

Erratum Dohm et al., *Genome Res.* 2007 17: 1697-1706, Table 2

An error occurred when finalising Table 2. The correct assembly property values for *H. influenzae* and *E. coli* are given below. The assembly properties of the assemblies for *S. cerevisiae* chromosomes 5 and 7 remain unchanged. We apologize for this mistake.

1	2	3	4	5	6	7	8	9	10	11
Species	GenBank	Seq. Length	Reads (Mio)	Read Length	Contigs	Mean	Max	N50	N80	Seq. cov. (%)
<i>S.cer 5</i>	NC_001137	576869	2.5	30	237	2379	41960	16096	5137	97.36
<i>S.cer 5</i>	NC_001137	576869	5	30	319	1793	54053	27975	17848	98.23
<i>S.cer 5</i>	NC_001137	576869	2.5	32	233	2423	42420	16987	5621	97.45
<i>S.cer 7</i>	NC_001139	1090946	10	30	330	3262	60516	24771	10280	98.32
<i>S.cer 7</i>	NC_001139	1090946	5	30	367	2914	32709	9737	3700	97.77
<i>S.cer 7</i>	NC_001139	1090946	5	32	300	3568	46493	15820	6715	97.88
<i>H. inf</i>	NC_007146.1	1913428	10	30	589	3183	48963	12323	5589	97.64
<i>H. inf</i>	NC_007146.1	1913428	10	32	554	3389	67333	18402	7227	97.78
<i>E. col</i>	NC_000913.2	4639675	15	30	2311	1969	35437	4506	2033	97.58
<i>E. col</i>	NC_000913.2	4639675	20	30	1401	3247	53973	10084	4733	97.77
<i>E. col</i>	NC_000913.2	4639675	20	32	1276	3570	73047	12754	6169	97.91

Table 2: Assembly properties for assemblies with simulated reads of *Saccharomyces cerevisiae* chromosome 5 (coverage 130-, 260-, 139-fold) and chromosome 7 (coverage 275-, 138-, 147-fold) and the complete genomes of *Haemophilus influenzae* (coverage 157- and 167-fold) and *Escherichia coli* (coverage 97-, 129-, 138-fold). Simulation assumptions were realistic, i.e. with missing reads and sequencing error rate of 0.6% per base; coverage range Column labels: 1: Species name (abbreviated). 2: GenBank accession number. 3: Length of GenBank reference sequence. 4: Number of reads used for assembly (in millions). 5: Read length (bases). 6: Number of contigs > 50 bp after assembly. 7: Average contig length. Only contigs >50 bp were counted. 8: Largest contig observed in assembly. 9: N50 length of assembly. 10: N80 length of assembly. 11: Percent coverage of reference sequence with SHARCGS contigs. All contigs could be aligned against the reference sequence error- and gap-free.