Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/26 03:11:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1781845.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR1781845 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1781845_1.fastq.gz SRR1781845_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Mar 26 03:11:34 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1781845.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	357,630,720
Mapped reads	349,344,035 / 97.68%
Unmapped reads	8,286,685 / 2.32%
Mapped paired reads	349,344,035 / 97.68%
Mapped reads, first in pair	175,646,172 / 49.11%
Mapped reads, second in pair	173,697,863 / 48.57%
Mapped reads, both in pair	346,186,112 / 96.8%
Mapped reads, singletons	3,157,923 / 0.88%
Secondary alignments	0
Supplementary alignments	1,347,981 / 0.38%
Read min/max/mean length	30 / 100 / 99.98
Duplicated reads (estimated)	37,671,173 / 10.53%
Duplication rate	10.43%
Clipped reads	15,343,688 / 4.29%

2.2. ACGT Content

Number/percentage of A's	10,188,078,150 / 29.38%
Number/percentage of C's	7,127,133,518 / 20.56%
Number/percentage of T's	10,164,076,885 / 29.31%
Number/percentage of G's	7,189,900,670 / 20.74%
Number/percentage of N's	3,862,130 / 0.01%

GC Percentage	41.29%

2.3. Coverage

Mean	11.2027
Standard Deviation	12.7077

2.4. Mapping Quality

Mean Mapping Quality	53.98

2.5. Insert size

Mean	41,101.06
Standard Deviation	1,991,243.27
P25/Median/P75	160 / 196 / 241

2.6. Mismatches and indels

General error rate	0.43%
Mismatches	144,027,168
Insertions	3,235,714
Mapped reads with at least one insertion	0.91%
Deletions	3,235,479
Mapped reads with at least one deletion	0.91%
Homopolymer indels	46.38%

