**Table S1:** Overview of mapped genomes of *P. luminescens* 1° and 2°. Sample ID DJC 1° and 2° are the original strains commonly used in the laboratory. Sample ID 1 indicate 1° cells and 2 indicate switched 2° cells after prolonged cultivation. A-F indicate the 6 different replicates of each tested phenotypic variant. The table indicates the mean GC-content of mapped reads of all sequenced genomes. Further the number of mapped reads against the reference genome (GenBank: CP024900.1) and the respective coverage information are represented.

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Sample ID | Mean GC-content of mapped reads  | Number of mapped reads | Coverage 1X | Coverage 10X(coverage depth) | Coverage mean fold | Coverage standard deviation | Mean mapping quality | SNPs |
| DJC 1° | 47.11% | 508,702 | 91.53% | 64.46% | 16.85 | 13.42 | 41.50 | 0 |
| DJC 2° | 46.20% | 849,897 | 94.48% | 81.68% | 29.41 | 19.27 | 41.50 | 0 |
| 1A | 42.35% | 4,337,166 | 95.33% | 94.38% | 56.28 | 19.39 | 41.47 | 1 |
| 1B | 42.24% | 5,163,856 | 95.37% | 94.99% | 66.82 | 21.34 | 41.47 | 4 |
| 1C | 41.02% | 239,859 | 86.16% | 1.06% | 3.14 | 2.48 | 41.40 | 0 |
| 1D | 41.75% | 516,314 | 96.17% | 92.56% | 23.97 | 9.09 | 41.62 | 0 |
| 1E | 41.74% | 1,230,841 | 96.34% | 95.39% | 58.55 | 21.13 | 41.64 | 3 |
| 1F | 42.35% | 5,881,125 | 95.37% | 94.79% | 77.21 | 25.40 | 41.47 | 1 |
| 2A | 42.70% | 5,685,937 | 95.37% | 95.00% | 69.18 | 23.99 | 41.47 | 2 |
| 2B | 42.32% | 4,474,680 | 95.37% | 94.96% | 59.39 | 19.41 | 41.46 | 1 |
| 2C | 42.77% | 5,384,675 | 95.37% | 94.96% | 66.96 | 23.18 | 41.46 | 2 |
| 2D | 42.27% | 1,452,522 | 96.35% | 95.64% | 72.81 | 23.94 | 41.64 | 6 |
| 2E | 41.92% | 890,401 | 96.27% | 94.66% | 42.40 | 15.56 | 41.62 | 3 |
| 2F | 41.96% | 3,146,817 | 95.36% | 94.71% | 41.64 | 14.48 | 41.47 | 1 |