Table S1. *Caulobacter crescentus* NA1000 genome sequencing and assembly statistics.

| | Run data | Paired end |
|---|---|---|
| Number of runs | 1.5 | 0.5 |
| Runs assembled | 738,099 | 96,978 |
| Average read length (bp) | 251 | 94 |
| Number of base pairs | 4,000,673 | |
| Number of contigs | 151 | |
| N50 contig size (bp) | 52,555 | |
| Largest contig size (bp) | 177,486 | |
| Depth of coverage | 24X | |