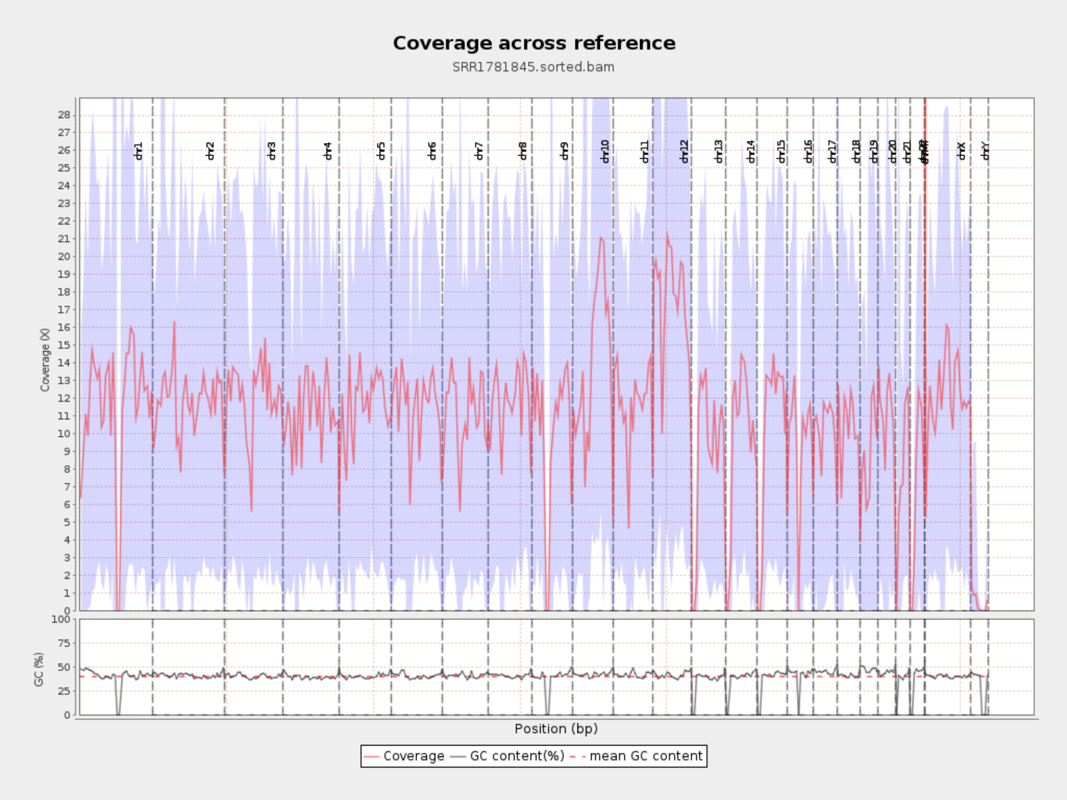
2.7. Chromosome stats

Name	**Length**	**Mapped**	**Mean**	**Standard**

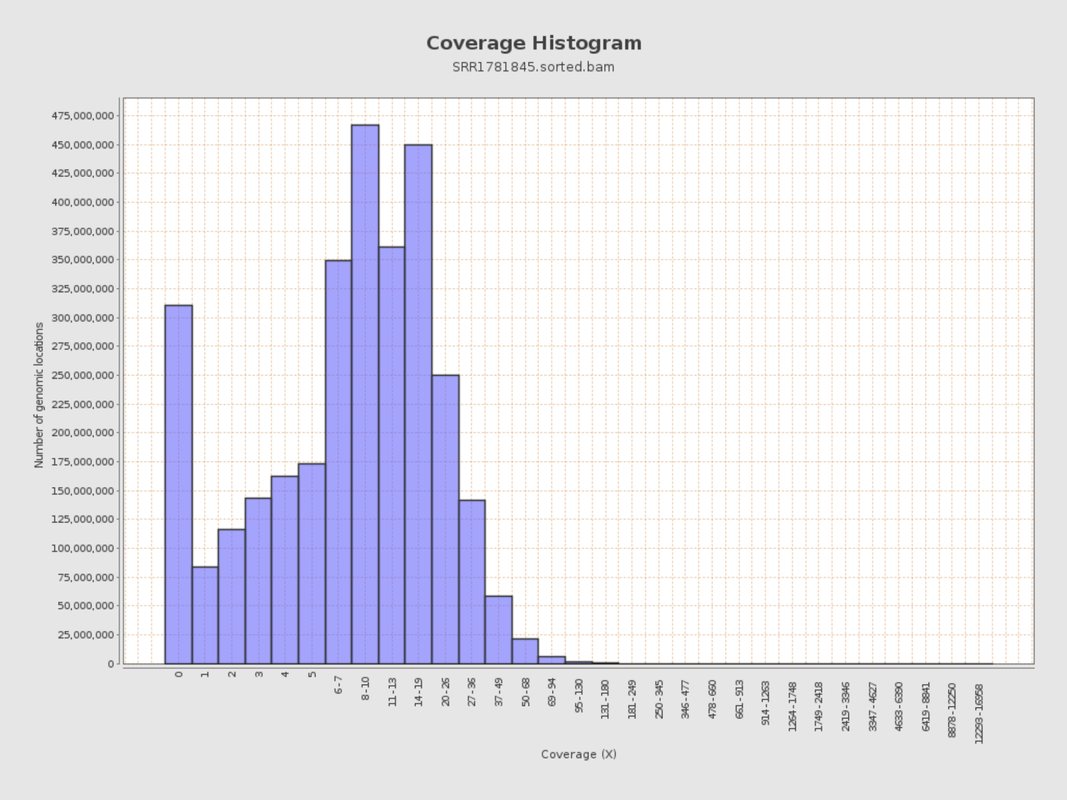
		bases	coverage	deviation
chr1	249250621	2895497575	11.6168	17.2566
chr2	243199373	2888170191	11.8757	17.2189
chr3	198022430	2398964932	12.1146	10.0787
chr4	191154276	2147333203	11.2335	10.7124
chr5	180915260	2096478192	11.5882	9.5931
chr6	171115067	2006489077	11.726	10.7054
chr7	159138663	1767412136	11.1061	11.0571
chr8	146364022	1737558121	11.8715	10.0188
chr9	141213431	1411307036	9.9941	12.2581
chr10	135534747	1949452678	14.3834	19.0702
chr11	135006516	1579583574	11.7001	10.5354
chr12	133851895	2358327989	17.6189	14.5159
chr13	115169878	1026778555	8.9153	8.995
chr14	107349540	1023880964	9.5378	9.848
chr15	102531392	1026416819	10.0108	10.4321
chr16	90354753	838571192	9.2809	9.809
chr17	81195210	839351467	10.3375	10.8903
chr18	78077248	815911004	10.45	11.5094
chr19	59128983	531274254	8.985	12.4902
chr20	63025520	699683954	11.1016	11.514
chr21	48129895	382568156	7.9487	13.8802
chr22	51304566	351163611	6.8447	9.4431
chrMT	16571	3309647	199.7252	51.9575
chrX	155270560	1878564887	12.0987	10.3402

