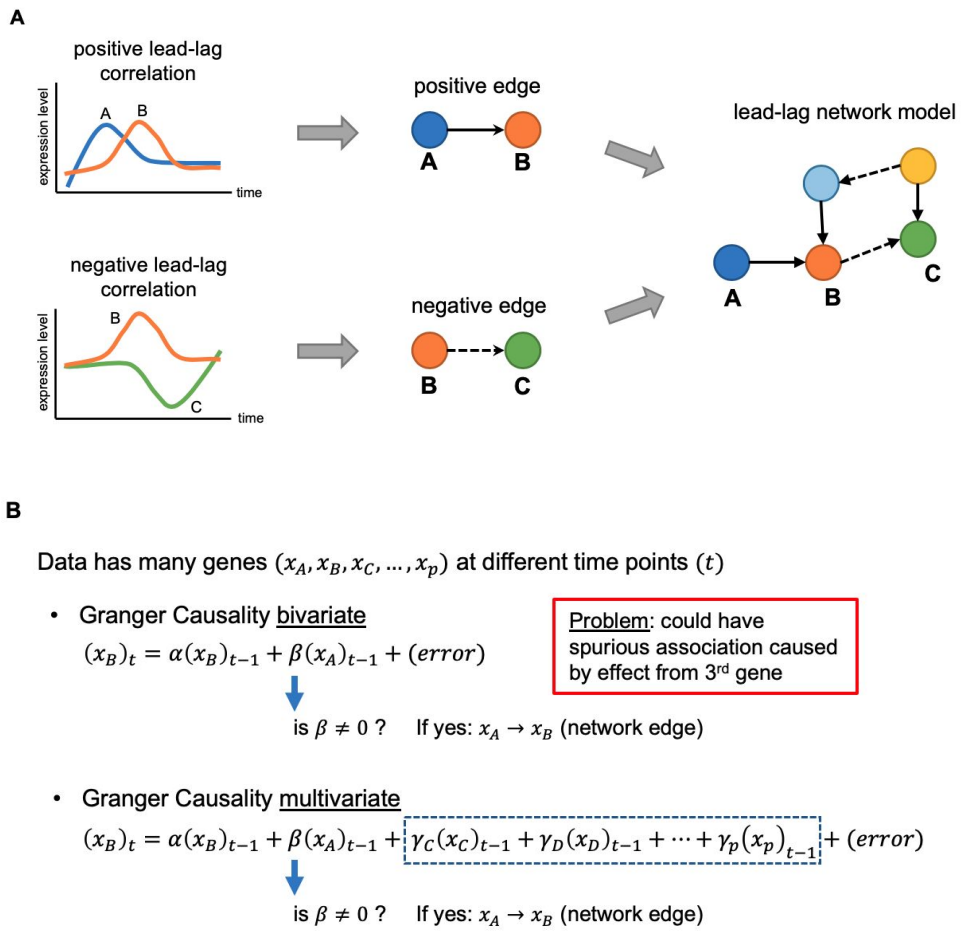

Figure 8. Diagram describing the process of constructing directed networks from Granger causality. (A) Lagged correlated expression between two genes (Granger causality) leads to the construction of a directed edge between two genes (nodes), which in turn is used to build directed lead-lag network models of putative interactions among genes. Edges can be positive or negative, based on the sign of lead-lag correlation between the two genes. **(B)** Bivariate associations are calculated between two genes at a time, while multivariate associations adjust for potential indirect association from all other genes in the gene set.

We constructed directed GC edges and networks of putative interactions among a subset of 258 genes. These genes changed at least 2-fold across the time course and had available functional annotations. We performed Granger causality analysis on sliding windows of 6 time points on the normalized counts of both replicates using bivariate and multivariate methods (see **Materials and Methods**). We investigated both positive and negative edges, reflecting positive and negative lagged correlations between genes. The overall unfiltered GC network has a multitude of relationships worth exploring, but limitations in the ability to distinguish different types of causality make widespread conclusions from the network challenging. Here, we discuss several examples of subnetworks which illustrate putative functional relationships among genes whose expression changes in response to LPS injection.

Based on our interest in identifying trade-offs between biological processes in infected animals, we first constructed a high-quality set of consistently significant GC edges of divergent expression (negative edges). To this end we first filtered the subnetwork by (a) removing all edges with a positive weight, (b) removing all nodes corresponding to cyclic genes identified earlier through the JTK_Cycle method, (c) using only pairs of nodes with significant edges (BHFDR < 0.05%) in at least 3 consecutive windows within the first 24 hr of the time course. After filtering, the resulting high-quality GC network contained 51 nodes and 35 edges in 16 connected components (**Figure S7**). This network, by design, should include the most interesting examples of divergent expression changes from our full dataset.

The largest connected component in this network (Component #1) is a multifunctional chain of 6 genes, which connects the down-regulation of four metabolic genes with the up-regulation of two genes that are involved in regulating proliferation and repair (**Figure 9A**). Two of the metabolic genes, *Sorbitol dehydrogenase 1* (*Sodh-1*) and *UGP*, both lead the divergent expression of *Claspin* (both 4 consecutive windows, 2 to 10 and 4 to 12, respectively) (**Figure 9C** & **S8A**). *Claspin* plays a role in DNA replication stress (Lee *et al.* 2012). It is known that there is an interplay between host immune systems and replication stress (Ubhi and Brown 2019). The immune system can detect and respond to replication stress, which is an important feedback loop necessary to remove defective cells (Liu *et al.* 2015). Furthermore, the activation of the immune response generates reactive oxygen species (ROS) and reactive nitrogen species (RNS), and can promote chronic inflammation, all of which can trigger DNA damage (Nakad and Schumacher 2016). *UGP* and *fbp* were identified earlier during gene set analysis to drive the down-regulation of metabolic pathways (**Figure 4B** and **4D**), and in this cluster they are both negatively directed by *LpR2* (3 consecutive windows, 6 to 13) (**Figure 9D** and **S8B**). *LpR2* is a lipophorin receptor, known to regulate the innate immune response by clearing serpin protease complexes from the hemolymph through endocytosis (Soukup *et al.* 2009). Lipophorin is a known humoral factor that contributes to clot formation (Karlsson *et al.* 2004; Krautz *et al.* 2014). Finally, *LpR2* is also shown to negatively direct *juvenile hormone acid methyltransferase* (*jhamt*) (4 consecutive windows, 1 to 9) (**Figure 9E**). JHAMT is an enzyme that activates juvenile hormone (JH) precursors at the final step of the JH biosynthesis pathway in insects (Shinoda and Itoyama 2003). JH is a known hormonal immunosuppressor in *Drosophila* (Rolff and Siva-Jothy 2002; Flatt *et al.* 2008; Schwenke and Lazzaro 2017).

Interestingly, *Claspin* was identified to be part of the same pathway as *Orc1* in our previous gene set analysis, showing similar patterns and window of up-regulation (mitotic DNA

replication checkpoint pathway, **Figure S9**). In our network, *Orc1* is part of an isolated edge with metabolic gene *ABGE* (Component #2, 4 consecutive windows, 4 to 12) (**Figure 9A** and **9E**). These prioritized subnetwork components suggest an interplay between metabolic pathways and other pathways such as proliferation and repair (**Figure 9B**), motivating follow-up studies to determine which pathways might be regulating and trading off with each other in the hours following an immune challenge.

In addition to these purely negative edges, we detected highly significant positive and negative edges among circadian rhythm genes. These included *cryptochrome* and *Smvt* (6 consecutive windows, 6 to 16) (**Figure S10A**), *vrille* and *takeout* (4 consecutive windows, 9 to 17) (**Figure S10B**), *period* and *takeout* (4 consecutive windows, 9 to 17) (**Figure S10C**), and *Smvt* and *takeout* (4 consecutive windows, 9 to 17) (**Figure S10D**). *Smvt* is predicted to encode a sodium-dependent multivitamin transporter, and *takeout* influences feeding behavior (Sarov-Blat *et al.* 2000; Wong *et al.* 2009). Metabolic processes and feeding are known to be under circadian control (Giebultowicz 2018). In addition, (So *et al.* 2000) reported that *takeout* is regulated by the circadian clock, but with a phase shift relative to *period*. This pattern is clearly visible in our dataset and was correctly identified using Granger Causality. This shows that Granger causality can be used to infer gene dependencies/interactions using global gene expression behavior.

Finally, among genes connected only by positive edges, we identified an edge from *period*, a regulator of the circadian clock (Smith and Konopka 1982; Reddy *et al.* 1984), to *Rhodopsin 5*, which encodes a G-protein-coupled receptor involved in phototransduction (**Figure S11A**). *Rh5* mRNA levels are known to demonstrate a cyclic pattern (Claridge-Chang *et al.* 2001), indicating regulation by the circadian clock. We further identified positive edges between genes that are likely co-regulated. These included edges between up-regulated genes that respond to NF-κB signaling: from genes encoding peptidoglycan recognition receptors (*PGRP-SD* and *PGRP-SB1*) to genes that encode secreted antibacterial peptides (*IM1*, *IM4*, *IM23, DptB*, and *AttC*) (**Figure S11B-F**). We also observed edges between down-regulated genes, such as from *CG18003* (predicted to play a role in lactate oxidation) to *AGBE* (a predicted hydrolase involved in glycogen synthesis) (**Figure S11G**). While the expression of these genes likely responds to similar signals, the observed lags between these genes' expression profiles suggest that there are differences in their transcriptional control, such as regulation by cofactors or differences in promoter affinity for certain transcription factors.

