

## 1 **Supplemental Data**

2 **Supplemental Figure S1. Correlation of biological replicates between hemocyte**  
3 **samples.** Venn diagrams of protein identities from independent biological replicates of  
4 non-selected sugar-fed hemocytes and mag-bead enriched hemocytes from sugar-fed,  
5 blood-fed, or *Plasmodium*-infected mosquitoes. Pearson-correlation identified strong  
6 reproducibility between experiments.

## 7 **Supplemental Figure S2. Ras family protein expression in hemocyte populations.**

8 Average normalized spectral counts of Ras superfamily GTPases across each of the  
9 respective treatments (phagocytosis, blood-feeding, and infection). All values are  
10 depicted as the Log2 average of normalized spectra, while significance (*P* value) is  
11 measured as the  $-\text{Log}_{10}$ . Dotted lines depict significance with a *P* value cutoff of 0.05.

## 12 **Supplemental Figure S3. Multiple Co-Inertia Analyses (MCIA) of comparisons of** 13 **hemocyte transcriptome and proteomes.** Using MCIA analysis, samples

14 corresponding to our granulocyte proteomes and previously reported hemocyte  
15 transcriptomes [8] are displayed as the global analysis of all hemocyte proteome data  
16 (A) or as immune-specific (B) and proliferation-specific (C) subsets. Transcriptome  
17 (green circle) or proteome (red triangle) profiles are displayed for each sample  
18 comparison: *P. falciparum*-infection (PF), blood-feeding (BF), and sugar-feeding  
19 (SF). The samples in this analysis were computed as log fold changes between two  
20 treatments: *P. falciparum* infection referenced to blood-feeding (PFvBF), *P. falciparum*  
21 infection referenced to sugar-feeding (PFvSF) and blood-feeding referenced to sugar-  
22 feeding (BFvSF). Additionally, the most highly expressed features (genes and proteins  
23 with the greatest distance from the origin) are projected in the MCIA result plots. Due to  
24 differences between the coordinates of the comparisons and of the most expressed  
25 features plots, different axes were generated. The relationships between sample  
26 comparisons are represented by the RV-coefficient (Hemocyte-specific, 0.958 with  $P =$   
27 0.023; Immune-specific, 0.940 with  $P = 0.033$ ; Proliferation-specific, 0.987 with  $P =$   
28 0.003). All data used for pairwise comparisons is presented in Supplemental Table S3.

29 **Supplemental Figure S4. qRT-PCR validation of enriched proteins.** Protein  
30 candidates with significantly increased spectral counts relative to their reference sample  
31 treatment (Table 1) were evaluated by qRT-PCR to measure correlations between  
32 transcript levels and protein abundance (A-C). Candidate genes with significant  
33 enrichment in phagocytic cells (A), following blood-feeding (B), or after *P. falciparum*  
34 infection (C) are displayed with the fold change in RNA (grey) or protein (colored)  
35 across each sample treatment. Each data point is the mean (+/- SEM) of three  
36 independent biological replicates. Genes examined are shown above each graph.

37 **Supplemental Figure S5. Efficiency of gene silencing on candidate phagocyte**  
38 **genes.** The efficiency of gene silencing was measured in sugar-fed mosquitoes after  
39 systemic injection of dsRNA for candidate phagocyte genes. Gene expression of the  
40 target gene is displayed as the expression level relative to dsGFP-injected control  
41 mosquitoes. The expression of rpS7 was used to normalize between samples and  
42 experiments.

43

44 **Supplemental Table S1. List of primers used in qRT-PCR analysis of enriched**  
45 **phagocyte populations.**

46 **Supplemental Table S2. Improved annotations list of unknown or hypothetical**  
47 **genes identified in our analysis.**

48 **Supplemental Table S3. List of primers used for the preparation of dsRNA and**  
49 **knockdown validation of candidate phagocyte genes.**

50 **Supplemental Table S4. Complete list of hemocyte proteins identified after MS**  
51 **analysis.**

52 **Supplemental Table S5. Significantly enriched phagocyte proteins (P<0.05)**  
53 **following phagocytosis, blood-feeding, or *Plasmodium* infection.**

54 **Supplemental Table S6. List of transcripts and proteins that feature prominently**  
55 **in MCI analysis.**