chrY	59373566	26200425	0.4413	4.8112

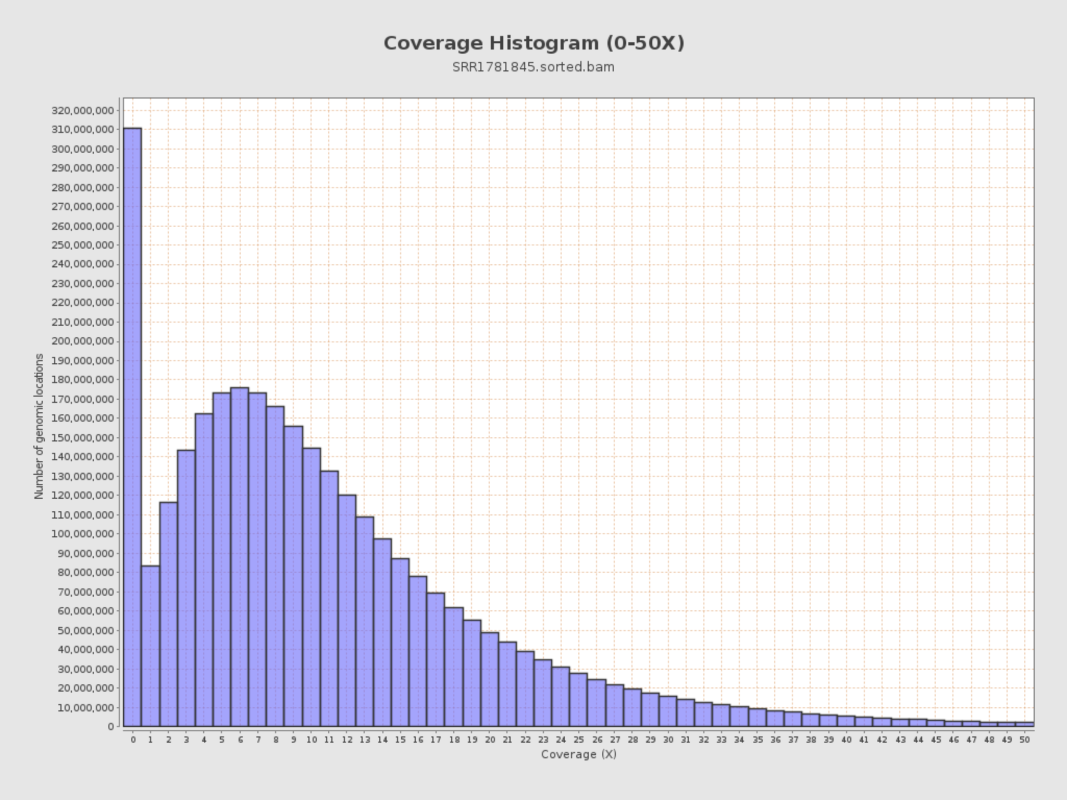
3. Results : Coverage across reference