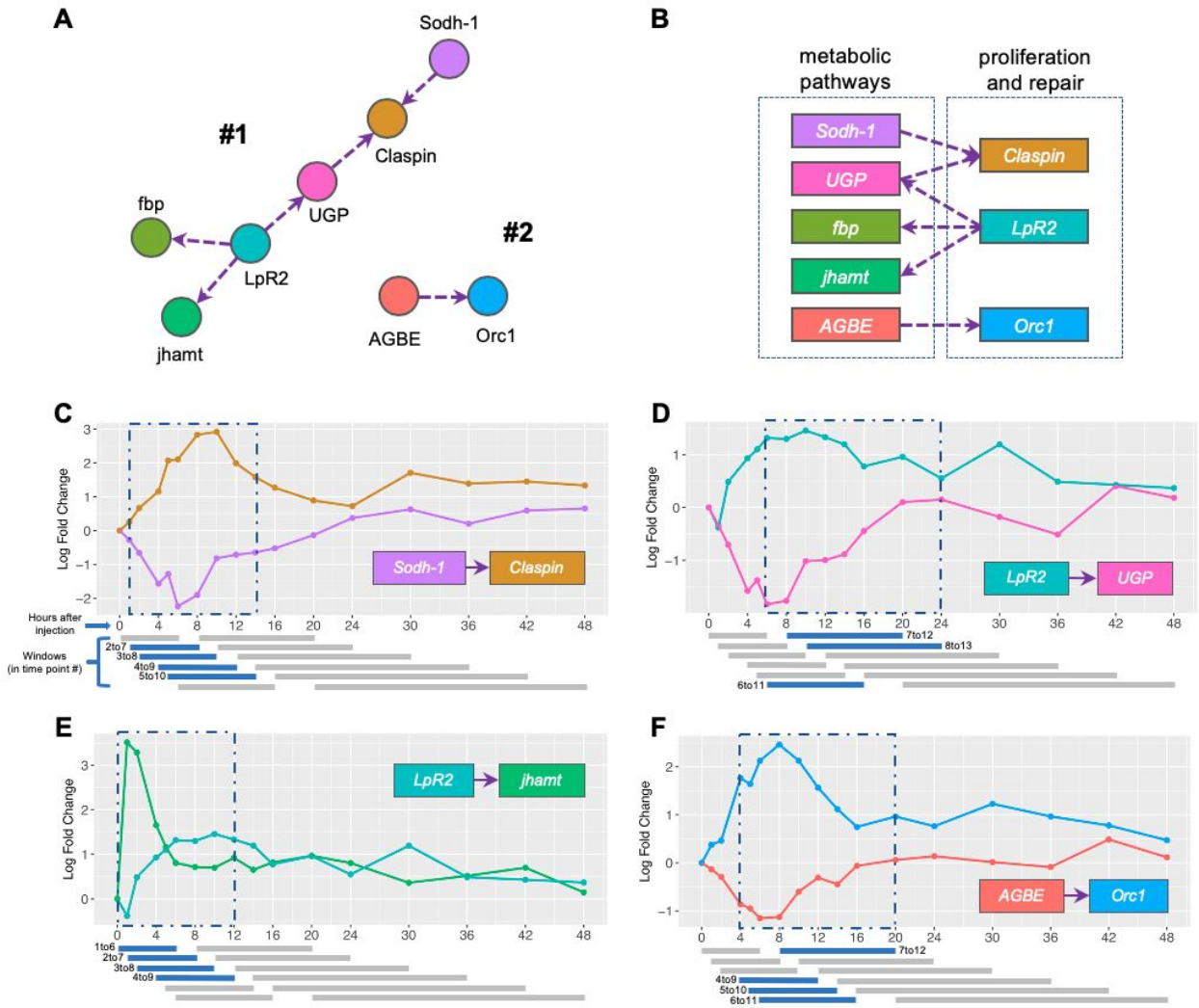

Figure 9. High-quality GC network components and their edges. (**A**) Components #1 and #2 from GC network (**Figure S4**). (**B**) Diagram summarizes interplay between main represented pathways on the selected components. (**C-F**) Selected edges from the components plotted against time. Significant windows colored in blue, non-significant colored in grey. Resulting overall consecutive windows are labeled in blue dashed rectangles. Individual windows represent 6 consecutive time points, but because time points are not at regular intervals, the windows have different time ranges, but identical numbers of samples.

DISCUSSION

We have produced a dense and high-quality time-course profiling of the *Drosophila* transcriptome response to commercial LPS injections using RNA-seq sampling over 20 time points in 5 five days. This profiling provides a high-dimensional dataset, which is available as a resource for the community. We analyzed this dataset using a broad range of statistical methods, including Granger causality, to investigate lead-lag relationships between genes. Because of the high dimensionality, it is not straightforward to analyze time series, as illustrated by the partially distinct results of spline fitting and pairwise comparisons. However, using a

combination of analysis methods allowed us to identify distinct patterns with high confidence, specifically responses to immune challenge with divergent initiation and resolution dynamics, as well as cyclic patterns of gene expression, and patterns of co-regulation and trade-offs. Below, we describe and discuss the main insights from these analyses, as well as limitations and future steps.

Genes vary in their initiation and resolution dynamics after immune challenge

Clusters of genes demonstrated distinct activation kinetics after immune challenge. This phenomenon has been observed both in fly (Boutros *et al.* 2002) and mammalian cells (Bahrami and Drabløs 2016), but as a result of the dense sampling, our dataset provides a highly detailed view of these initiation dynamics. In addition, because we sampled up to five days post-injection, we could also compare the long-term responses of exposure to commercial LPS.

First, genes that are part of distinct functional groups showed a maximal up- or down-regulation after immune challenge within 4 different time frames. AMPs showed the fastest up-regulation within the first 1-2 hr after immune challenge (**Figure 3A, S3A** and **Figure 6A**), a pattern we also observed in several transcription factors (**Figure 4A**). Metabolic genes and IMs reached their lowest and highest point of expression respectively at 5-8 hr after immune challenge (**Figure 4, 5** and **6B**). Proliferation and repair genes reached their highest point of expression at 8-10 hr (**Figure 9**). Finally, stress-related Turandot genes reached their highest point of expression at 10-12 hr (**Figure 6C**), following a pattern of delayed response, in line with observations by Ekengren and Hultmark (2001).

The resolution dynamics of these gene sets differed as well. A fast recovery of gene expression levels was observed for a cluster containing metabolic genes (e.g. *FASN1*, *UGP*, *fbp*, and *mino*; **Figure 4**). After an initial down-regulation, the expression of these genes recovered to the pre-challenge state around 12-24 hr after LPS injection. A slower recovery was observed for two clusters mainly composed of known immune-induced molecules (IMs, or Bomanins (Clemmons *et al.* 2015)) and stress-induced Turandot genes. The expression of genes in these clusters returned to a pre-challenge state after 2 to 5 days (**Figure 4**). Finally, the expression of genes in the cluster containing mainly antimicrobial peptides (AMPs) remained up-regulated during the entire five-day time course (**Figure 6A**).

Several interesting biological questions come forward from these time-course dynamics. First, the expression IMs and certain AMPs (e.g. *Mtk*) is activated downstream of Toll activation (Clemmons *et al.* 2015, Lin *et al.* 2020), but Toll-regulated AMPs were up-regulated significantly earlier than IMs and remained up-regulated for longer, suggesting additional layers of regulation downstream of Toll. Second, it is striking that AMP expression did not recover to pre-injection levels even after five days. In the absence of LPS measurements over time, we cannot conclude whether the prolonged AMP up-regulation was due to remaining commercial LPS in flies or whether it is typical for AMPs to be expressed at a higher level for a certain time after LPS has been cleared. Troha *et al.* (2018) also observed prolonged AMP up-regulation after bacterial infection, even when levels of bacteria were below detection threshold. These observations further raise the question of what it means to return to normality, if normality is achieved at all after infection. Third, the speedy recovery of metabolic genes, despite sustained expression of AMPs, suggests that the early stages of infection likely involve the greatest

trade-offs, at least in response to commercial LPS. These dynamics might differ in flies infected with live bacteria and might differ depending on the strain of bacteria (Troha *et al.* 2018). For example, infections with *Mycobacterium marinum* were shown to induce wasting, or an excessive loss of energy stores in flies (Dionne *et al.* 2006). Thus, future comparisons between the response to commercial LPS presented here, and the response to various strains of bacteria should provide more information on the regulation of metabolism dynamics during immune challenge, and how that contributes to long term effects either detrimental or beneficial.

