**Supplemental Table S5a.** Number of differentially methylated CpG sites and differentially expressed or spliced genes

|  |  |  |  |
| --- | --- | --- | --- |
| Differentially Methylated CpG Sitesa | Both differentially methylated and expressed genesb | Differentially spliced genesc | Both differentially methylated and spliced genes |
| **Bacteriocytes vs. Body cells** | | | |
| 3,474 | 441 | 3,859 | 702 |
| **Fava bacteriocytes vs. Alfalfa bacteriocytes** | | | |
| 294 | 3 | 47 | 3 |

**Supplemental Table S5b.** Number of differentially methylated CpG sites be genic regions

|  |  |  |  |
| --- | --- | --- | --- |
| Differentially methylated CpG sitesa - Total | Differentially methylated CpG sites - Exon | Differentially methylated CpG sites - Intron | Differentially methylated CpG sites - Intergenic |
| **Bacteriocytes vs. Body cells** | | | |
| 3,474 | 1,625 (47%) | 1,215 (35%) | 630 (18%) |
| **Fava bacteriocytes vs. Alfalfa bacteriocytes** | | | |
| 294 | 141 (48%) | 89 (30%) | 64 (22%) |

Each group has 6 biological replicates from alfalfa and fava feeding aphids.

1. Differentially methylated sites were determined with > 10% difference level, FDR-adjusted p-value < 0.01, with minimum of 10 read cutoff
2. Differentially expressed genes were determined with FDR-adjusted p-value < 0.05, 1.5X cutoff based on normalized read counts
3. Significance determined based on Jensen-Shannon divergences of splicing isoforms (see *SI Materials and Methods*)