**S4 Table. Percentage of reads aligned to the three reference sequences by Bowtie2.**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Sequenced sample** | **total reads** | **% mapped to *E. coli*** | **% mapped to *P. putida*** | **% mapped to R388** |
| **NP\_1** | 111,226,753 | 52.81 | 46.70 | 0.00 |
| **NP\_2** | 111,226,753 | 52.74 | 45.92 | 0.00 |
| ***ardC +*\_1** | 94,606,221 | 51.84 | 43.72 | 1.73 |
| ***ardC +*\_2** | 94,606,221 | 51.43 | 43.18 | 1.84 |
| ***ardC -*\_1** | 115,128,076 | 35.35 | 62.63 | 1.03 |
| ***ardC -*\_2** | 115,128,076 | 35.40 | 61.76 | 1.03 |