Initiation of the immune response coincides with a down-regulation of metabolic processes

Our dataset showed distinct global dynamics pointing to a divergence in the functional responses to immune challenge. Both clustering and gene set analysis demonstrated the striking divergence in expression between immune and metabolic processes (both carbohydrate and lipid metabolism), with the most up-regulated pathways related to the immune response, and the most down-regulated pathways related to metabolic functions. Such a strong trade-off was not reported previously in a post-infection gene expression time course in *D. melanogaster* (Boutros *et al.* 2002, DeGregorio *et al.* 2001). *FASN*, which showed the strongest down-regulation in both glycogen metabolic process and triglyceride biosynthetic process, is a lipogenic gene whose down-regulation might indicate a need to have easily accessible nutrients instead of storing them. Indeed, infections in mammals are known to induce adipose tissue lipolysis (Wolowczuk *et al.* 2008) and bacterial peptidoglycan is a ligand that stimulates lipolysis as well (Chi *et al.* 2014). The gene with the strongest down-regulation in the gluconeogenesis pathway was *fbp*, which codes for fructose-1,6-bisphosphatase, the rate limiting enzyme for gluconeogenesis. This gene was significantly down-regulated in a study that reported that *Listeria monocytogenes* infection in *Drosophila* causes a decrease in energy stores, with reduced levels of triglycerides and glycogen (Chambers *et al.* 2012). The divergent dynamics detected in our dataset are thus in agreement with known individual mechanisms characterized in the immune response.

We further saw implications of functional interplays using the Granger Causal (GC) network analysis. Main subnetwork components showed significant GC directional edges between down-regulated metabolic genes (such as *Sodh-1*, *UGP*, *fbp*, and *AGBE*) and up-regulated genes with cell proliferation and repair functions (*Claspin*, *LpR2*, and *Orc1*) (**Figure 9**). These results further suggest an underlying interplay between metabolic pathways and proliferation and repair mechanisms such as regulation of DNA replication stress, endocytosis, and clot formation. While functional genetics studies have demonstrated such trade-offs previously (e.g. DiAngelo *et al.* 2009; Clark *et al.* 2013), our dataset reveals the extent and dynamics of these trade-offs on a genome-wide scale.

Predicting function by association

Using clustering analysis, we identified several genes with no well-established functions that clustered tightly with well-studied genes. Co-clustering suggests that genes with unknown functions might be members of the functional pathways enriched among genes with known functions that are part of the same clusters (Eisen *et al.* 1998).

Temporal clustering analysis identified *CG43236, CG43920, CR44404* and *CR45045*, which shared similar expression dynamics with AMP pathway associated genes (**Figure 6A**). Observations from literature are consistent with our dynamics-based implication of these uncharacterized genes as AMPs: All four genes were previously found to respond to infection (Katzenberger *et al.* 2016, Troha *et al.* 2018), and *CG43236* and *CG43920* have been shown to encode small proteins predicted to be cationic (Im 2018), properties shared by known AMPs (Lemaitre and Hoffmann 2007). *CR44404* and *CR45045* were predicted to physically interact with antimicrobial peptide transcripts (Im 2018). Both *CR44404* and *CR45045* used to be classified as lncRNAs, but are now predicted to encode small, secreted proteins (Valanne *et al.* 2019). *CR44404* overexpression resulted in higher levels of hemocytes and hemolymph glucose, leading Valanne *et al.* (2019) to suggest that *CR44404* functions as a link between immunity and metabolism. *CR44404*'s co-expression with established AMPs in our dataset suggests that *CR44404* could act as an AMP itself, but an alternative hypothesis is that *CR44404* is not an AMP itself, but that its expression is tightly linked to AMP expression, and perhaps sustains AMP expression, by supporting hemocyte numbers and available glucose.

The dense sampling nature of this time course allowed us to discern the clear cycling patterns of differentially expressed genes such as *period*, *timeless*, *takeout*, *vrille*, and *cryptochrome*, all of which have well-characterized circadian rhythm functions (Konopka and Benzer 1971; Myers *et al.* 1996; So *et al.* 2000; Cyran *et al.* 2003; Collins *et al.* 2006). Clustered with these genes, our analysis identified genes that showcase cyclic behavior but are not canonically circadian-associated genes. This includes eight genes which do not have assigned circadian functions but do have some evidence of cyclic behavior in previous literature. It also includes ten genes that had not been reported to exhibit any cyclic expression before this study (**Table 1**). The identification of canonical circadian rhythm patterns both validates our methods of data normalization and differential expression analysis, and increases the certainty that we are accurately profiling novel temporal dynamics. It is important to note, however, that proper validation of the cycling behavior of our novel cyclic genes should be performed under normal *Drosophila* conditions, as we do not know whether immune challenge affected their expression.

Overall, we were able to implicate these uncharacterized genes as potential members of these functional pathways due to the strong similarity of their expression dynamics. This is impactful both in the novel functional implication of these genes, but also in demonstrating the potential this method of guilt-by-association has to assign function to other uncharacterized genes through RNA expression time-course experiments.

Limitations and future steps

This time-course experimental design lacks time-matched controls to account for expression changes associated with phenomena outside the immune challenge, such as aging. However, it is still highly valuable to develop and improve methods for analyzing time-course transcriptional data lacking time-matched control samples since they are needed to analyze processes such as development, where such controls are not possible.

In our dataset, Granger Causality analysis excelled at showcasing the relationships between divergent gene pairs, but was overly sensitive to the extreme temporal correlation between large groups of genes when analyzing positive edges. To avoid a prohibitively dense

network for analysis, we relied on heuristic network trimming criteria, which was effective, but is likely not generalizable to other similar experiments. Developing co-integration methods that take into account the specific bias found in high-dimensional RNA-seq datasets would provide a more robust statistical analysis of the causal relationships observed in this type of data. Using Granger Causality, we further did not observe edges between transcription factors and potential target genes. This is likely due to the complexity of transcription and translation, which involves more layers of regulation than can be inferred from mRNA abundance. However, Granger causality was successful at identifying what are likely the downstream results of divergent regulation, and it was successful at identifying positive lead-lag relationships between genes that likely respond to similar signals, but might differ in their exact transcriptional control. These statistical causal relationships provide hypotheses that can be tested with direct experimental disruptions of a system, to demonstrate biological causality.

Overall, this analysis motivates innovation in computational methods for longitudinal omics data, both to account for their inherent high-dimensionality and the complex underlying architecture that contains both causal and spurious coordination. Further, this should serve as a proof of concept for the future of high-density time-course RNA-seq in other model organisms.

MATERIALS AND METHODS

1. Fly lines, injections, and sample collection

Male adult *Drosophila* of about 4 days old from an F1 cross from two *Drosophila melanogaster* Genetic Reference Panel (DGRP) lines: line 379, which has shown to have low bacterial resistance, and line 360, which has high bacterial resistance (Early *et al.* 2017b). Flies were kept on a 12:12 dark-light cycle.

Flies were injected in the abdomen with 9.2 µl of commercial lipopolysaccharide (LPS) (*Escherichia coli* 055:B5 Sigma) derived from the outer membrane of Gram-negative bacteria. LPS is a known non-pathogenic elicitor used to stimulate a full but transient immune response in *Drosophila* (Imler *et al.* 2000, Leulier *et al.* 2003). Using commercial LPS instead of living bacteria also gives the advantage of avoiding the confounding effects from the mechanisms the bacteria use to circumvent immune responses (Graham *et al.* 2011). While it is now argued that purified LPS by itself does not induce an immune response in *Drosophila*, it has been shown that commercial 'crude' LPS preparations do (Imler *et al.* 2000, Leulier *et al.* 2003, Kaneko *et al.* 2004, Handu *et al.* 2015), most probably due to contaminating peptidoglycan in the latter (Kaneko *et al.* 2004). For this reason, commercial LPS was chosen for this study, and its ability to induce an immune response was confirmed using qPCR, as explained in the next section.

Flies were injected using a Nanoinjector (Nanoject II, catalog #3-000-204, Drummond), which allows high-throughput fly injections with a constant injection volume. Injections were performed in the abdomen, as it has been shown to be less detrimental to the fly compared to thorax injury (Chambers *et al.* 2014).

Flies were sampled for a total of 21 time points throughout the course of five days, which included an uninfected un-injected sample as control at time zero, and 20 time points after LPS injection (1, 2, 3, 4, 5, 6, 8, 10, 12, 14, 16, 20, 24, 30, 36, 42, 48, 72, 96, 120 hr). This sampling was performed in two blocks, using flies from the same stock, in two consecutive days. Therefore, all samples have two replicates, giving a total of 42 samples. During collection, a group of ~10 pooled flies corresponding to the sampled time point were flash frozen in dry ice and stored at -80 C for later RNA extraction.

2. Experimental validation using qPCR

The immune inducibility of commercial LPS was confirmed using qPCR. Adult male *Drosophila* were injected with 9.2 µl or 40 µl of 1 mg/mL LPS and flash frozen at 8 and 24 hr for RNA extraction. Uninfected un-injected flies were used as control. Each sampled time point consisted of a group of ~10 pooled flies. Each sample had two replicates. Genes *AttA* and *DptB* were measured to confirm immune inducibility. Gene *Rp49* was used as a baseline for expression normalization. Results showed a significant up-regulation of *AttA* and *DptB* at both volumes (9.2 µl and 40 µl) for both time points (8 and 24 hr). We decided to use 9.2 µl so as to cause the least amount of disruption to flies during infections, while still eliciting an immune response.

3. RNA extraction, RNA sequencing, and quality control filtering

RNA extraction was performed using Trizol (Life Technologies) following the manufacturer's instructions. cDNA libraries were prepared using the TruSeq RNA Sample Preparation Kit (Illumina). RNA purity was assessed using a Nanodrop instrument. RNA concentration was determined using a Qubit (Life Technologies) instrument. Sequencing was performed on an Illumina Hi-Seq 2500, single-end, and a read length of 75 bp, at Cornell Biotechnology Resource Center Genomics Facility.