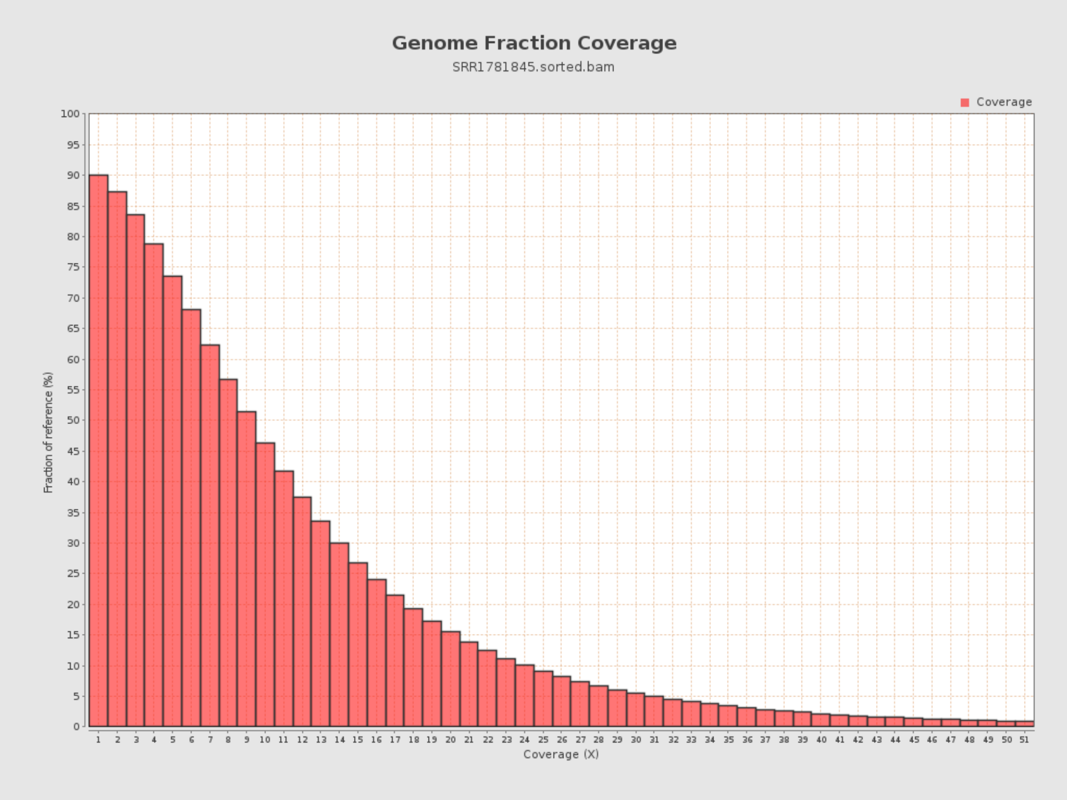
4. Results : Coverage Histogram



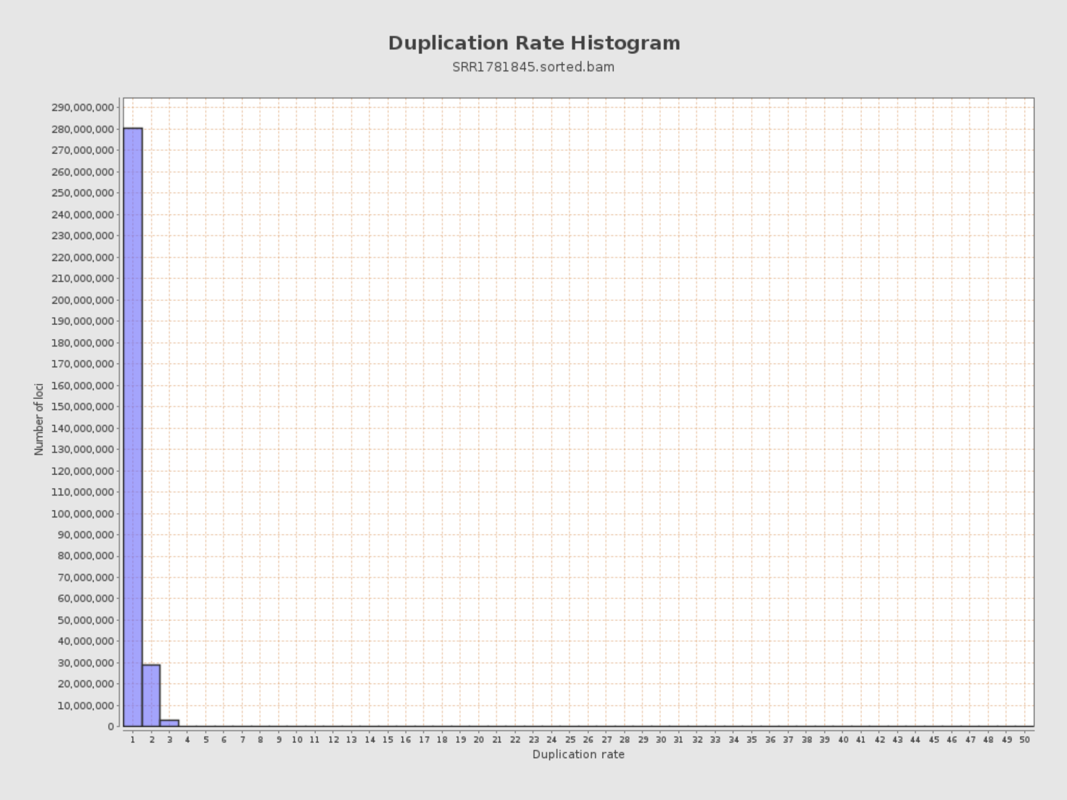
5. Results : Coverage Histogram (0-50X)



