

Table 1: The start and end positions of high-quality read regions

Read	Start ^a	End	Read length
R1+	5	849	860
R2+	55	888	1022
R3+	55	870	918
R4+	4	790	799
R5+	17	599	920
R6+	70	789	850

^a Positions are relative to raw reads in given orientation.

Table 2: The start and end positions of similar read regions

Read	Start ^a	End	Read	Start	End
R1-	2	427	R4+	374	799
R1-	2	239	R5+	390	628
R1-	2	311	R6+	518	827
R1+	12	829	R2+	55	873
R1+	12	829	R3+	55	874
R2-	27	545	R4+	282	799
R2-	34	357	R5+	304	628
R2-	27	429	R6+	426	827
R2+	55	838	R3+	55	838
R3-	4	441	R4+	364	799
R3-	90	253	R5+	464	628
R3-	4	325	R6+	508	827
R4+	46	611	R5+	52	628
R4+	18	683	R6+	152	827
R5+	52	628	R6+	181	755

^a Positions are relative to raw reads in specified orientation.

Table 3: The start and end positions of clean regions

Read	Start ^a	End	Read length
R1+	12	859	860
R2+	55	996	1022
R3+	55	915	918
R4+	18	799	799
R5+	52	628	920
R6+	152	827	850

^a Positions are relative to raw reads in given orientation.

Table 4: The positions and scores of overlaps

Read	Start ^a	End	Length ^b	Read	Start	End	Length	Score
R1+	1	848	848	R3+	1	850	861	53378
R3+	1	861	861	R2+	1	861	942	51554
R1+	1	848	848	R2+	1	849	942	50668
R6+	1	676	676	R4+	1	666	782	36206
R4+	357	782	782	R1-	1	426	848	19848
R4+	265	782	782	R2-	1	519	942	19133
R4+	347	782	782	R3-	1	438	861	18011
R5+	1	577	577	R4+	29	594	782	10311
R6+	275	676	676	R2-	1	403	942	10308
R5+	1	577	577	R6+	30	604	676	10211
R6+	367	676	676	R1-	1	310	848	10047
R6+	357	676	676	R3-	1	322	861	8516
R5+	246	577	577	R2-	1	331	942	3021
R5+	339	577	577	R1-	1	238	848	2473
R5+	327	577	577	R3-	1	250	861	1871

^a Positions are relative to clean reads in specified orientation.

^b Length is the length of a clean read without poor end regions.

Table 5: The strengths and availability of the sequence assembly programs

Program	Strength	Availability
CAP3	Assembly of ESTs	genome.cs.mtu.edu/cap/cap3.html
Celera Assembler	Assembly of large genomes	www.celera.com
GAP4	Interactive assembly	www.mrc-lmb.cam.ac.uk/pubseq
Phrap	Assembly of reads with quality values	www.phrap.org
TIGR Assembler	Assembly of clean reads	www.tigr.org