Samples had an average of 24.8 M raw reads. Samples went through quality control using FastQC (version 0.11.5) (Andrews 2010). Truseq adapter sequences were removed from any sample that showed any level of adapter contamination using cutadapt (version 1.14) (Martin 2011). Low quality bases in the beginning and end of the reads were trimmed using fastx_trimmer (version 0.0.13, http://hannonlab.cshl.edu/fastx_toolkit/). Reads were mapped to the *Drosophila melanogaster* genome (r6.17) using STAR (version 2.5.2b) (Dobin *et al.* 2012). BAM files were generated using SAMtools (version: 1.3.2) (Li *et al.* 2009). Only one sample (4B, at 3 hr) out of the original 42 failed to pass the quality thresholds, and all subsequent analysis used the remaining 41 samples. An average of 92.97% reads per library mapped uniquely to the *Drosophila melanogaster* genome. We ended up with an average of 23.4 million uniquely mapped reads per library.

Reads mapping to genes were counted using the R package *GenomicAlignments* (Lawrence *et al.* 2013). Genes with zero counts across all samples were removed (923 genes out of 17,736). Samples were normalized to library size. A "+1" count number was added to all genes before performing $\log_2$ transformation, to make sure values after transformation are finite, and stabilize the variance at low expression end. After normalization and $\log_2$ transformation, only genes with more than 5 counts in at least 2 samples were kept (removing 4,156 genes). We ended up with 12,657 genes for downstream analysis.

A heatmap of the row Z-scores of normalized counts for all 12,657 genes indicated that sample 6A (5 hr after commercial LPS injection) was an outlier for a subset of the 12,657 genes (**Figure S12A**), even though sample 6A did not appear as an outlier using Principal Component Analysis (see below and **Figure 1B**). We identified outlier genes in sample 6A by subtracting replicate A row Z-scores of normalized counts from replicate B. While for most time points the difference between samples A and B varied between -4 and 4, samples 6A and 6B demonstrated larger differences for 1,439 genes (**Figure S12B**). These genes were enriched for GO terms related to neuron signaling and development (based on PANTHER GO statistical overrepresentation test with FDR 0.05). Only 40 of the 1,439 genes were annotated as immune genes by Early *et al.* (2017), and none of the 1,439 genes were among the DE genes detected as differentially expressed using pairwise comparisons or spline fitting. Library sizes for samples 6A and 6B were similar (26,256,507 for replicate A and 22,980,006 for replicate B). We think the difference between the replicates at 5 hr post-injection could be caused by unknown variation in the flies' environment. It did not influence our data analysis and conclusions, but it is necessary to be aware of when using this dataset for other analyses.

4. Principal component analysis

Principal components analysis (PCA) was performed using function *plotPCA* from the R package *DESeq2* (Love *et al.* 2014) after regularized-logarithm transformation of raw counts, using the design ~time+time:time to create the DEseqDataSet. Genes with zero counts across all samples were first removed. The default number of 500 top genes with highest row variance was used to calculate the principal components.

5. Differential expression analysis

In order to identify genes that had differential expression over the time course, we adopted the linear model-based methodology proposed in (Law *et al.* 2014) and available in the R package *limma*. We first transformed the normalized RNA-seq read counts (before $\log_2$ transformation) using the *voom* transformation, which estimates the heteroscedastic mean variance relationships of log-counts and adds a precision weight to each observation to make them amenable to the usual linear modeling pipelines that rely on normality. We used gene-wise linear models to fit cubic splines (with 3 degrees of freedom) with time, TMM normalization method (Robinson and Oshlack 2010), and standard empirical Bayes *F*-tests to select genes whose expression levels were significantly altered across the time course in both replicates.

We also fit 3 degree polynomials across the first 48h using the R package maSigPro (Conesa *et al.* 2006; Nueda, Tarazona, and Conesa 2014). We used default parameters, including counts=F to model the data based on a normal distribution, since we ran maSigPro on counts that were normalized using Limma-Voom. We selected 169 genes as significantly time dependent if they had alfa (Benjamini-Hochberg corrected) < 0.05 and a goodness of fit R^2 value of at least 0.6.

Next, we checked for differential expression of every gene between time point 0 (control) and time point *t*, for *t* = 1, 2, …, 48 hr. For each test, a multiple testing correction at 5% False Discovery Rate (FDR) using the Benjamini-Hochberg method (Benjamini and Hochberg 1995) was adopted. Venn diagrams to compare results were adapted from those generated using web tool Venny (http://bioinfogp.cnb.csic.es/tools/venny/) (Oliveros 2007).

6. Functional annotation

Gene Ontology (GO) enrichment analysis was performed using PANTHER Statistical Overrepresentation Test (http://pantherdb.org/, version 14.1, released 2019/04/29) (Mi *et al.* 2018) using default settings ("GO biological process complete" as annotation dataset, Fisher's Exact test, FDR < 0.05). Transcription factors were identified among differentially expressed genes based on a list of 753 putative site-specific transcription factors available via the FlyTF database (version 1) (Pfreundt *et al.* 2010). Gene set analysis was done using the R package *GSA*, which uses a Gene Set Analysis algorithm (Efron and Tibshirani 2007) that improves the GSEA algorithm (Subramanian *et al.* 2005) by allowing testing for associations between gene sets and time-dependent variables (Efron and Tibshirani 2007; Mullighan *et al.* 2009). Gene set membership was assigned from GO data downloaded from FlyBase.org in January 2019. Normalized counts for both replicates at each time point from 1 to 120 h were compared against

both control replicates (0 h), using a two-class paired vector (-1, 1, -2, 2) which corresponds to (control_replicateA, timepointX_replicateA, control_replicateB, timepointX_replicateB). We used 100,000 permutations to estimate false discovery rates. Only pathways with *P*-values below 0.05 and with 5 or more genes from our full dataset were kept. A subset of most relevant pathways was compiled by selecting pathways that had at least one gene from the subset of 551 most predominant time-dependent genes, and had a score of 2.5 or more in at least one time point from 1 to 48 hr. This gave us 41 unique pathways as shown in **Figure 9**.

7. Cluster analyses

Hierarchical clustering of 91 core genes was performed using R package *hclust*, using Euclidean correlation as a distance metric. Hierarchical clustering of 551 predominant time-dependent genes was done using the default Pearson correlation with R package *pheatmap*. Temporal clustering was performed using the R package *TSclust* (Montero and Vilar 2014). Normalized counts of both replicates were clustered using dissimilarity measures from Autocorrelation-based method (ACF), which computes the dissimilarity between two time series as the distance between their estimated simple autocorrelation coefficients (Galeano and Peña 2000). This method was used with a *P*-value cutoff of 0.05, and only top 1% correlation edges were further explored.

Cyclic gene patterns were identified using the JTK_Cycle algorithm (Hughes *et al.* 2010) available in R package *JTK_Cycle*. Nine regularly distributed time points were subset from both replicates every 6 hr (0, 6, 12, 18, 24, 30, 36, 42, 48 hr). The time point corresponding to 18 hr was approximated by averaging normalized gene counts between time points 16 and 20 h. We looked for rhythms between 18-30 hr (4 to 6 time points) with a cutoff of BH *Q*-value < 0.05 and amplitude > 0.5.

8. Network inference

Granger causality-based methods (Granger 1969) were used to construct putative interaction networks among genes in the form of directed graphs with individual genes as nodes. A directed edge from gene *A* to gene *B* is added if the time course of gene *A* Granger-causes the time course of gene *B*. The notion of 'Granger causality' is popular in learning lead-lag relationships among two or more time series. Formally, if the time series of gene *A*, given by x_t, has some power in predicting the expression of gene *B* at time $t+1$, called y_{t+1}, over and above y_t and conditioned on an information set I_t, then gene *A* is said to exert a *Granger causal* effect on gene *B*. Bivariate Granger causality uses a small information set $I_t = \{x_{1:t}, y_{1:t}\}$ and captures Granger causal relationship from gene *A* to gene *B* by testing whether the regression coefficient β in the following bivariate regression is different from zero:

$$y_{t+1} = \alpha y_t + \beta x_t + error_{t+1}$$

A master set of 258 genes was constructed from the 551 predominant time-dependent genes by picking those that had available functional annotation and that had differential expression of at least 2-fold. Using linear regression (function lm() in R), we conducted bivariate (pairwise) Granger causality tests for every pair of genes among this set of 258 genes using data on sliding windows of *t* = 6 consecutive time points and the two replicates (sample size =

12), and ranked them in order of increasing *P*-values (BH method used for calculating FDR), keeping the top resulting edges (BHFDR < 0.05%).

