**Table S4.** Summary of the *aioA*, *arrA*, and *arsM* sequence reads during quality control assessment

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | T1\_*aioA* | T2*\_aioA* | T1\_*arrA* | T2\_*arrA* | T1\_*arsM* | T2\_*arsM* |
| Raw reads (reads) | 119,891 | 54,654 | 138,093 | 56,016 | 87,552 | 56,853 |
| Joint sequence after blastx (reads) | 92,410 | 5,548 | 1,064 | 242 | 54,134 | 9,964 |
| Filtering sequence1 (reads) | 49,688 | 3,360 | 498 | 78 | 32,158 | 7,487 |
| OTUs (clusters) | 13,513 | 1,753 | 131 | 30 | 11,507 | 1,803 |

1Sequences were filtered with 80% coverage and 80% similarity.