**Supplemental Table S3a.** Pathways significantly enriched in aphid bacteriocytes feeding on fava or alfalfa using Gene Set Enrichment Analysis (GSEA)

|  |  |  |  |
| --- | --- | --- | --- |
| **Description** | **Set sizea** | **NESb** | **P\_adjc** |
| **Bacteriocytes vs. Body cells** | | |  |
| Glycine, serine and threonine metabolism\*\* | 20 | 1.5 | 0.008 |
| Glyoxylate and dicarboxylate metabolism\*\* | 18 | 1.49 | 0.017 |
| Phenylalanine metabolism\*\* | 8 | 1.48 | 0.07 |
| Pentose phosphate pathway\*\* | 17 | 1.46 | 0.044 |
| Nicotinate and nicotinamide metaboslim\*\* | 10 | 1.43 | 0.027 |
| Vitamin B6 metabolism\*\* | 3 | 1.4 | 0.037 |
| Folate biosynthesis\*\* | 13 | 1.39 | 0.045 |
| Biosynthesis of amino acids\* | 50 | 1.39 | 0.085 |
| Phenylalanine, tyrosine and tryptophan biosynthesis\* | 3 | 1.36 | 0.074 |
| Lipoic acid metabolism\*\* | 3 | 1.34 | 0.016 |
| Hippo signaling pathway - fly\* | 43 | -1.3 | 0.072 |
| Notch signaling pathway\*\* | 19 | -1.39 | 0.017 |
| Other glycan degradation\* | 16 | -1.44 | 0.087 |
| Phototransduction - fly\*\* | 16 | -1.46 | 0.002 |
| Neuroactive ligand-receptor interaction\*\* | 27 | -1.69 | 0 |

\*p-value <0.1; \*\*p-value <0.05; aNumber of genes included in a gene set; bNormalized Enrichment Score; cNormalized p-value; Shaded rows indicate the pathways enriched in body cells.

**Supplemental Table S3b.** Pathways significantly enriched in aphid bacteriocytes feeding on alfalfa relative to fava using Gene Set Enrichment Analysis (GSEA)

|  |  |  |  |
| --- | --- | --- | --- |
| **Description** | **Set sizea** | **NESb** | **P\_adjc** |
| **Alfalfa bacteriocytes vs. Fava bacteriocytes** | | |  |
| Synthesis and degradation of ketone bodies\* | 5 | 1.43 | 0.096 |
| Vitamin B6 metabolism\*\* | 3 | 1.39 | 0 |
| Aminoacyl-tRNA biosynthesis\*\* | 32 | 1.35 | 0 |
| Pyruvate metabolism\* | 30 | 1.35 | 0.097 |
| Jak-STAT signaling pathway\* | 18 | 1.29 | 0.092 |
| Lipoic acid metabolism\*\* | 3 | 1.28 | 0 |
| Butanoate metabolism\*\* | 15 | 1.27 | 0 |

\*p-value <0.1; \*\*p-value <0.05; aNumber of genes included in a gene set; bNormalized Enrichment Score; cNormalized p-value

**Supplemental Table S3c.** Pathways significantly enriched in aphid bacteriocytes relative to body cells feeding on both host plants from differentially methylated genes between bacteriocytes relative to body cells using Gene Set Enrichment Analysis (GSEA)

|  |  |  |  |
| --- | --- | --- | --- |
| **Description** | **Set sizea** | **NESb** | **P\_adjc** |
| **Alfalfa bacteriocytes vs. Fava bacteriocytes** | | |  |
| Metabolic pathways \*\* | 47 | 1.68 | 0.006 |
| Lysosome \*\* | 8 | 1.65 | 0 |
| Protein processing in endoplasmic reticulum\*\* | 7 | 1.51 | 0.04 |
| Selenocompound metabolism\* | 2 | 1.47 | 0.002 |
| Tryptophan metabolism\*\* | 3 | 1.34 | 0.083 |

\*p-value <0.1; \*\*p-value <0.05; aNumber of genes included in a gene set; bNormalized Enrichment Score; cNormalized p-value;