A well-known critique of bivariate Granger causality is its use of a small information set that does not contain any other factors except genes *A* and *B* (Mukhopadhyay and Chatterjee 2006). This failure to account for other potential confounding variables can give rise to many spurious edges in our network (Mukhopadhyay and Chatterjee 2006), where Granger causal effects from gene *A* to gene *B* is an artefact of gene *C*, which is causal for one or both genes. To address this, we adopted multivariate (or network) Granger causality (Basu *et al.* 2015), allowing us to avoid such spurious inferences through multiple linear regression. In this framework, we start with *p* genes, and Granger causal relationship of Gene *A* on Gene *B* is tested by regressing y_{t+1} on y_t, x_t and the time courses of the other *p* - 2 genes $z_{1t}, z_{2t}, ..., z_{pt}$.

$$y_{t+1} = \alpha y_t + \beta x_t + \gamma_1 z_{1t} + \gamma_2 z_{2t} + ... + \gamma_{p-2} z_{p-2,tt} + error_{t+1}$$

For small sample size and large *p*, the above regression is not possible to run using ordinary least squares (OLS), so we use LASSO (Tibshirani 1996) regression. To test if the regression coefficient β in the above regression is different from zero, we used two different variants of de-biased LASSO (Javanmard and Montanari 2014, Dezeure *et al.* 2015), each of which corrects the bias of lasso and allows quantifying uncertainty of regression coefficients one at a time. A non-zero coefficient in the above multivariate regression suggests that gene *A* is Granger causal for gene *B*, even after accounting for the effects of the other *p*-2 genes. Using this method on the master set of 258 genes, we reconstructed putative directed networks of multivariate Granger causality and ranked the edges in increasing order of *P*-values, following the same parameters used in the bivariate (pairwise) Granger causality method (sliding window of 6 consecutive time points in both replicates, keeping the top resulting edges (BHFDR < 0.05%)).

11. Data availability

The RNA-seq data will be available at NCBI SRA, BioProject ID PRJNA641552. The pipeline scripts and intermediary data files will be made available through GitHub. A script will allow any user to query a gene of interest and download a table of raw counts, normalized counts, log fold change, and plots of gene trajectory over time.

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AUTHOR CONTRIBUTIONS

F.S., A. E., and A.G.C. conceived the study. F.S. collected the samples and generated the time course data. F.S., S.B., M.T.W., and A.G.C. conceived the computational and statistical analyses. F.S., S.Y.N.D., and S.B. performed the computational and statistical analyses. F.S., S.Y.N.D., S.B., and A.G.C. wrote the manuscript.

SUPPORTING INFORMATION

Figure S1. Plots of normalized counts of housekeeping genes and immune response genes.

Figure S2. Venn Diagram showing overlap and differences of DE genes identified using limma-voom spline fitting vs. maSigPro fitting of polynomials.

Figure S3. Heatmap of 214 genes

Figure S4. Temporal dynamics of gene expression of the most strongly up-regulated genes .

Figure S5. Expression profiles of DE genes encoding transcription factors.

Figure S6. Gluconeogenesis pathway

Figure S7. GC filtered network of negative edges

Figure S8. Negative GC edges

Figure S9. Pathway corresponding to ‘mitotic DNA replication checkpoint’

Figure S10. GC edges of circadian rhythm genes plotted against time.

Figure S11. Positive GC edges

Figure S12. Outlier explanation

Table S1. Genes that encode transcription factors and respond to commercial LPS injection.

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SUPPLEMENTAL FIGURES

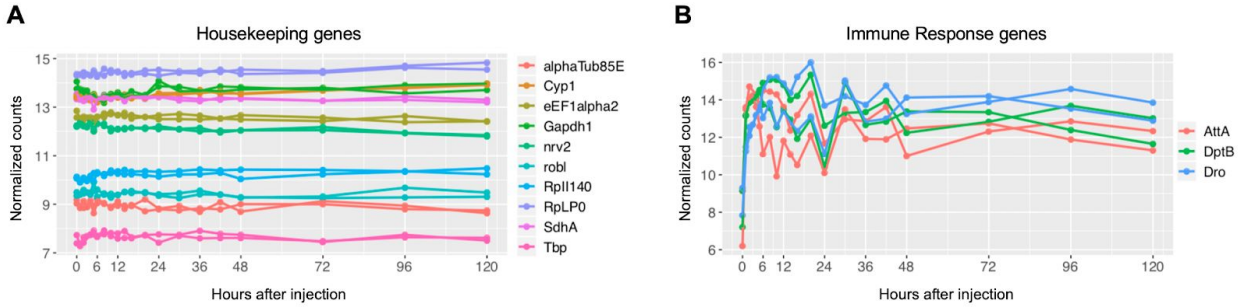

Figure S1. Plots of normalized counts of housekeeping genes (**A**) show little change across time as expected under proper data normalization, while immune response genes (**B**) show up-regulation within the first time points, as expected after a successful immune challenge.

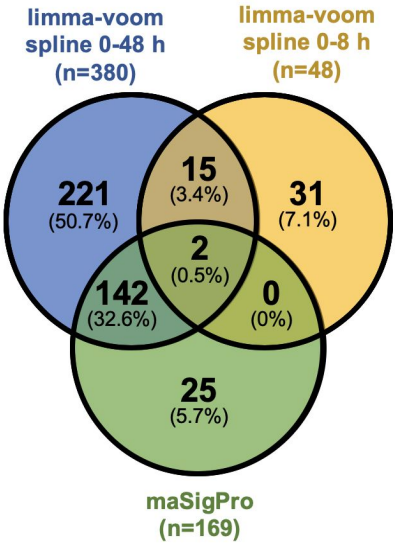

Figure S2. Venn Diagram showing overlap and differences of DE genes identified using limma-voom spline fitting vs. maSigPro fitting of polynomials.

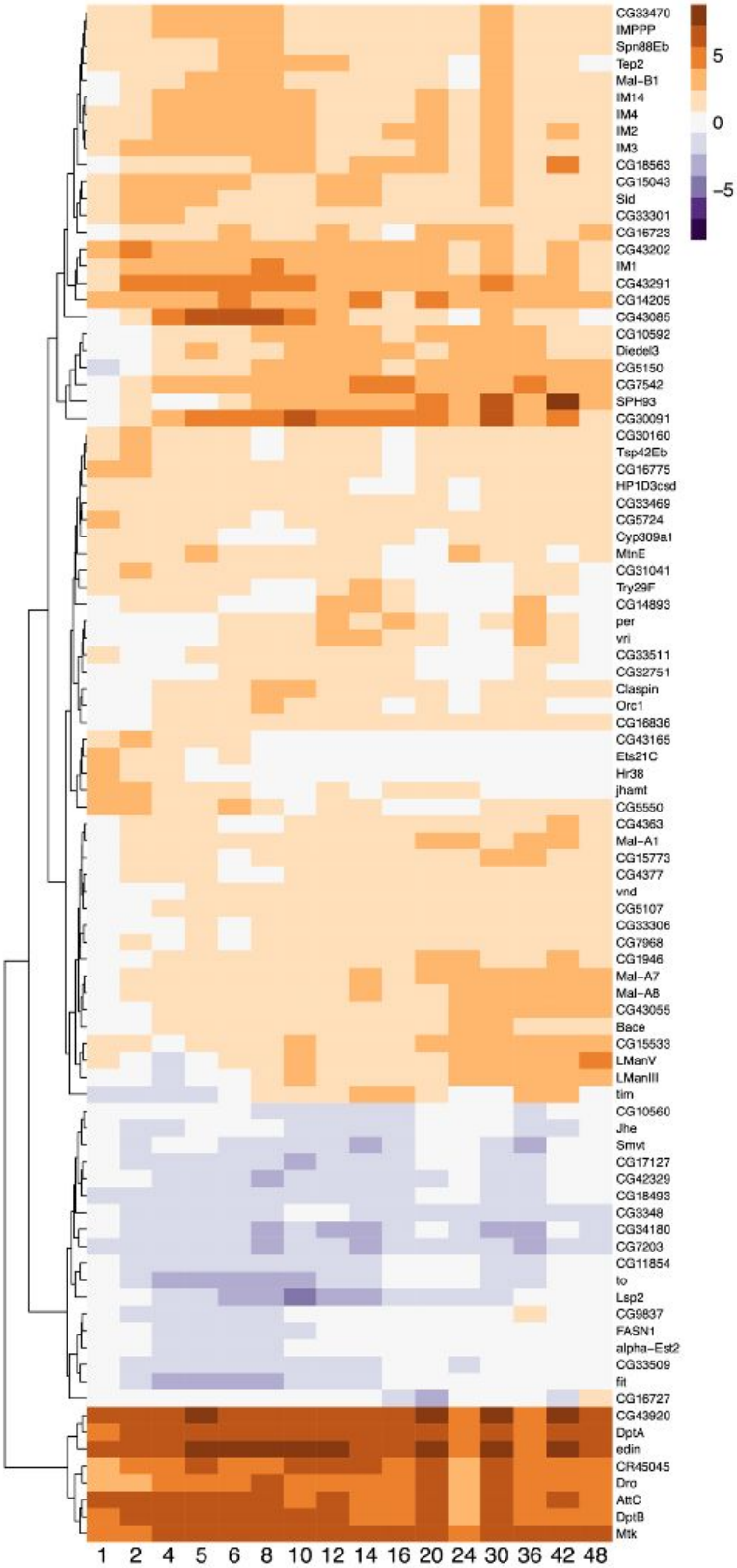

Figure S3. Heatmap of 214 genes differentially expressed following injection with LPS. Scale is log2-fold change, with lower expression in purple and higher expression in dark orange.

