|  |  |  |  |
| --- | --- | --- | --- |
| **Sample** | **Raw reads** | **Reads mapped uniquely to** | |
| **Prochlorococcus** | **Alteromonas** |
| 9313 1 | 12,837,336 | 9,047,467 | 24,965 |
| 9313 2 | 11,470,536 | 7,763,792 | 1,454 |
| 9313+1A3 1 | 16,543,508 | 222,393 | 4,277,697 |
| 9313+1A3 2 | 15,233,874 | 146,901 | 4,239,022 |
| 9313+ Diluted 1A3 1 | 814,989 | 275,172 | 258,330 |
| 9313+ Diluted 1A3 2 | 12,001,482 | 1,208,792 | 1,051,797 |
| MED4 1 | 14,044,568 | 7,976,819 | 122,351 |
| MED4 2 | 13,301,262 | 8,716,916 | 8,596 |
| MED4+1A3 1 | 14,121,601 | 266,277 | 5,826,824 |
| MED4+1A3 2 | 7,500,307 | 165,430 | 3,669,183 |
| 1A3 1 | 14,719,446 | 0 | 8,474,619 |
| 1A3 2 | 12,191,652 | 2 | 8,746,409 |

**Supplementary Table S1**: Total raw reads from each sequencing library and the number of uniquely-mapping reads to the genomes of *Prochlorococcus* and *Alteromonas* after the quality control and data cleaning procedures described in the supplementary text. The numbers after each sample name represent the biological replicate.