

## 1 SUPPLEMENTARY MATERIALS

### 1.1 Command line options

All assemblers were run in 16 threads with command line options and recommended parameters. For PBcR, the options were *length 500 -partitions 200 -s pacbio.spec -t 16* where *pacbio.spec* file contained one string *"merSize=14"*. Cerulean was run without any additional options except the thread quantity; blasr used by Cerulean was run as recommended with options *-minMatch 10 -minPctIdentity 70 -bestn 30 -nCandidates 30 -maxScore -500 -nproc 16 -noSplitSubreads*. SPAdes was run with no command line options except *-t 16*

### 1.2 Time and memory usage

All benchmarking was performed on 64 cores server with 1Tb of memory in 16 threads. The provided running times are rough estimates since the server was used by various other tools at the same time.

**Table 1.** Memory usage in gigabytes

	Memory			
	HYBRIDSPADES	Cerulean	selfPBcR	hybridPBcR
ECOLI100	9	3	32	95
ECOLI200	9	5	76	131
ECOLI-NANO	9	-	-	-
MRUBER	5	2	28	17
STREPTO	9	3	-	6
TM6	9	3	20	-

**Table 2.** Running time

	Time			
	HYBRIDSPADES	Cerulean	selfPBcR	hybridPBcR
ECOLI100	1h:11m	1h:33m	1h:10m	2d:22h:17m
ECOLI200	1h:28m	4h:16m	2h:57m	3d:15h:43m
ECOLI-NANO	1h:15m	-	-	-
MRUBER	22m	33m	3h:38m	16h:12m
STREPTO	5h:53m	1h:27m	-	10h:24m
TM6	1h:12m	1h:10m	1h:50m	-

### 1.3 Datasets

#### 1. *Streptomyces PAMC26508*:

- Reference genome: Accession number CP003990.1
- Illumina reads: Accession number SRR628254
- PacBio reads: Accession number SRX208159

#### 2. *E. coli K12 subsp MG1655*:

- Reference genome: Accession number U00096.2

- Illumina reads: Accession number ERA000206
- PacBio reads: Available at PacBio DevNet, <https://github.com/PacificBiosciences/DevNet/wiki/E.-coli-20kb-Size-Selected-Library-with-P6-C4> and <https://github.com/PacificBiosciences/DevNet/wiki/E.-coli-20kb-Size-Selected-Library-with-P4-C2>

- Nanopore reads: Accession number ERX593920

#### 3. *M. ruber DSM 1279*:

- Reference genome: Accession number NC\_013946.1
- Illumina reads: Available at Illumina BaseSpace, <https://basespace.illumina.com/sample/15029026/mei01>
- PacBio reads: Accession number SRX260496

#### 4. *candidate division TM6 bacterium JCVI TM6SC1*:

- Reference assembly: Accession number ASM38563v1
- Illumina reads: <http://spades.bioinf.spbau.ru/tm6/>
- PacBio reads: <http://spades.bioinf.spbau.ru/tm6/>

**Table 3.** Statistics of datasets containing long reads. To define “N50 read length” parameter, we ordered all reads in the decreasing order of their lengths and computed their total length *TotalLength*. We further selected the minimum number of reads from the top of this list whose total length exceeds *TotalLength/2*. The parameter “N50 read length” is defined as the length of shortest read in the selected dataset. .

	Long reads		
	longest read	N50 read length	av. coverage
ECOLI100	22609	7566	94
ECOLI200	41390	15724	208
ECOLI-NANO	115979	7566	144
MRUBER	15409	3542	124
STREPTO	7844	2376	25
TM6	21827	3145	44

**Table 4.** Statistics of datasets containing short reads.

	Short reads		
	read length	insert size	average coverage
<i>E. coli str. K12</i>	100	215	230
<i>M. ruber DSM 1279</i>	150	3500	20
<i>Streptomyces sp. PAMC26508</i>	150	280	95
TM6	100	270	265