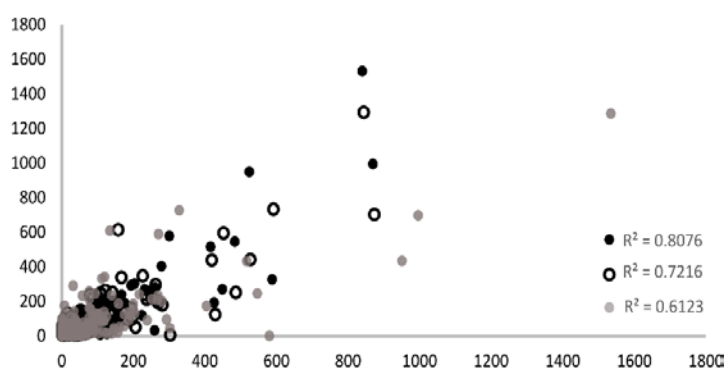
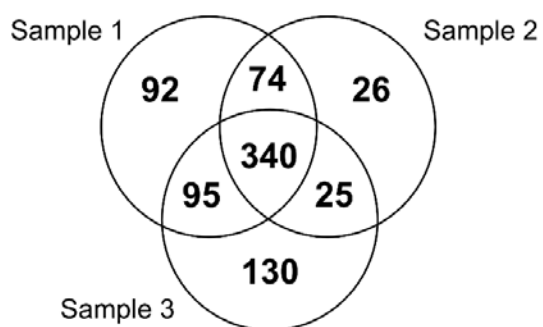
56 **Supplemental Table S7. Correlations between the log fold-change from the gene**  
57 **expression data and phagocytic granulocyte protein abundance.**

58 **Supplemental Table S8. List of proteins that correspond to each cluster group**  
59 **following cluster analysis.**

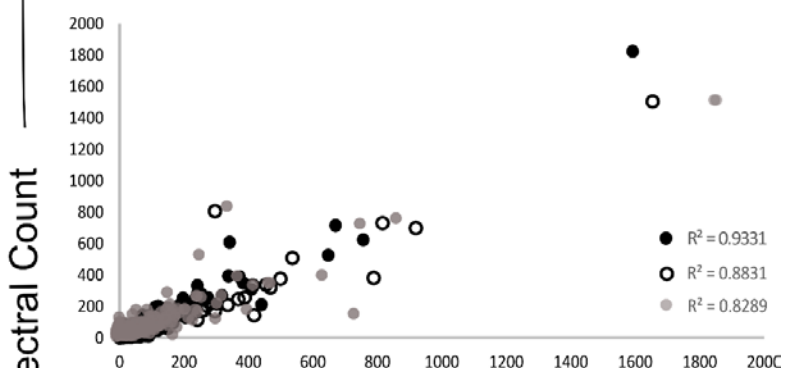
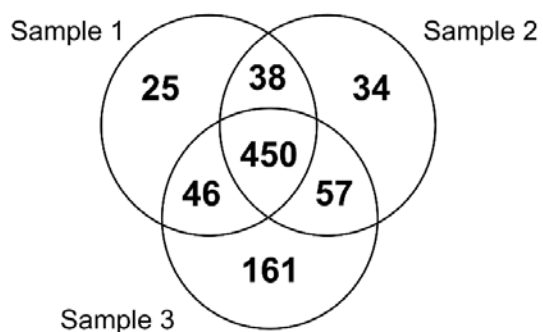
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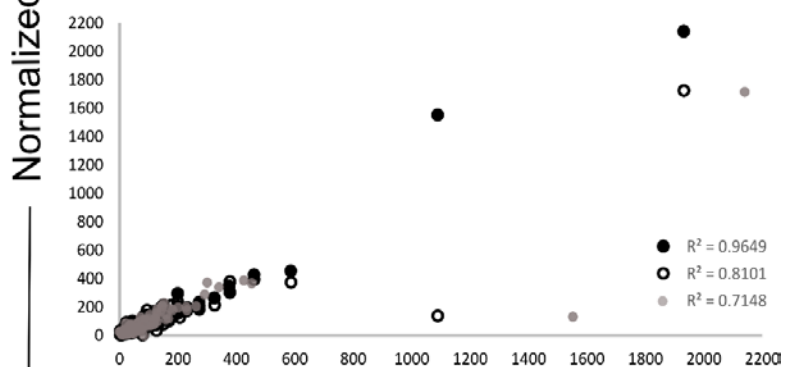
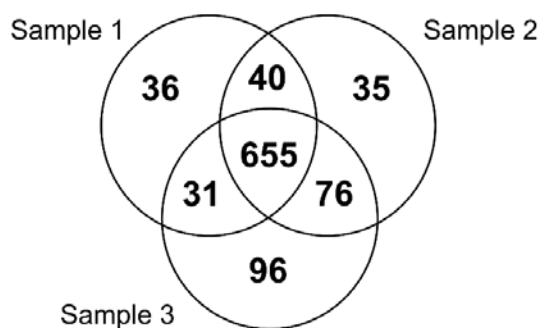
## Non-selected sugar-fed hemocytes