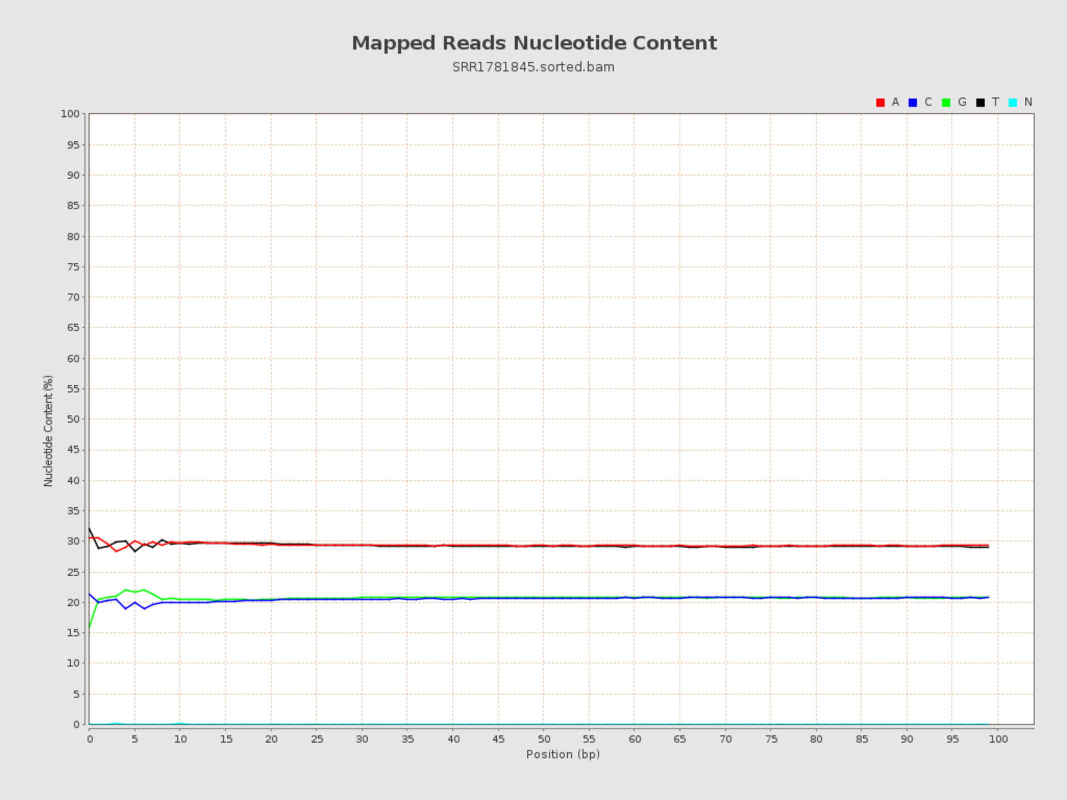
6. Results : Genome Fraction Coverage



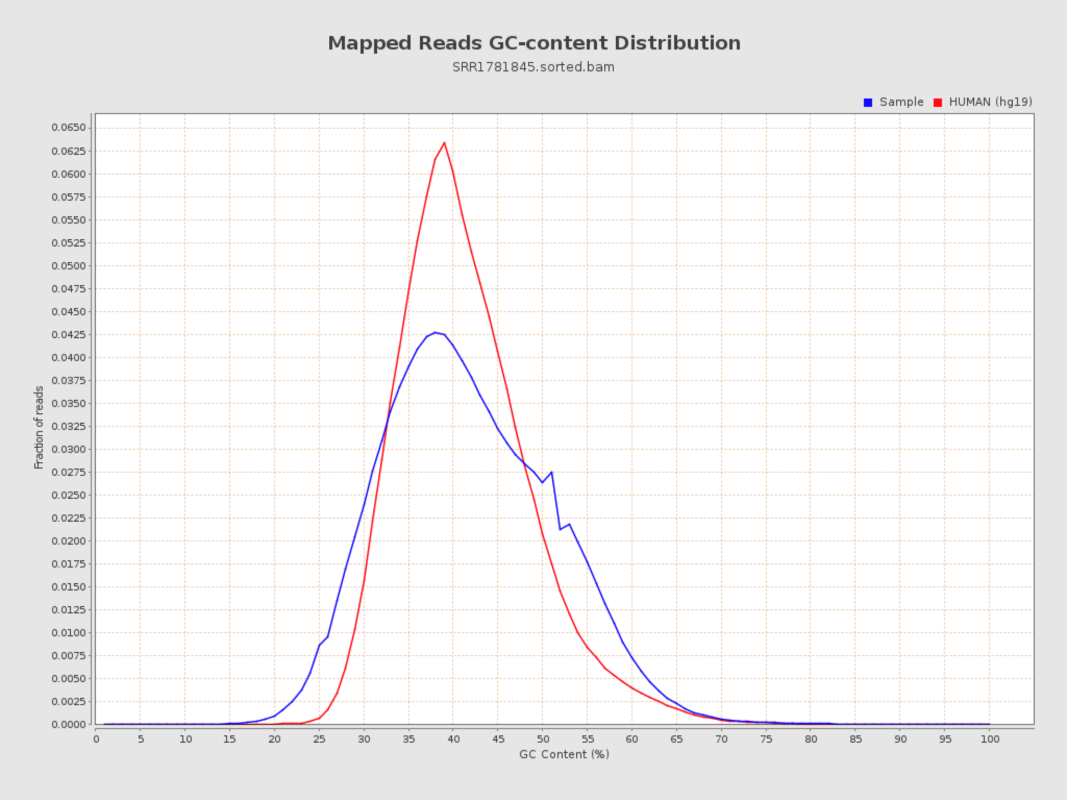
