Table S1. Internal standards utilized in lipidomic and untargeted metabolomic analysis.

Internal Standard	Molecule Class	Analysis
1-heptadecanoyl-2-hydroxy-sn-glycero-3-phosphocholine	Lysophosphatidylcholine	Lipidomics
1,2-diheptadecanoyl-sn-glycero-3-phosphocholine	Phosphatidylcholine	Lipidomics
1,2-diheptadecanoyl-sn-glycero-3-phosphoethanolamine	Phosphatidylethanolamine	Lipidomics
1,2-diheptadecanoyl-sn-glycero-3-phospho-L-serine	Phosphatidylserine	Lipidomics
N-heptadecanoyl-D-erythro-sphingosylphosphorylcholine	Sphignomyelin	Lipidomics
cholest-5-en-3ß-yl heptadecanoate	Ceramide	Lipidomics
1-palmitoyl-2-oleoyl-sn-glycerol	Diadylglyercolipid	Lipidomics
1-heptadecanoyl-rac-glycerol	Monoadylglyercolipid	Lipidomics
1,2,3-triheptadecanoyl-glycerol	Triadyglycerolipid	Lipidomics
N-heptadecanoyl-D-erythro-sphingosine	Ceramide	Lipidomics
1,2-diheptadecanoyl-sn-glycero-3-phosphate	Glycerophosphate	Lipidomics
1,2-diheptadecanoyl-sn-glycero-3-phospho-(1'-rac-glycerol)	Phosphoglycerol	Lipidomics
Epibrassinolide	Plant steroid	Metabolomics
L-Tryptophan-$^{15}N_2$	Heavy amino acid	Metabolomics
Zeatin	Plant hormone	Metabolomics
L-[^{15}N]-Anthranilic Acid	Heavy aromatic acid	Metabolomics
Thymine-d4 (methyl-d3,6-d1)	Heavy nucleic acid	Metabolomics

Table S2. Metabolites in University of Michigan Metabolomics Resource Core in-house database at time of analysis.

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Table S3. Diapause incidence for experimental samples.

Diapause/Non-Diapause	Replicate	Total Eggs	% Diapause
Non-Diapause	1	672	10.4%
Non-Diapause	2	356	6.9%
Non-Diapause	3	290	14.0%
Non-Diapause	4	961	6.3%
Non-Diapause	5	394	11.4%
Non-Diapause	6	491	8.8%
Non-Diapause	7	1047	12.3%
Non-Diapause	8	597	11.3%
Diapause	1	560	100.0%
Diapause	2	393	99.7%
Diapause	3	486	99.8%
Diapause	4	593	99.2%
Diapause	5	544	99.2%
Diapause	6	344	99.3%
Diapause	7	204	100.0%

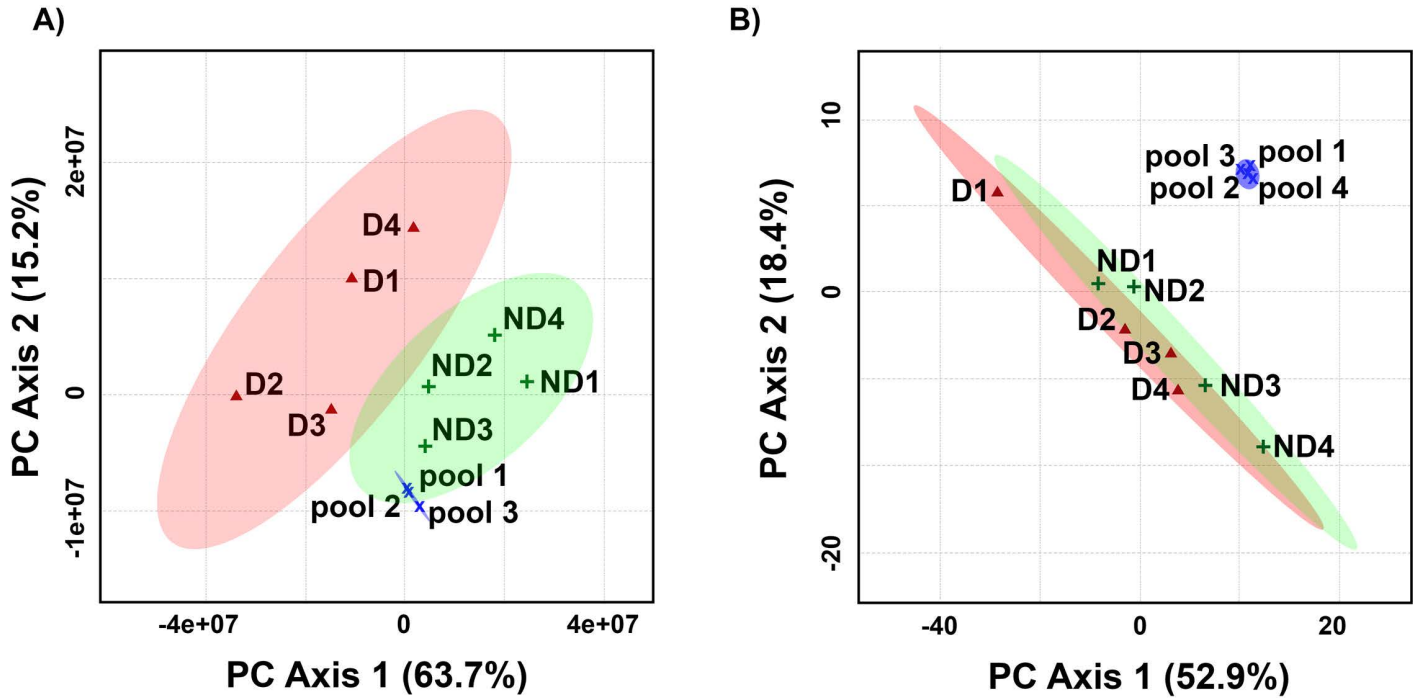**Table S4. Log2FC for all features with RSD<30% measured in experiment.**

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Table S5. HMDB classification of annotated metabolites co-eluting with diapause-exclusive features

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Table S6. Metabolites by pathway for QEA top 10.