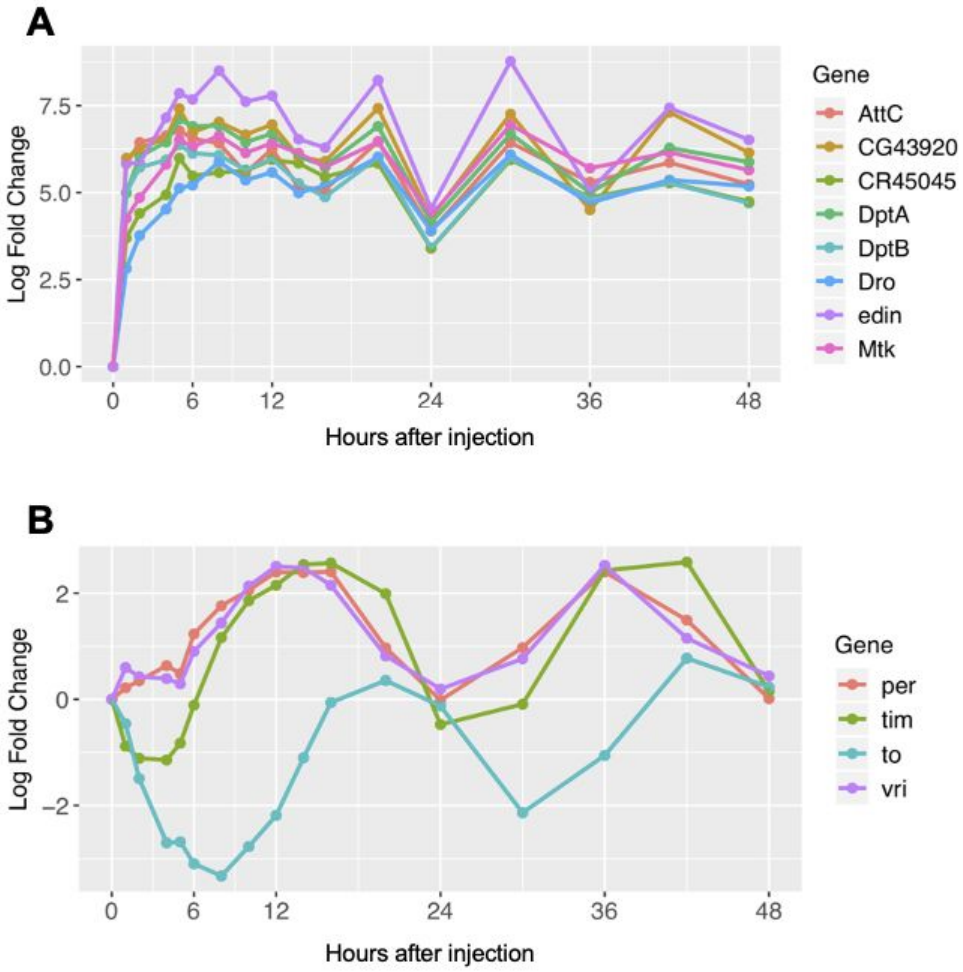

Figure S4. (A) Temporal dynamics of the most strongly up-regulated genes (*DptB*, *AttC*, *Mtk*, *Dro*, *CR45045*, *DptA*, *CG43920*, and *edin*) in the first 48 hr after injection. These genes are part of the 91 "core" DE genes that underwent at least a 4-fold change in expression in at least two time intervals after injection, with an FDR < 0.01 (**Figure 3**). (**B**) Temporal dynamics of gene expression of circadian rhythm genes (*per*, *tim*, *to*, *vri*) show a classic and well characterized 24 hr periodic expression.

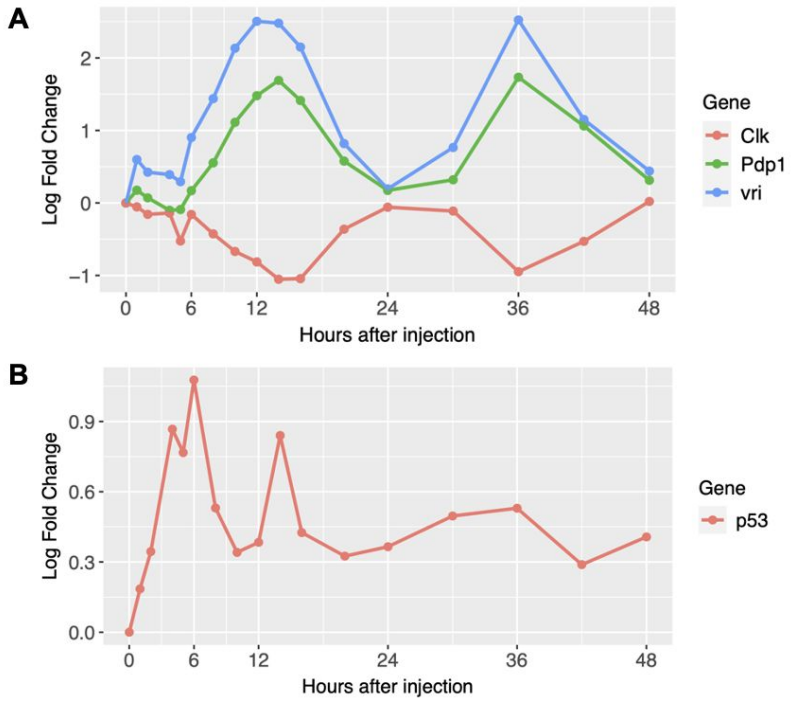

Figure S5. Expression profiles of DE genes encoding transcription factors. (A) Genes involved in regulation of the circadian clock. **(B)** *p53*, which encodes a transcription factor involved in DNA repair and genotoxic stress.

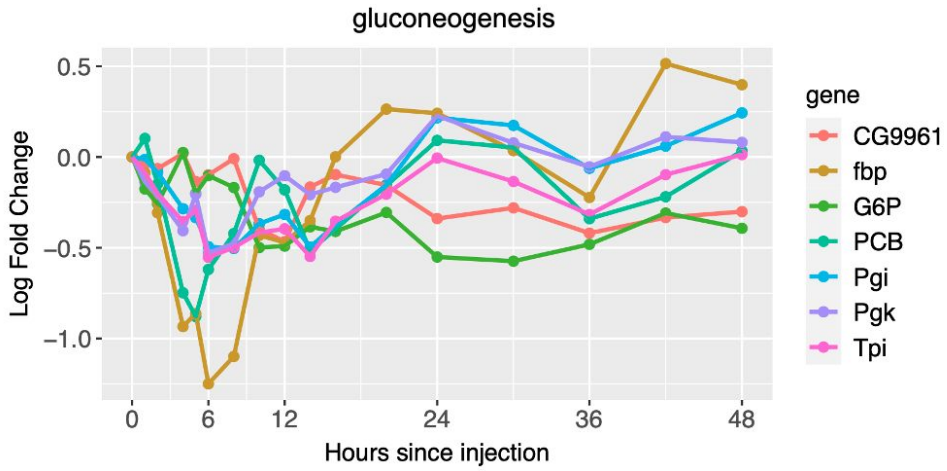

Figure S6. Gluconeogenesis pathway

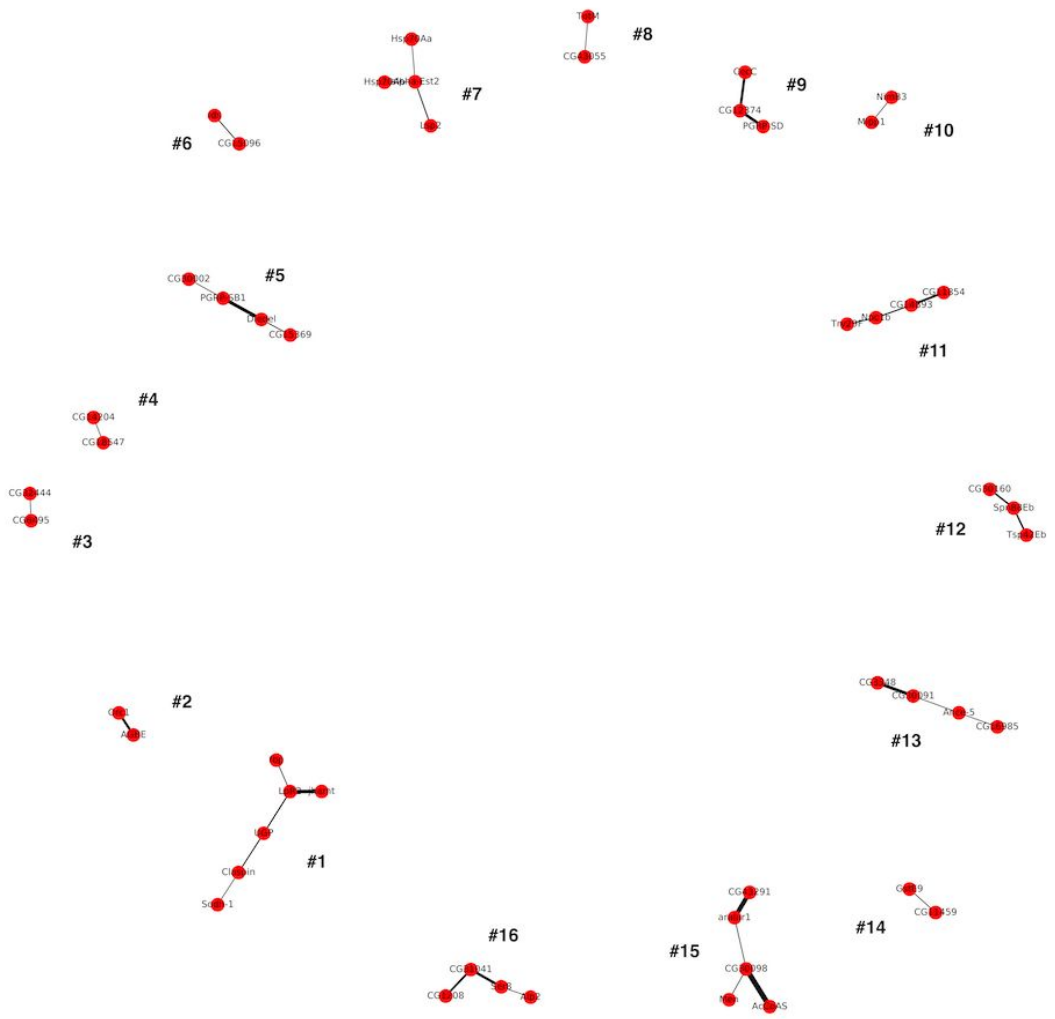

Figure S7. GC filtered network. The network was pruned to only the edges with at least three consecutive windows of GC significance, have a negative GC relationship, and excludes genes identified with JTK_Cycle.