7. Results : Duplication Rate Histogram



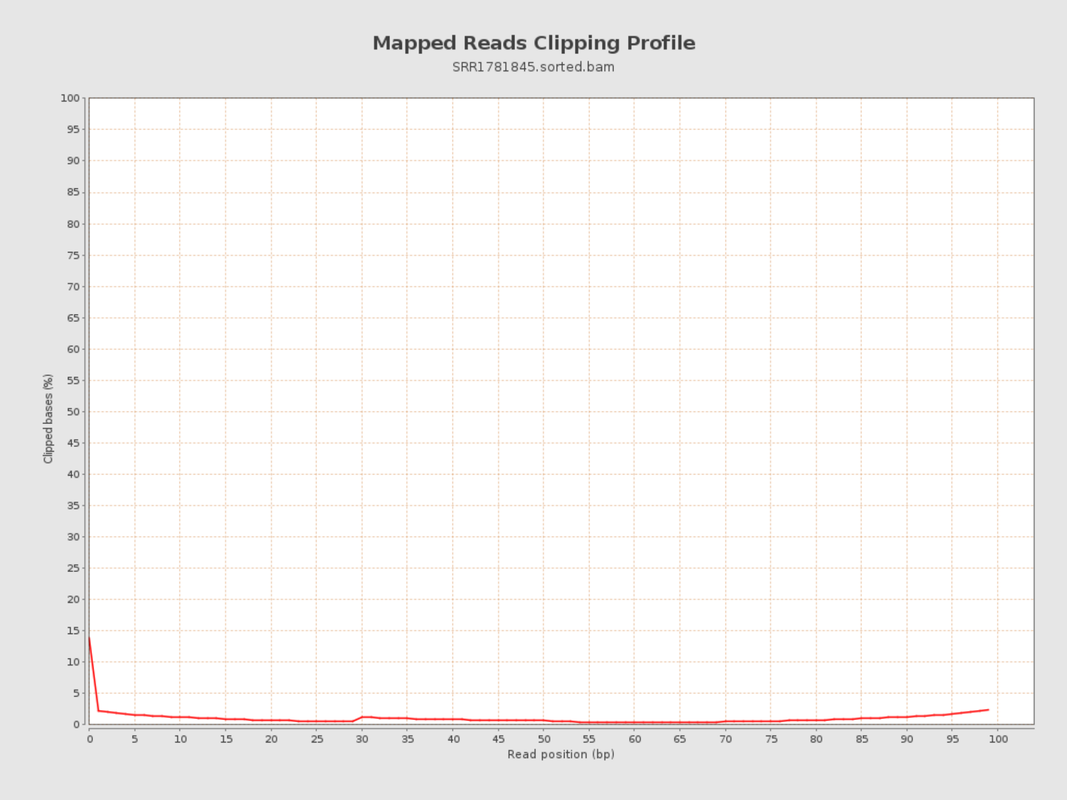
8. Results : Mapped Reads Nucleotide Content