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Fig. S1. Pooled quality control samples show consistent overall profiles across repeated measurements. Principal 955 component analysis (PCA) plot of [A] lipidomic profiles with pooled QC samples and in [B] untargeted 956 metabolomics profiles with pooled QC samples. In both plots, red triangles represent biological replicates of 957 diapause eggs reared under short-day photoperiod (8 h light: 16 h dark). Green crosses represent biological 958 replicates of non-diapause eggs reared under long-day photoperiod (16 h light: 8 h dark). Blue X's represent 959 technical replicates of pooled QC samples. Red, green, and blue shaded regions surrounding the points represent 960 the 95% confidence interval for diapause eggs, non-diapause eggs, and pooled QC samples, respectively. The tight 961 clustering of QC sample reads indicates low machine drift and consistency of the analytical platform across 962 experiment.
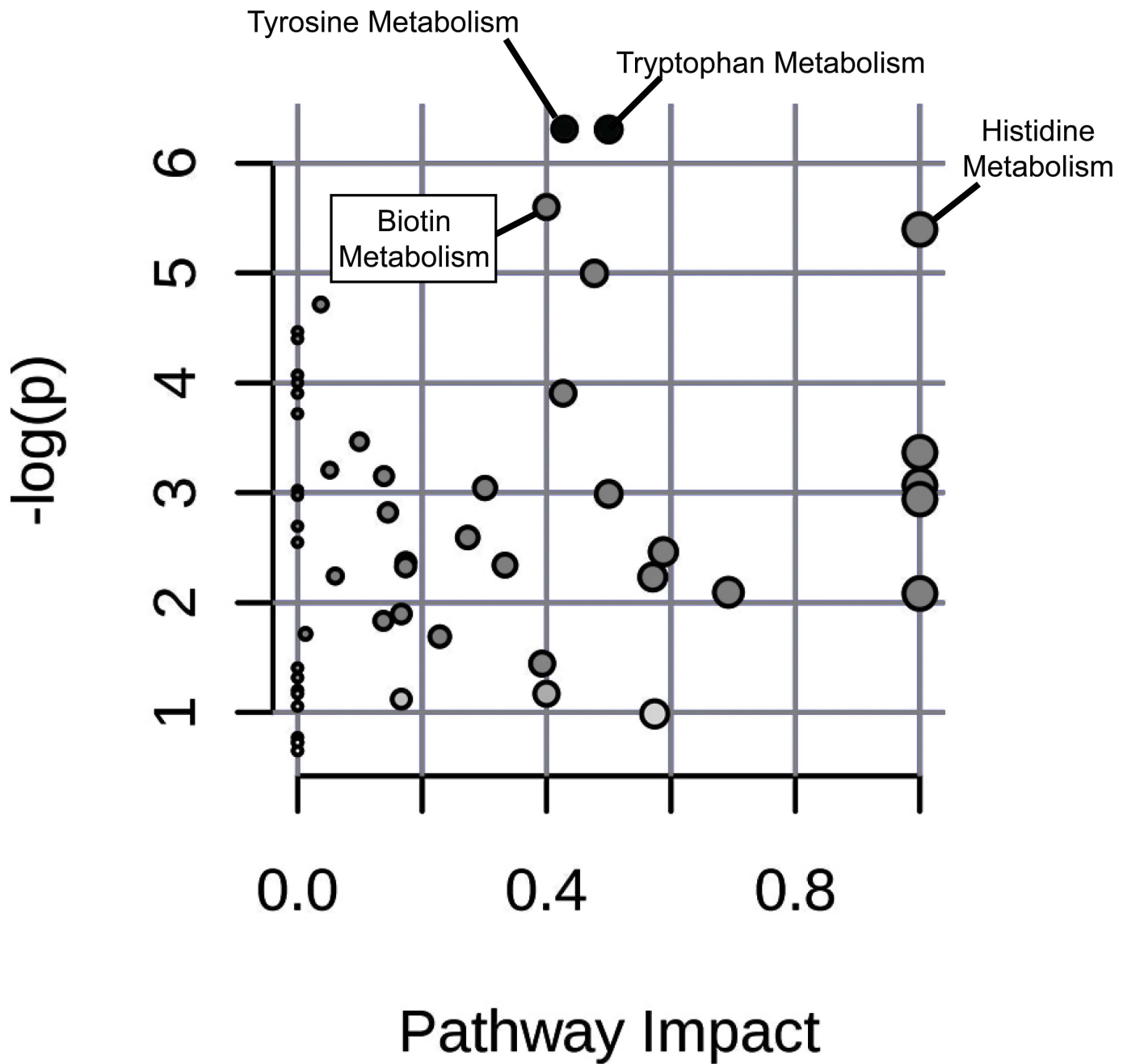
Fig. S2. Altered pathways identified to Pathway Enrichment Analysis. Pathway impact is a measure 965 ranging from zero to one that quantifies topological information about the affected metabolites. 966 Metabolic pathways with large changes in well-connected metabolites score higher corresponding to a 967 larger predicted effect on the overall pathway. Each dot represents a pathway. Light gray dots represent 968 non-significant impacts while black dots represent statistically significant impacts (p < 0.05 after FDR). 969 The size of the dot reflects the number of molecules affected on a given pathway.