

Table 1 Sequence assembly details

Feature	Chromosome						
	1	2	3	4	5	6	All
<b>Chromosomal assemblies</b>							
Assembly span (bp)*	4,919,822	8,467,571	6,358,352	5,430,575	5,062,323	3,578,828	33,817,471
Assembly sequence (bp)†	4,911,622	8,437,971	6,334,852	5,397,875	5,032,273	3,547,128	33,661,721
Total contigs	11	40	32	65	107	44	309
Mean contig size (bp)	446,511	210,949	197,964	83,044	47,031	80,617	108,938
Number of sequence gaps	4	12	10	34	81	14	155
Number of repeat gaps	8	29	23	9	4	11	84
Number of clone gaps	0	0	0	22	22	20	64
Total estimated gap size (bp)‡	8,200	29,600	23,500	32,700	30,050	31,700	155,750
Number of HAPPY markers (mean spacing in kb)	749 (6.6)	615 (12.5)§	684 (9.3)	628 (8.6)	628 (8.1)	598 (6.0)	3,902 (8.7)
<b>Floating contigs  </b>							
Number of floating contigs	0	22	3	9¶		0	34
Total size of floating contigs (bp)	0	171,670	16,360	37,309		0	225,339
<b>Combined (assemblies plus floating contigs)</b>							
Total sequence (bp)	4,911,622	8,609,641	6,351,212	5,416,529¶	5,050,928¶	3,547,128	33,887,060
Mean coverage (fold)	9.1	6.5	6.7	9.6	9.9	10.3	8.3

\*Total end-to-end length of the chromosomal assembly, including any gaps.

†Sequenced bases covered by chromosomal assembly, not counting gaps.

‡Sequence, repeat and clone gaps are taken to have average sizes of 50 bp, 1,000 bp and 1,000 bp, respectively.

§Does not include the second copy of the 755-kb inverted duplication.

||Includes only those contigs that can be assigned to specific chromosomes.

¶Floating contigs from chromosomes 4 and 5 cannot be distinguished. In calculating total chromosomal sequence, we assume that half of these floating contigs are from each of chromosomes 4 and 5.