

**Supplemental table S2.** QCAST analysis of gap-closed *E. coli*, *S. cerevisiae* and *C. elegans* draft genome assemblies.

	<i>E. coli</i> K12 (4,686,137 bp)				<i>S. cerevisiae</i> S288c (12,071,326 bp)				<i>C. elegans</i> Bristol N2 (100,272,607 bp)			
	Original assembly	Sealer	GapCloser	GapFiller	Original assembly	Sealer	GapCloser	GapFiller	Original assembly	Sealer	GapCloser	GapFiller
Number of sequences*	535	<b>526</b>	534	527	1750	<b>1682</b>	1737	1687	5846	4701	4970	<b>4179</b>
Largest sequence (bp)	66338	66338	66338	66338	59854	59854	59854	59854	384642	1349218	1349228	762554
N50 (bp)	14251	<b>14601</b>	14251	<b>14601</b>	10397	<b>10724</b>	10429	<b>10724</b>	39508	52267	48508	<b>59358</b>
NG50 (bp)	13120	<b>13190</b>	13120	13150	9497	<b>9963</b>	9626	9934	41165	55074	51773	<b>59732</b>
Mis-assemblies	<b>2</b>	3	<b>2</b>	<b>2</b>	<b>14</b>	15	<b>14</b>	<b>14</b>	<b>231</b>	440	370	362
N's per 100 kbp	0.00	0.09	0.00	0.00	1.25	1.45	0.00	0.00	1.54	5.58	0.00	0.00
Mis-match per 100 kbp <sup>1</sup>	<b>2.01</b>	2.67	<b>2.01</b>	3.06	81.02	82.19	82.53	<b>80.60</b>	<b>15.53</b>	22.24	22.81	20.63
Complete genes	3765	<b>3787</b>	3771	3779	5089	<b>5149</b>	5103	5122	47405	<b>47743</b>	47645	46269

\* All statistics are based on sequences of size  $\geq 500$

<sup>1</sup> Sealer introduces IUPAC ambiguity codes when a base is uncertain, which is assessed as a mismatch by QCAST