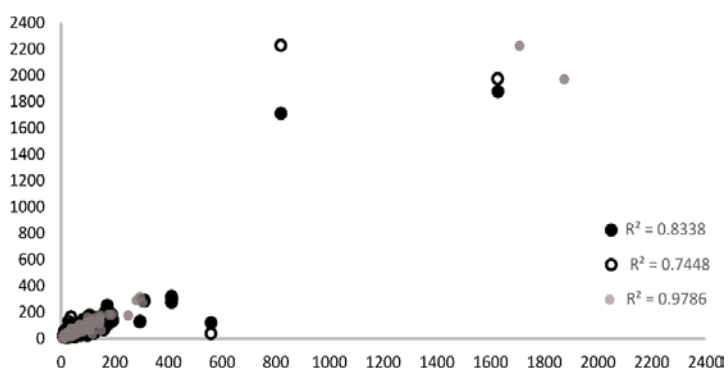
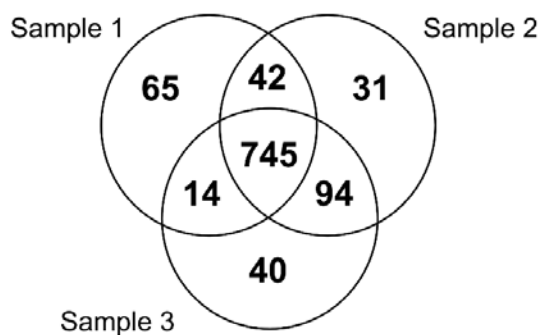
## SF-enriched granulocytes



