**Supplemental Table S4.** Total whole genome bisulfite sequencing reads, high quality reads successfully mapped as pairs, and total read coverage for the whole genome, CpG sites, and genes for each bacteriocyte and body tissue sample in aphid host-plant treatments.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **DNA samples** | **Total reads** | **Mapped reads (paired) *Buchnera*** | **Mapped reads (paired) aphid** | **Total read coverage aphid genome** | **Total read coverage CpGs (%)a** | **Total read coverage genes (%)b** |
| **Fava sub-lines** | | | | | | |
| F1 Bacteriocytes | 101,895,398 | 59,637,111 | 14,278,056 | 1.2x | 46.8 | 49.6 |
| F1 Body Cells | 45,538,395 | 0 | 26,129,311 | 4.8x | 58.9 | 54.4 |
| F2 Bacteriocytes | 131,924,346 | 85,647,711 | 14,063,069 | 1.2x | 47.5 | 46.1 |
| F2 Body Cells | 56,394,111 | 0 | 31,477,892 | 5.8x | 62.9 | 62.9 |
| F3 Bacteriocytes | 61,926,293 | 39,367,593 | 6,830,107 | 0.9x | 37.3 | 36.2 |
| F3 Body Cells | 44,062,440 | 0 | 24,627,528 | 4.6x | 55.7 | 54.6 |
| **Alfalfa sub-lines** | | | | | | |
| A1 Bacteriocytes | 107,886,414 | 73,506,570 | 11,090,840 | 0.9x | 33.5 | 42.2 |
| A1 Body Cells | 28,669,685 | 0 | 17,578,080 | 3.2x | 58.8 | 48.3 |
| A2 Bacteriocytes | 112,822,307 | 75,303,932 | 11,830,822 | 0.9x | 48.6 | 43.1 |
| A2 Body Cells | 28,405,921 | 0 | 17,928,345 | 3.3x | 53.0 | 50.6 |
| A3 Bacteriocytes | 81,042,088 | 54,282,855 | 7,982,616 | 0.7x | 38.7 | 38.5 |
| A3 Body Cells | 88,555,344 | 0 | 22,527,414 | 3.1x | 55.4 | 52.7 |

F1, F2, and F3 denote 3 biological replicates of aphid lines with fava bean treatment. A1, A2, and A3 denote 3 biological replicates of aphid lines with alfalfa treatment.

a Total read coverage CpGs are the percentage value of the CpG sites that are covered by the high quality mapped reads with ≥10x coverage.

b Total read coverage genes are the percentage value of the aphid genes that are covered entirely by the high quality mapped reads with ≥10x coverage.