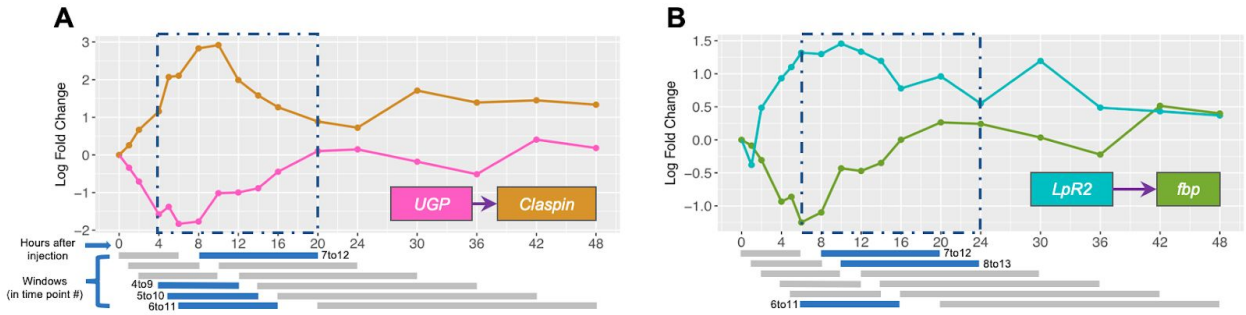

Figure S8. Negative GC edges. (A) between *Claspin* and *UGP.* (B) between *LpR2* and *fbp* Windows in which a significant Granger Causal relationship is established are colored in blue and are contained in a dashed blue box marking the plot area, non-significant windows are grey below the plot.

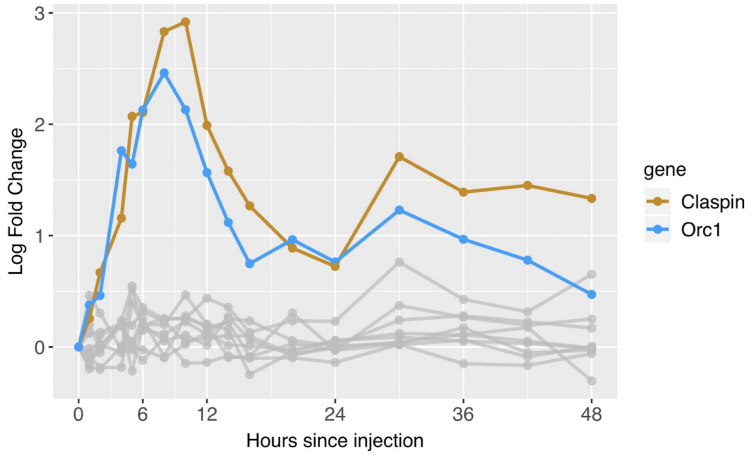

Figure S9. Pathway corresponding to 'mitotic DNA replication checkpoint'

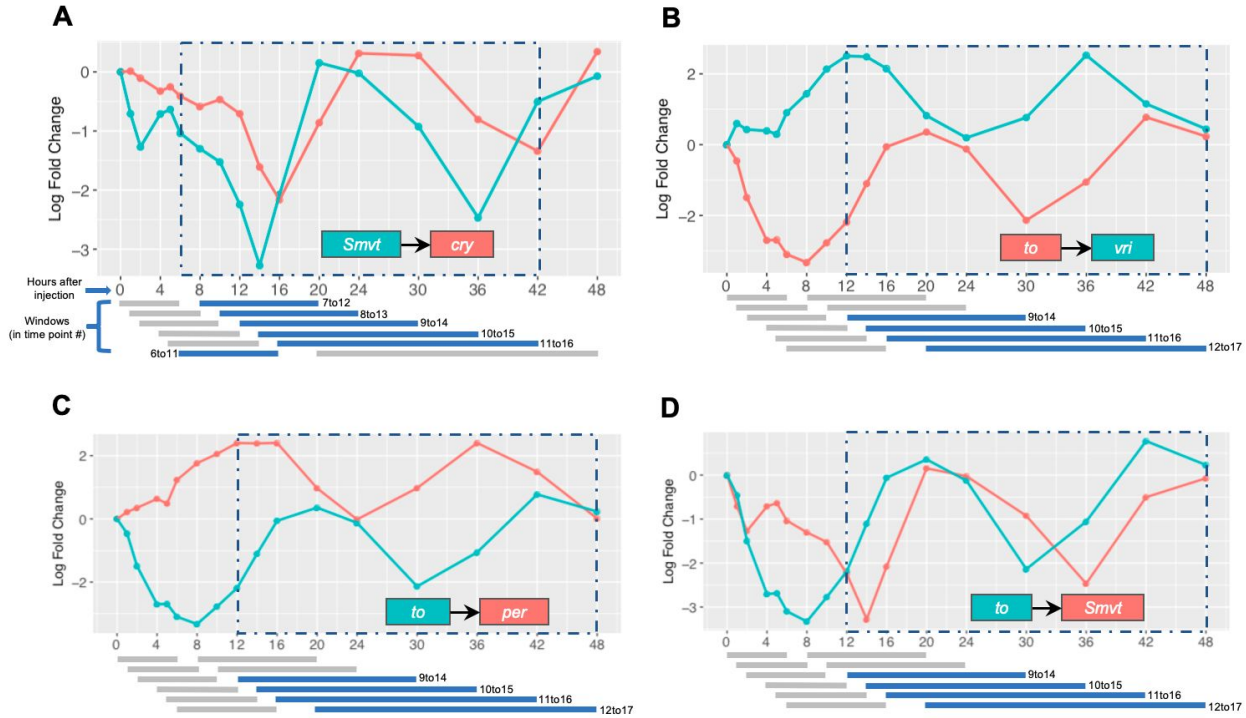

Figure S10. GC edges of circadian rhythm genes plotted against time. (**A**) Positive lead-lag correlation between *Smvt* and *cry*. (**B**) Negative lead-lag correlation between *to* and *vri*. (**C**) Negative lead-lag correlation between *period* and *takeout*. (**D**) Positive lead-lag correlation between *Smvt* and *takeout*. Significant windows are colored in blue, non-significant windows are colored in grey. Resulting overall consecutive windows are labeled in blue dashed rectangles. Individual windows represent 6 consecutive time points. Note that time points are not regularly distributed with time, therefore windows have different time ranges, but identical number of samples.

