

Table S-1. Evaluation with various coverage of the *E. coli* long reads. The coverage in tests (a)-(d) is 50x, 80x, 150x and 200x, respectively. The error corrected long reads by MECAT and FLAS (below dashed line), and the other existing self-correction algorithms HGAP, LoRMA, FALCON, Canu and Canu+ (above dashed line) are compared in each test. The best result in each column is shown in boldface. The performance measurements are listed in section 3.2.2.

Method	Throughput (bp)	Alignment ratio	Alignment identity	Time (h)	Memory (GB)
<i>(a) Long reads of 50x coverage (250,204,859 bp)</i>					
HGAP	123,745,180	95.4%	99.3%	1.0	2.4
LoRMA	107,523,523	85.7%	<b>99.8%</b>	0.3	24.8
FALCON	211,654,731	<b>98.3%</b>	99.3%	0.6	32.3
Canu	124,024,894	96.5%	99.0%	0.3	<b>1.6</b>
Canu+	215,937,028	96.6%	99.1%	0.7	2.1
MECAT	177,717,383	97.3%	99.4%	<b>0.1</b>	2.4
FLAS	<b>217,459,369</b>	96.7%	99.3%	0.2	2.4
<i>(b) Long reads of 80x coverage (397,486,752 bp)</i>					
HGAP	173,564,650	95.4%	99.4%	2.0	7.2
LoRMA	310,602,850	92.7%	<b>99.9%</b>	0.9	36.4
FALCON	245,895,710	97.0%	99.4%	1.3	46.2
Canu	158,007,936	95.6%	98.9%	0.3	<b>2.7</b>
Canu+	315,881,753	96.5%	99.2%	1.5	3.4
MECAT	284,138,161	<b>97.2%</b>	99.6%	<b>0.1</b>	2.9
FLAS	<b>346,737,024</b>	96.8%	99.6%	0.2	2.9
<i>(c) Long reads of 150x coverage (795,178,646 bp)</i>					
HGAP	309,120,988	95.4%	99.5%	4.1	9.6
LoRMA	561,802,249	97.0%	<b>99.9%</b>	2.8	48.6
FALCON	488,661,417	96.7%	99.5%	5.8	59.6
Canu	258,445,060	<b>97.4%</b>	99.3%	1.0	<b>3.4</b>
Canu+	471,025,187	96.2%	99.1%	1.9	4.3
MECAT	574,049,529	97.3%	99.7%	<b>0.3</b>	5.0
FLAS	<b>671,662,346</b>	96.8%	99.7%	0.6	5.0
<i>(d) Long reads of 200x coverage (1,078,811,834 bp)</i>					
HGAP	397,553,406	95.3%	99.4%	5.5	10.7
LoRMA	739,372,112	96.1%	<b>99.9%</b>	6.2	52.8
FALCON	677,623,010	96.6%	99.5%	10.6	60.2
Canu	262,676,389	<b>97.8%</b>	99.4%	1.0	<b>3.4</b>
Canu+	672,908,829	96.3%	99.1%	3.0	4.3
MECAT	795,567,126	97.2%	99.7%	<b>0.5</b>	6.3
FLAS	<b>916,699,023</b>	96.7%	99.7%	1.0	6.3

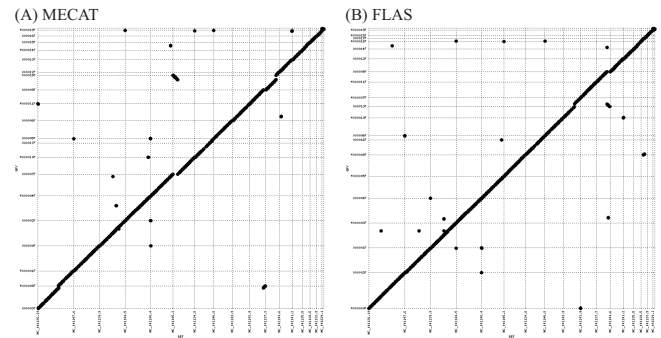


Fig. S-1: MUMmer plots of the *S. cerevisiae* contigs by FALCON\*, assembled from the MECAT corrected long reads (A) and FLAS corrected long reads (B), respectively.

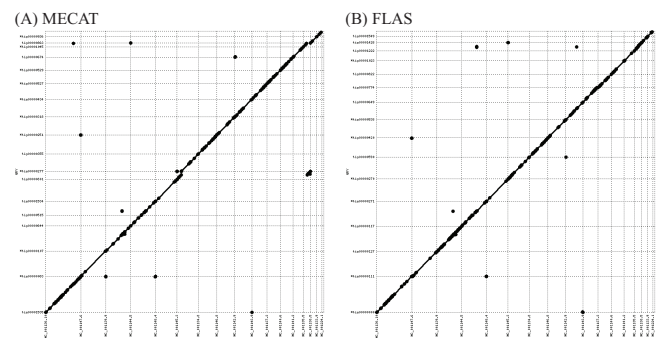


Fig. S-2: MUMmer plots of the *S. cerevisiae* contigs by Canu\*, assembled from the MECAT corrected long reads (A) and FLAS corrected long reads (B), respectively.

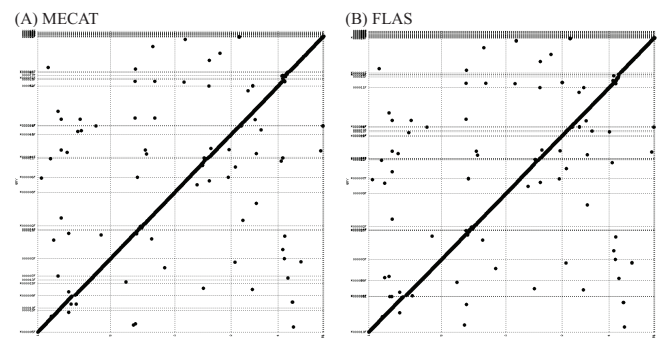


Fig. S-3: MUMmer plots of the *A. thaliana* contigs by FALCON\*, assembled from the MECAT corrected long reads (A) and FLAS corrected long reads (B), respectively.