## BF-enriched granulocytes

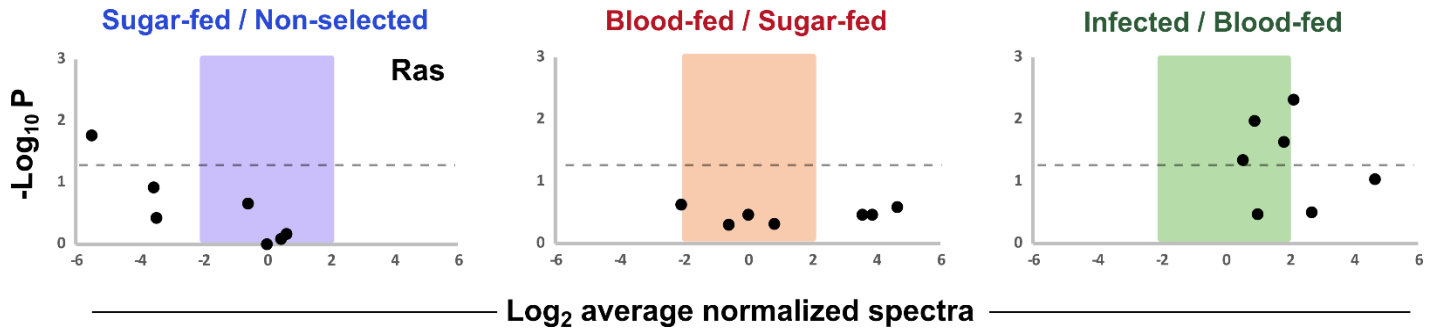


## PF-enriched granulocytes



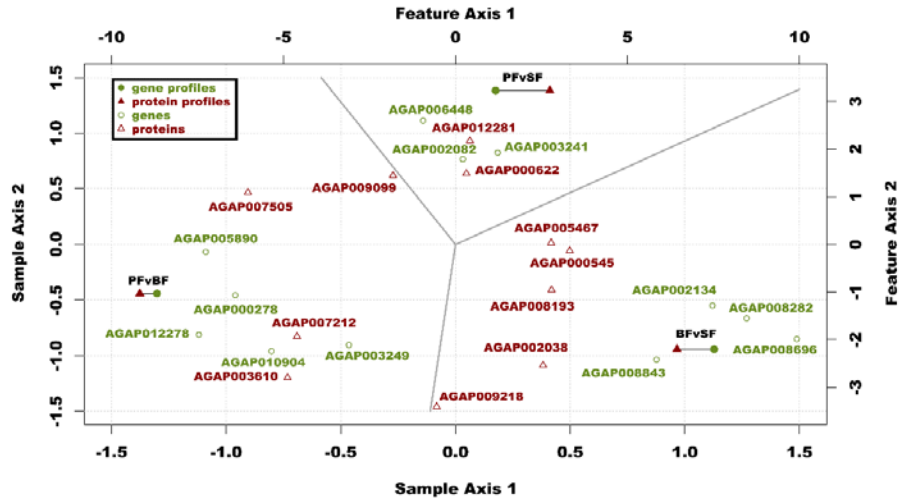
Normalized Spectral Count

Normalized Spectral Count

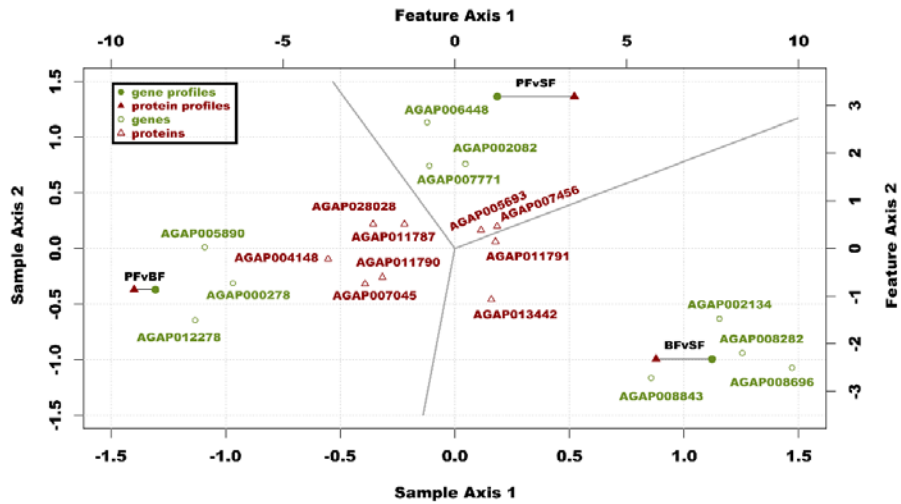


Supplemental Figure S2

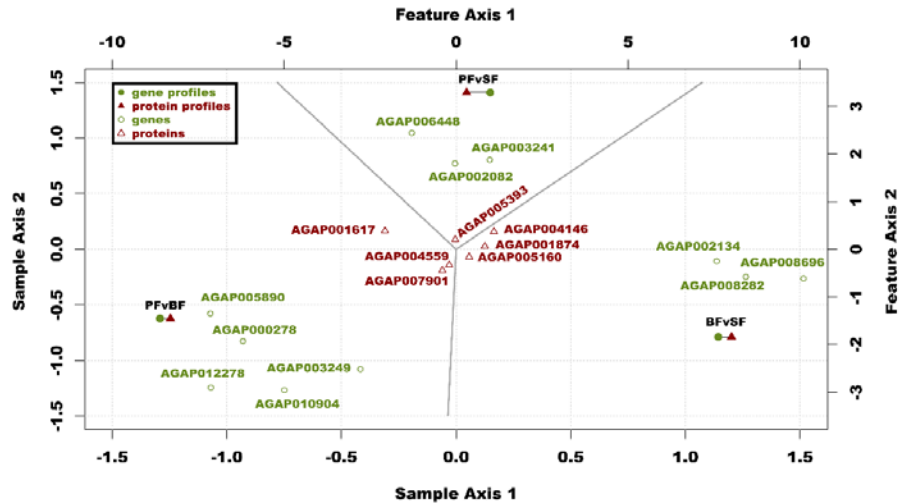
# A HEMOCYTE-SPECIFIC



# B IMMUNE-SPECIFIC

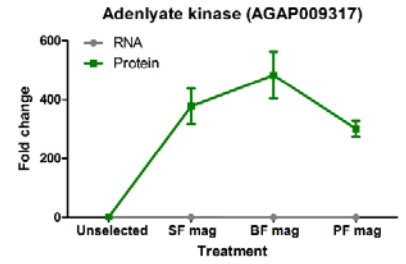
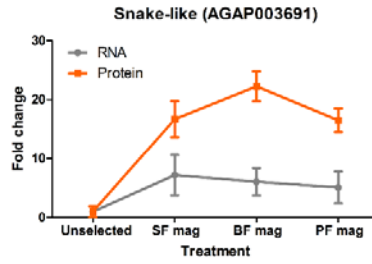
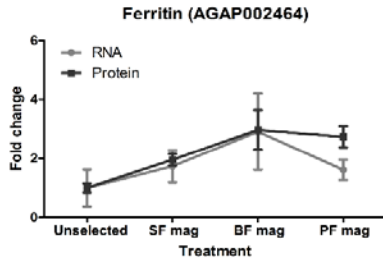


# C PROLIFERATION-SPECIFIC



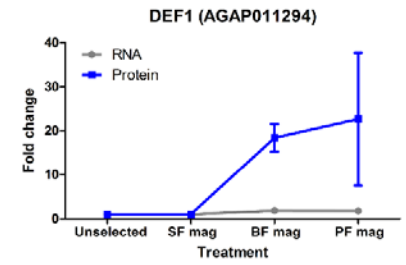
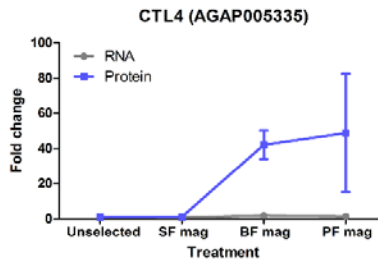
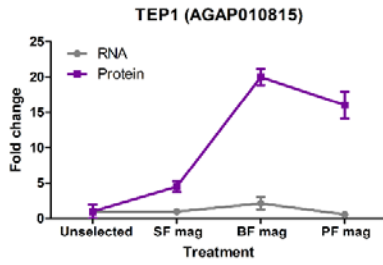
# A

