|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Blast nr nucleotide databas** | **Aligned nucleotide%** |  |  |  | 23.34 | 51.53 | 14.54 |  | 14.36 | 17.00 | 25.38 |
| **ANI%** |  |  |  | 86.69 | 92.68 | 86.46 |  | 87.39 | 84.89 | 91.09 |
| **Length (bp)** |  |  |  | 178,249 | 178,249 | 178,249 |  | 178,249 | 183,806 | 178,249 |
| **Name** | No significant hit | No significant hit | No significant hit | Prochlorococcus phage P-SSM4 (AY940168.2) | Prochlorococcus phage P-SSM4 (AY940168.2) | Prochlorococcus phage P-SSM4 (AY940168.2) | No significant hit | Prochlorococcus phage P-SSM4 (AY940168.2) | Prochlorococcus phage P-HM2 (GU075905.1) | Prochlorococcus phage P-SSM4 (AY940168.2) |
| **483 scaffolds** | **Aligned nucleotide%** | 64.33 | 64.33 | 100.00 | 100.00 | 100.00 | 58.77 |  | 38.69 | 100.00 | 49.32 |
| **ANI%** | 98.08 | 98.19 | 99.73 | 99.25 | 97.63 | 99.49 |  | 99.36 | 99.40 | 95.25 |
| **Length (bp)** | 8,327 | 8,327 | 10,777 | 37,975 | 27,949 | 43,974 |  | 43,974 | 8,048 | 37,975 |
| **Name** | NTLX01000256.1 | NTLX01000256.1 | NTLX01000174.1  | NTLX01000012.1  | NTLX01000030.1 | NTLX01000006.1 | No hit found | NTLX01000006.1 | NTLX01000263.1 | NTLX01000012.1 |
| **GOV database** | **Aligned nucleotide%** | 97.51 | 6.25 | 99.98 | 86.78 | 92.4 | 37.41 | 93.09 | 38.5 | 99.81 | 55.00 |
| **ANI%** | 97.51 | 89.5 | 95.06 | 90.73 | 90.95 | 89.21 | 97.78 | 90.88 | 92.03 | 90.78 |
| **Length (bp)** | 8,146 | 6,690 | 28,306 | 12,004 | 37,113 | 37,113 | 8,146 | 37,113 | 3,592 | 37,113 |
| **Name** | GOV\_bin\_1296\_contig-100\_1 | GOV\_bin\_892\_contig-100\_6 | Tp1\_32\_SUR\_0-0d2\_scaffold20227\_1 | Tp1\_18\_DCM\_0-0d2\_scaffold48213\_1 | Tp1\_18\_DCM\_0-0d2\_scaffold31884\_1 | Tp1\_18\_DCM\_0-0d2\_scaffold31884\_1 | GOV\_bin\_1296\_contig-100\_1 | Tp1\_18\_DCM\_0-0d2\_scaffold31884\_1 | GOV\_bin\_5370\_contig-100\_47 | Tp1\_18\_DCM\_0-0d2\_scaffold31884\_1 |
| **Avg coverage** | 93.0 | 103.6 | 48.5 | 338.0 | 67.4 | 327.2 | 102.9 | 312.4 | 123.2 | 223.1 |
| **Length** | 193,112 | 155,659 | 136,254 | 132,604 | 93,939 | 86,648 | 80,620 | 76,528 | 73,892 | 72,532 |
| **Name** | S0 | S1 | S2 | S3 | S4 | S5 | S6 | S7 | S8 | S9 |

Table 1: The longest ten scaffolds of the 268 scaffolds generated by applying FVE-novel to the ocean metagenome sample collected from Aylward et al. showing ANI and aligned nucleotide percentage between the reference (GOV database) scaffold and the extended scaffold. These 10 scaffolds are also compared with the 483 scaffolds assembled in the original Aylward et al. study and blast nr nucleotide database using Blast, the best hit from Blast is selected.