**Table S2.** Sequencing yields for both reactors and sequencing platforms after quality control and trimming. OLR, oxygen-limited bioreactor; NLR, nitrogen-limited bioreactor; MiSeq, Illumina MiSeq platform; ONT, Oxford Nanopore Technologies platform.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Reactor** | **Sequencer** | **Read count\*** | **Read bps****(total)** | **Read length (mean)** |
| OLR | MiSeq | 7,568,591 | 2,031,927,441 | 268 |
| OLR | ONT | 318,070 | 3,128,778,886 | 9,837 |
| NLR | MiSeq | 8,733,498 | 2,300,830,797 | 263 |
| NLR | ONT | 416,527 | 4,014,258,886 | 9,638 |

\* Paired read counts and bps for Illumina data, *i.e.*, total R1 and R2 reads and bps divided by 2.