## Enrichment in SF mag-beads



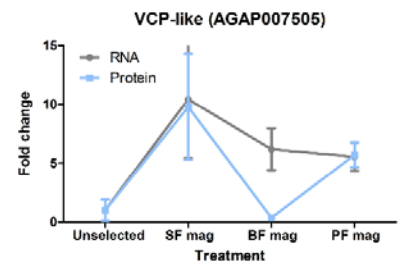
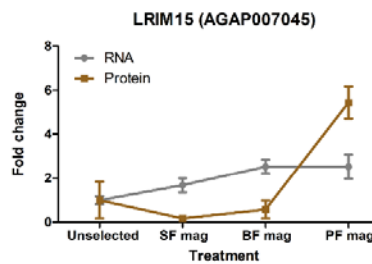
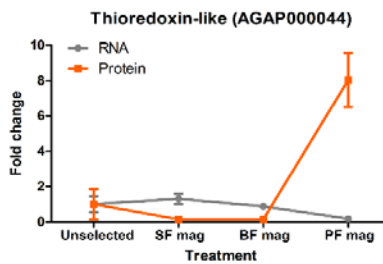
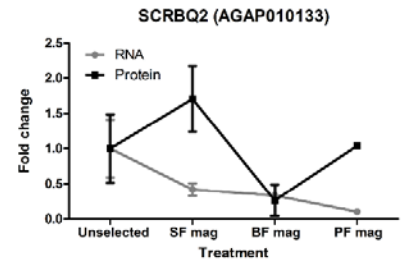
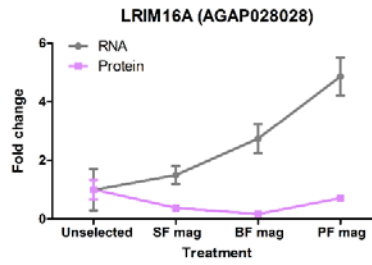
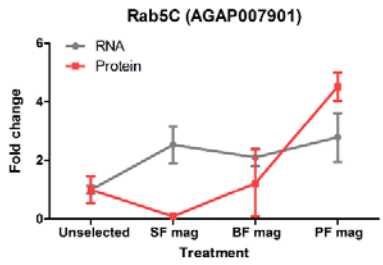
# B

## Enrichment in BF mag-beads

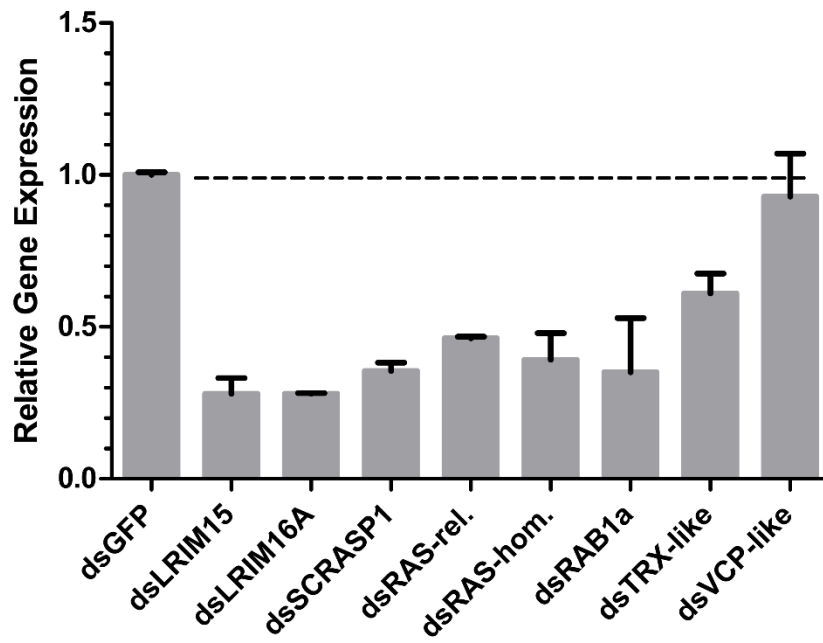


# C

## Enrichment in PF mag-beads



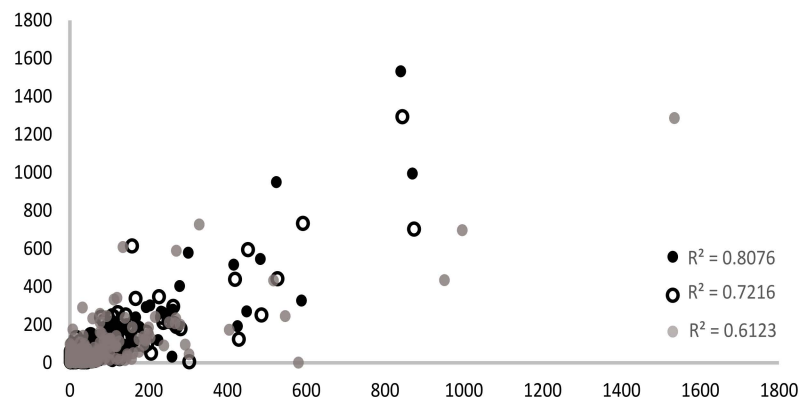
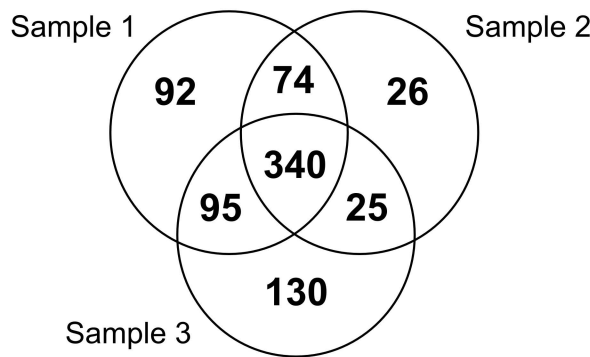
Supplemental Figure S4



