

## Rhodobacter SRX264781

The tables 1, 2, 3, 4, and 5 are similar to the tables in the main text, with the addition of *R. sphaerooides* accession SRX264781 data set. This extra data set is the same strand as the other *R. sphaerooides* data set but is a PCR free library and was sequenced more recently (2012 vs. 2010). The relative performance of QuorUM versus the other error corrector is identical on this more recent data set.

**Table 1. Percent of false 31-mers remaining and true 31-mers missing in error corrected reads.**

Corrector	Rhodobacter			Staphylococcus			Mouse C16			R. SRX264781		
	False remain (55 M)	True missing (4.6 M)	Score $\pi$	False remain (33 M)	True missing (2.9 M)	Score $\pi$	False remain (410 M)	True missing (87 M)	Score $\pi$	False remain (48 M)	True missing (4.6 M)	Score $\pi$
none	100	0.36	40	100	0.037	4	100	0.069	7	100	0.15	20
trim20B	55	0.39	20	64	0.085	5	50	<b>0.076</b>	4	64	0.16	10
trimQual5	9.4	0.71	7	96	0.039	4	34	0.10	3	19	0.19	4
Coral	69	0.38	30	56	0.13	7	52	0.22	10	49	0.33	20
Echo	60	<b>0.36</b>	20	55	<b>0.029</b>	2	-	-	-	38	<b>0.15</b>	6
HiTec	42	1.1	50	33	0.23	8	-	-	-	26	0.22	6
Quake	8.3	0.71	6	3.3	0.24	0.8	4.6	0.16	0.7	9.0	0.18	2
SGA	2.3	1.5	3	0.49	0.61	0.3	7.1	0.16	1	0.53	0.22	0.1
Racer	40	0.93	40	35	0.26	9	30	0.27	8	25	0.24	6
Musket	40	0.52	20	44	0.067	3	29	0.15	4	36	0.18	6
QuorUM	<b>0.29</b>	0.40	<b>0.1</b>	<b>0.22</b>	0.087	<b>0.02</b>	<b>2.0</b>	0.11	<b>0.2</b>	<b>0.24</b>	0.16	<b>0.04</b>

**Table 2. Idealized contig size statistics (in kb).**

Corrector	Rhodobacter		Staphylococcus		Mouse C16		R. SRX264781	
	N50	E-size	N50	E-size	N50	E-size	N50	E-size
none	2.7	4.1	43	42.4	32	40.4	67	74.8
trim20B	3.9	5.8	17	20.4	32	40.1	58	77.6
trimQual5	3.2	4.3	35	42.3	38	47.8	36	51.8
Coral	4.7	6.9	65	87.7	17	22.6	100	142
Echo	5.6	8.0	<b>100</b>	110	-	-	120	<b>171</b>
HiTec	5.7	8.1	55	56.3	-	-	110	132
Quake	3.2	4.3	21	23.1	36	45.1	36	57.2
SGA	4.7	6.8	15	16.2	38	48.1	68	94.4
Racer	5.7	9.3	39	44.3	24	30.2	99	128
Musket	5.1	7.8	61	78.1	31	38.6	90	120
QuorUM	<b>12</b>	<b>18</b>	86	<b>112</b>	<b>40</b>	<b>49.0</b>	<b>140</b>	167

**Table 3. Percentage of the original reads that are perfect after error reduction, and percentage of bases contained in perfect reads compared with bases in original reads.**

Corrector	Rhodobacter		Staphylococcus		Mouse C16		R. SRX264781	
	Reads (2 M)	Sequence (200 M)	Reads (1.2 M)	Sequence (120 M)	Reads (41 M)	Sequence (4.2 G)	Reads (2.0 M)	Sequence (200 M)
none	21	21	33	33	48	48	39	39
trim20B	44	36	46	37	79	64	52	42
trimQual5	76	51	35	35	78	72	68	52
Coral	58	58	74	74	81	81	80	80
Echo	56	56	65	65	-	-	79	79
HiTec	61	61	78	78	-	-	84	84
Quake	81	59	69	60	89	81	66	55
SGA	62	62	75	75	85	85	81	81
Racer	63	63	78	78	84	84	86	86
Musket	76	70	80	78	88	86	86	84
QuorUM	<b>90</b>	<b>77</b>	<b>84</b>	<b>81</b>	<b>92</b>	<b>88</b>	<b>90</b>	<b>86</b>

**Table 4. Number of chimeric reads per 10 000 after correction.**

Corrector	Rhodobacter	Staphylococcus	Mouse C16	R. SRX264781
none	11	7.3	59	2.0
trim20B	7.9	4.9	46	1.5
trimQual5	2.9	7.1	26	0.81
Coral	11	9.3	52	1.7
Echo	9.6	7.6	-	1.3
HiTec	35	12	-	6.8
Quake	<b>0.100</b>	<b>5.2</b>	<b>11</b>	0.68
SGA	3.8	5.7	14	0.56
Racer	18	8.8	65	2.3
Musket	15	8.6	40	1.7
QuorUM	0.17	7.2	13	<b>0.24</b>

**Table 5. Runtime of each program in hours:minutes:seconds, using 16 threads, and memory usage in giga-bytes.**

Corrector	Rhodobacter 4.6 Mb		Staphylococcus 2.9 Mb		Mouse C16 98.2 Mb		R. SRX264781 4.6 Mb	
	Time	Mem	Time	Mem	Time	Mem	Time	Mem
Coral	0:09:46	35	0:06:18	33	-	-	0:08:24	-
Echo	2:10:46	58	1:06:11	39	-	-	2:02:37	-
HiTec	0:41:51	4.0	0:22:09	2.3	-	-	0:37:30	-
Quake	0:03:01	0.37	0:04:18	1.3	1:13:30	5.7	0:03:01	-
SGA	0:05:14	0.34	0:03:23	0.28	0:32:33	2.1	0:04:07	-
Racer	0:01:58	2.0	0:01:01	1.4	0:34:35	11	0:01:27	-
Musket	0:06:54	<b>0.23</b>	0:01:49	<b>0.22</b>	0:58:11	<b>0.38</b>	0:03:09	-
QuorUM	<b>0:00:53</b>	0.44	<b>0:00:17</b>	0.74	<b>0:23:12</b>	8.8	<b>0:00:30</b>	-