Supplemental Table S1 Overview of the metatranscriptomic libraries.

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| --- | --- | --- |
|  | Control | Treatment |
| Number of total reads | 8,295,242 | 9,351,598 |
| Average length of raw reads | 184 | 185 |
| Number of paired-end high quality reads | 7,074,470 | 7,919,816 |
| Average length of high quality reads | 171 | 170 |
| Number of total mRNA reads | 609,578 | 757,690 |
| Number of reads with significant hits to the NCBI nr database | 155,848 | 195,998 |
| Number of reads with SEED annotation | 64,940 | 67,842 |
| Number of reads with KEGG annotation | 74,727 | 98,712 |