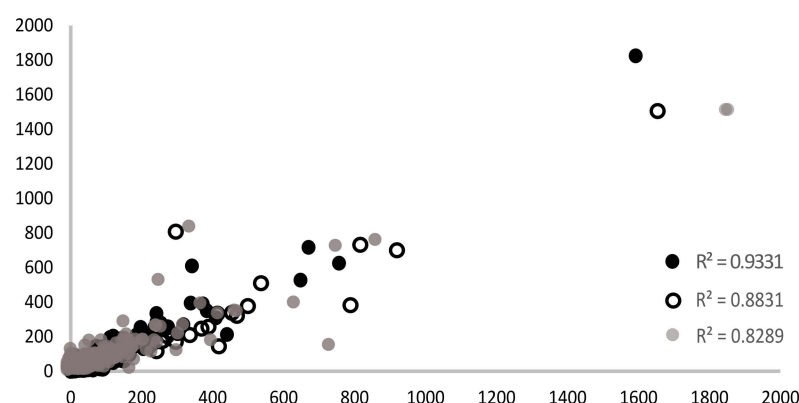
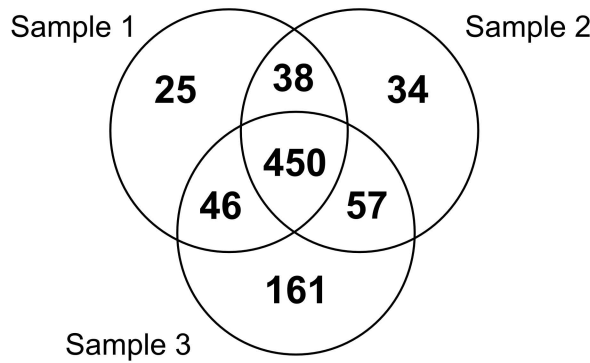
Supplemental Figure S5



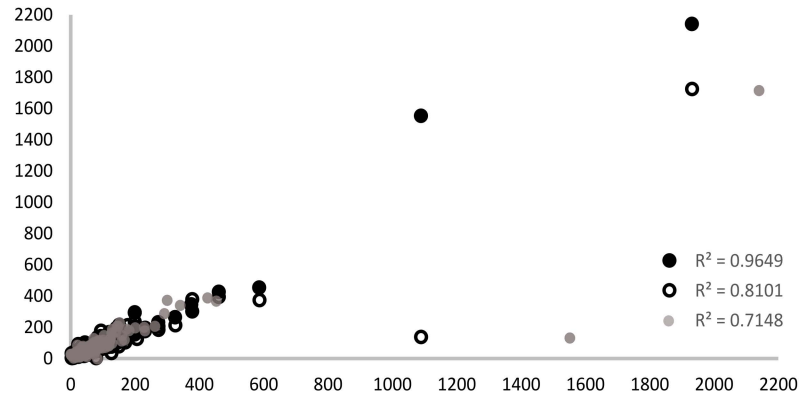
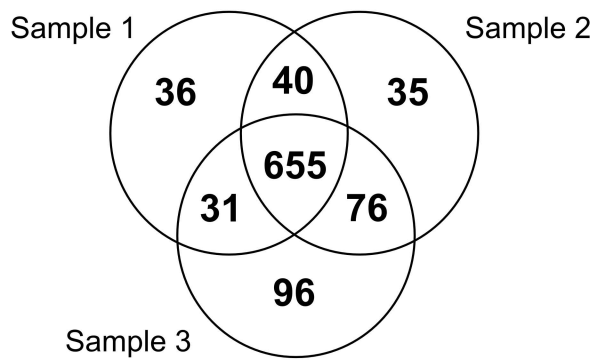
# Non-selected sugar-fed hemocytes



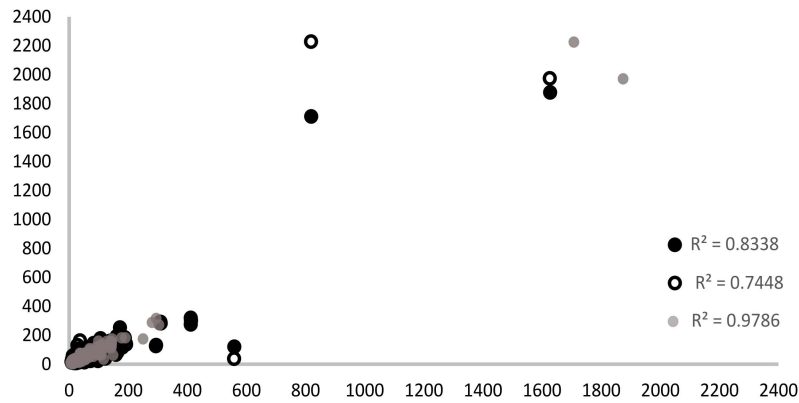
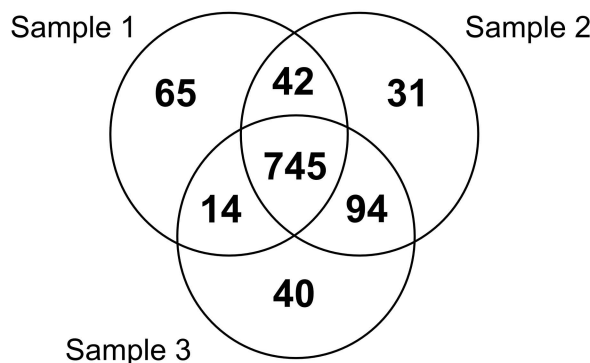
## SF-enriched granulocytes