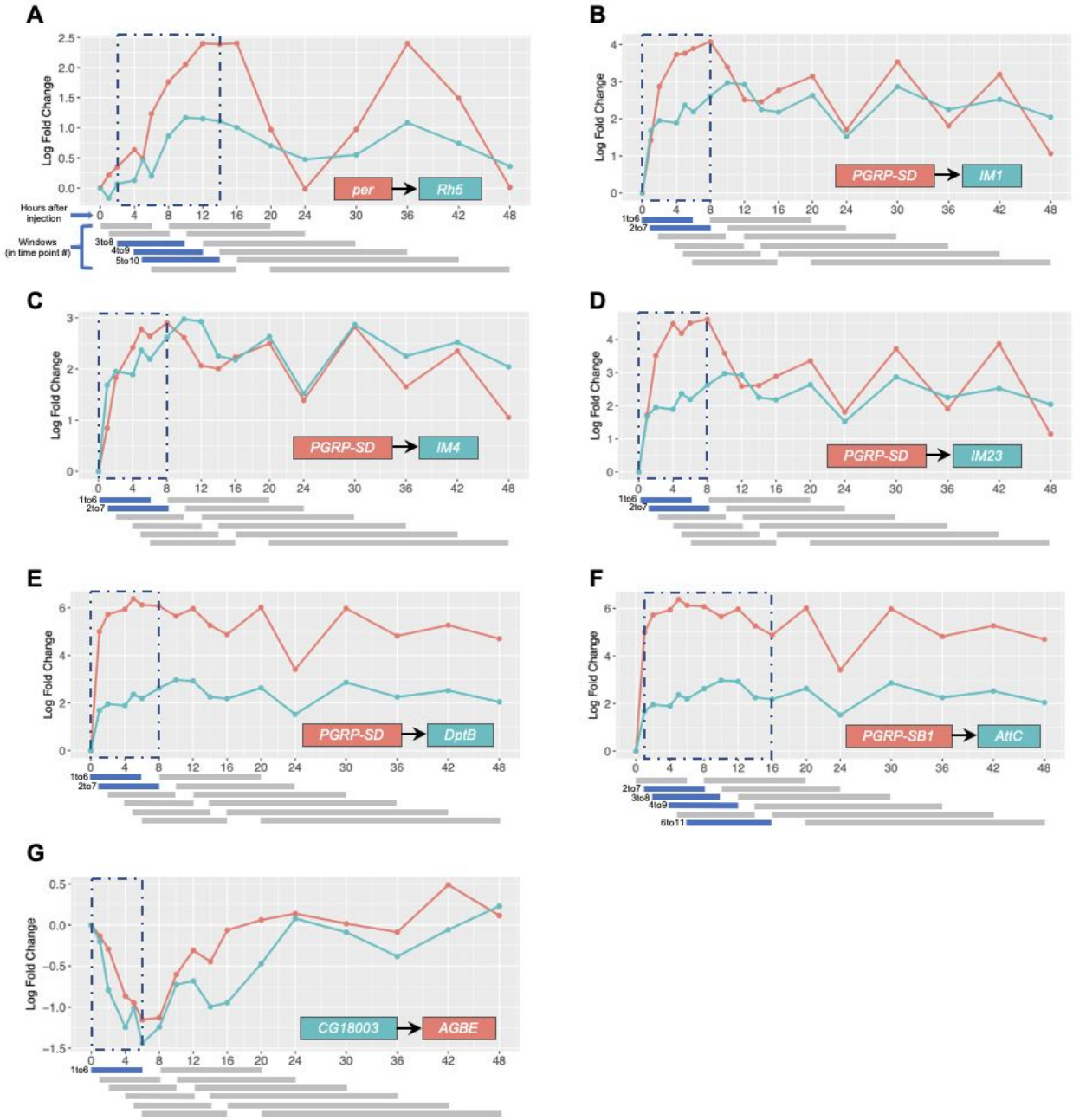

Figure S11. Positive GC edges. Positive lead-lag correlation between (**A**) *period* and *Rh5*, (**B**) *IM1* and *PGRP-SD,* (**C**) *IM4* and *PGRP-SD,* (**D**) *IM23* and *PGRP-SD,* (**E**) *DptB* and *PGRP-SD,* (**F**) *AttC* and *PGRP-SB1,* and (**G**) *AGBE* and *CG18003.* Significant windows are colored in blue, non-significant windows are colored in grey. Resulting overall consecutive windows are labeled in blue dashed rectangles. Individual windows represent 6 consecutive time points. Note that time points are not regularly distributed with time, therefore windows have different time ranges, but identical number of samples.

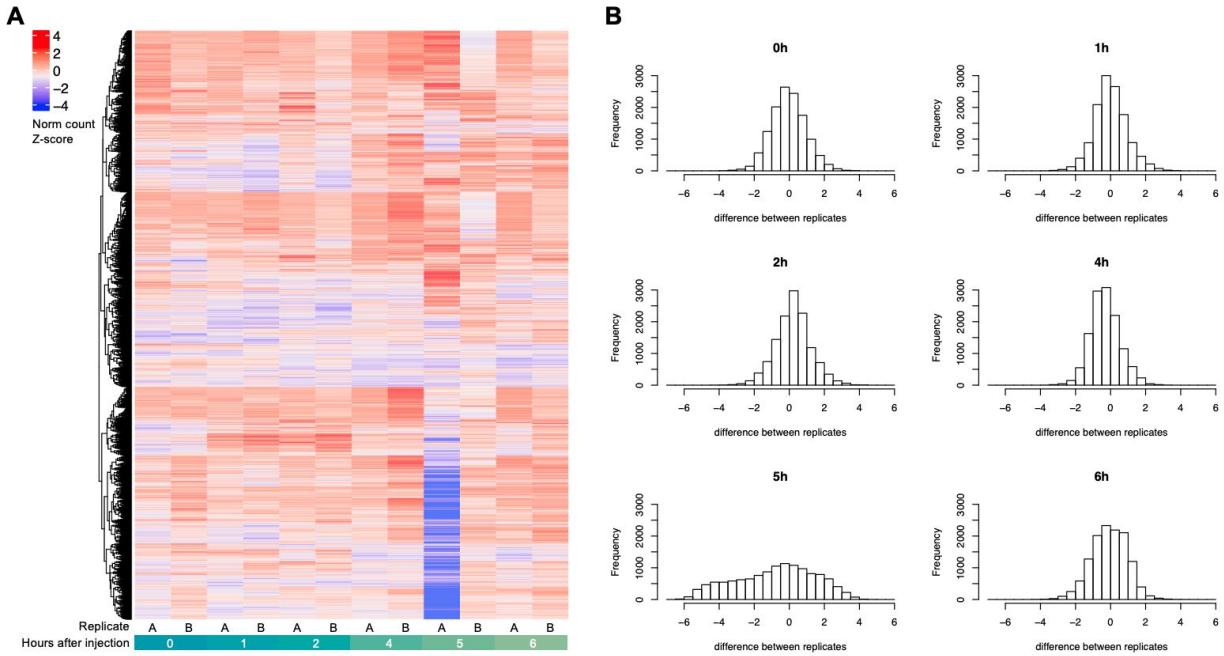

Figure S12. Sample 6A is an outlier for a subset of genes. (**A**) Heatmap showing row Z scores of normalized counts for all 12,657 genes in the filtered datasets. Each row represents a gene; each column represents a replicate, from pre-injection (0 hours) up to 6 hr post-injection. (**B**) Distribution of differences between normalized count Z scores for replicates A and B for each time point.

Table S1. 20 genes that respond to commercial LPS injection encode transcription factors.

Symbol	Flybase ID	Flybase snapshot
E(spl)m3-HLH	FBgn0002609	Enhancer of split m3, helix-loop-helix (E(spl)m3-HLH) is a member the enhancer of split gene (E(spl)) complex. E(spl)m3-HLH encodes a transcriptional repressor executing Notch-mediated cellular differentiation.
GATAe	FBgn0038391	GATAe (GATAe) encodes a endoderm-specific GATA factor. It regulates endoderm differentiation and intestinal stem cell maintenance.
CG10147	FBgn0035702	NA
exex	FBgn0041156	extra-extra (exex) encodes a homeodomain transcription factor that is expressed in and regulates the differentiation of motor neurons that project axons to ventral body wall muscles. Within the central nervous system, the product of exex negatively interacts with the products of Lim3 and eve to govern neuronal specification and differentiation. The roles of the product of exex include neuronal specification and differentiation.
CG2678	FBgn0014931	NA
Vri	FBgn0016076	vrille (vri) encodes a bZIP transcription factor acting as an enhancer of dpp phenotypes both in embryo and in wing. It is involved in hair and cell growth and in tracheal development. Vri is a clock-controlled gene acting as a repressor of the products of Clk and cry.
Pdp1	FBgn0016694	PAR-domain protein 1 (Pdp1) encodes a member of the PAR domain bZip family of sequence-specific transcription factors. It regulates gene expression in muscles and in circadian clock neurons.
Clk	FBgn0023076	NA
Unpg	FBgn0015561	NA
Cbt	FBgn0043364	cabut (cbt) encodes a transcription factor that controls Dpp signaling and is involved in dorsal closure and wing disc morphogenesis.
Sr	FBgn0003499	stripe (sr) encodes a transcription factor that induces the fate of tendon cells in the embryo as well as in the adult fly. It works upstream of tendon specific genes including Tsp, slow and Lrt.
CrebA	FBgn0004396	Cyclic-AMP response element binding protein A (CrebA) encodes a leucine-zipper transcription factor that upregulates genes encoding protein components of the canonical secretory pathway and tissue-specific genes in the salivary gland and epidermis.
Ets21C	FBgn0005660	Ets at 21C (Ets21C) encodes a stress-inducible transcription factor that binds specifically to purine-rich DNA motifs. It cooperates with transcription factors acting downstream of the MAP kinase pathways to fine tune gene expression in response to stress, such as infection or oncogene activation.
Dif	FBgn0011274	Dorsal-related immunity factor (Dif) encodes a transcription factor that contributes to zygotic function of the Toll pathway, notably the regulation of antimicrobial peptides, but it is not involved in dorsoventral patterning of the embryo.
Rel	FBgn0014018	Relish (Rel) encodes a transcription factor and the downstream component of the immune deficiency pathway, which regulates the antibacterial response and other less characterized cellular processes.
Hr38	FBgn0014859	Hormone receptor-like in 38 (Hr38) encodes a protein that can heterodimerize with the U adult cuticle and for the proper uptake and storage of glycogen in larvae.
Luna	FBgn0040765	NA
P53	FBgn0039044	p53 (p53) encodes a transcriptional factor required for adaptive responses to genotoxic stress, including cell death, compensatory proliferation and DNA repair.
Hand	FBgn0032209	Hand (Hand) encodes a transcription factor that contributes to cardiogenesis, hemopoiesis, and muscle function.
Fer3	FBgn0037937	48 related 3 (Fer3) encodes a basic helix-loop-helix (bHLH) transcription factor expressed in the ventral nerve cord.