## BF-enriched granulocytes



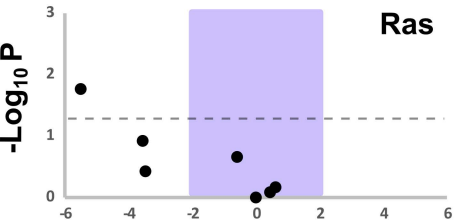
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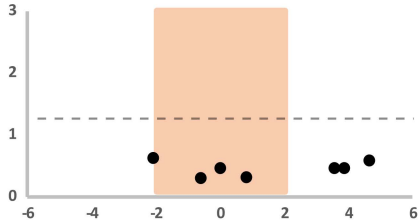
Normalized Spectral Count

Normalized Spectral Count

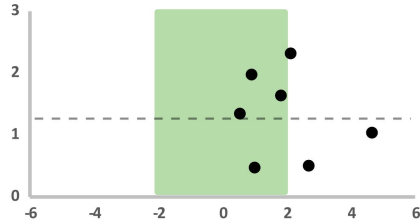
**Sugar-fed / Non-selected**



**Blood-fed / Sugar-fed**

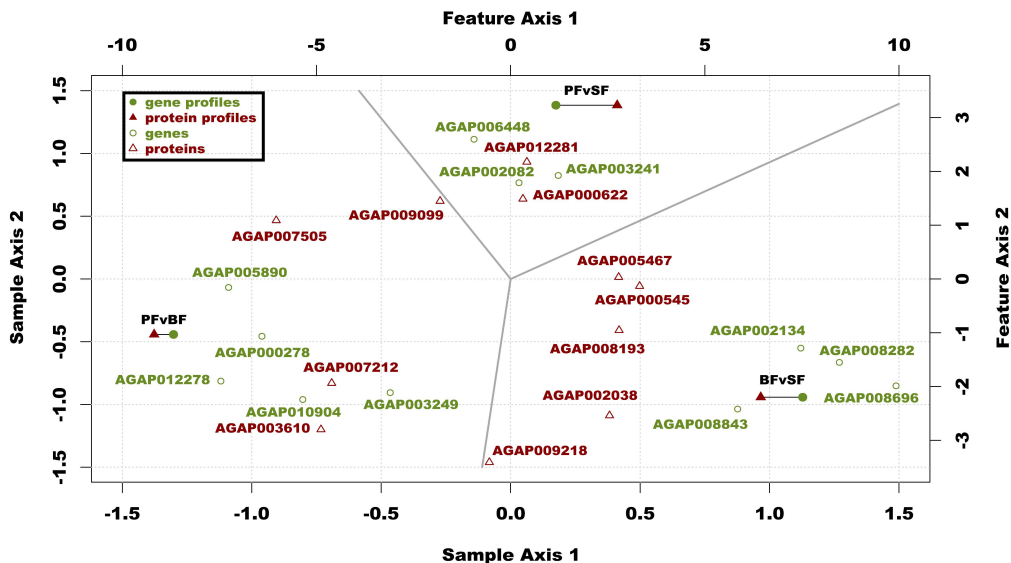


**Infected / Blood-fed**

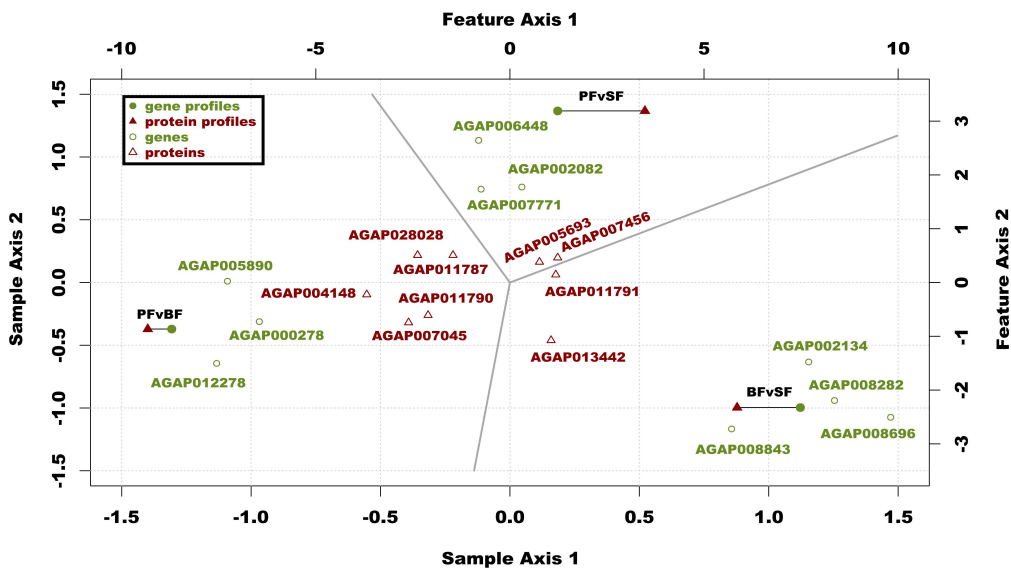


**Log<sub>2</sub> average normalized spectra**

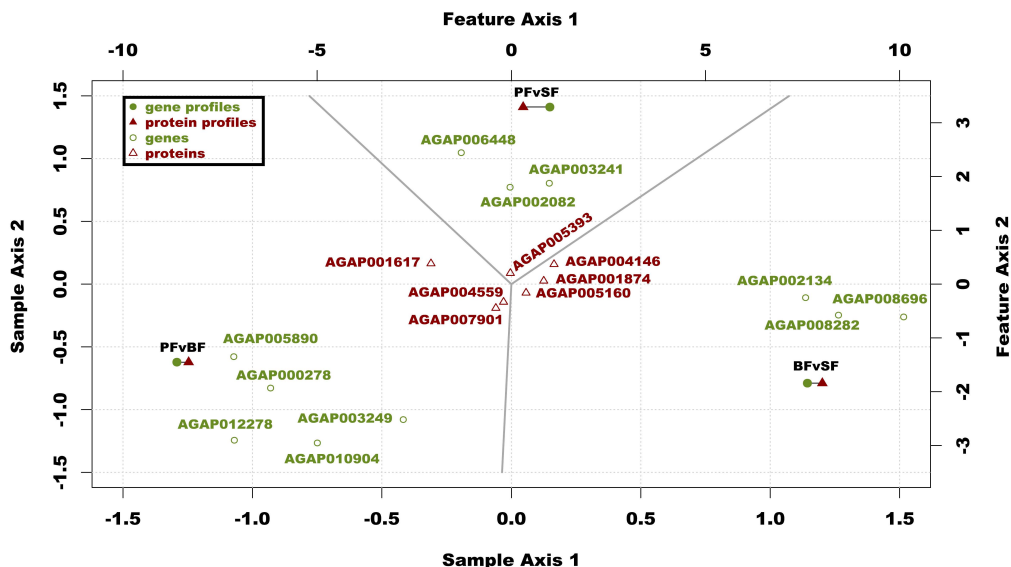
# A HEMOCYTE-SPECIFIC

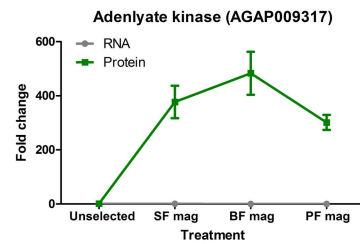
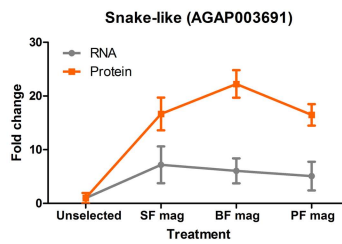
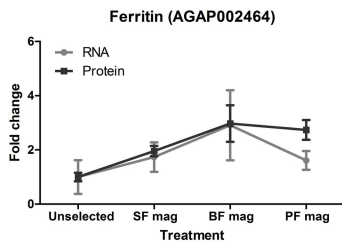
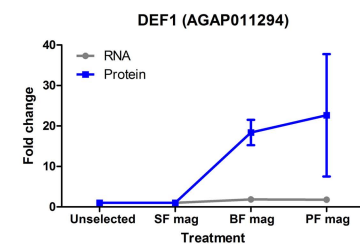
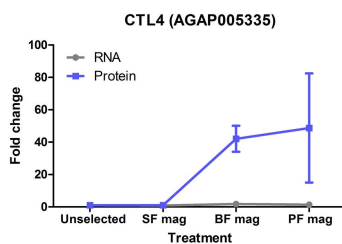
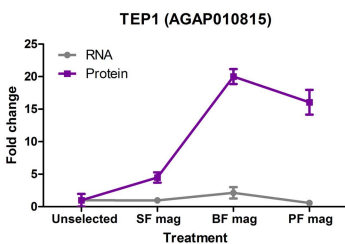


# B IMMUNE-SPECIFIC



# C PROLIFERATION-SPECIFIC



**A****Enrichment in SF mag-beads****B****Enrichment in BF mag-beads****C****Enrichment in PF mag-beads**