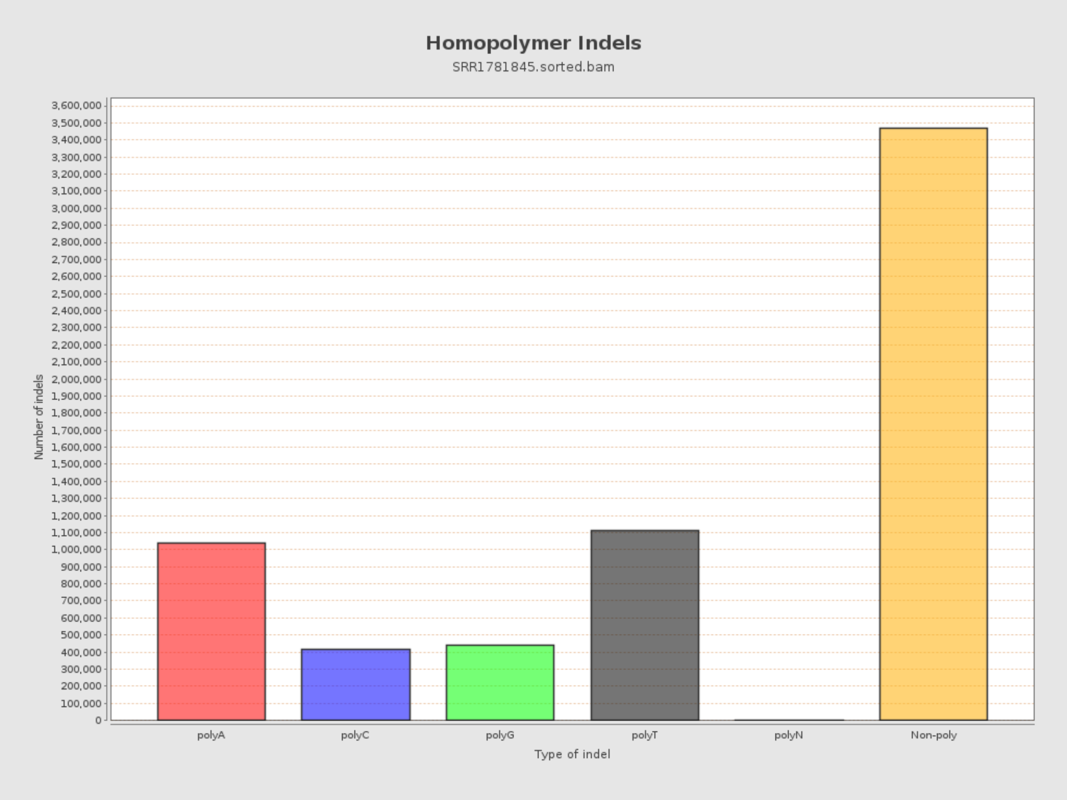
9. Results : Mapped Reads GC-content Distribution



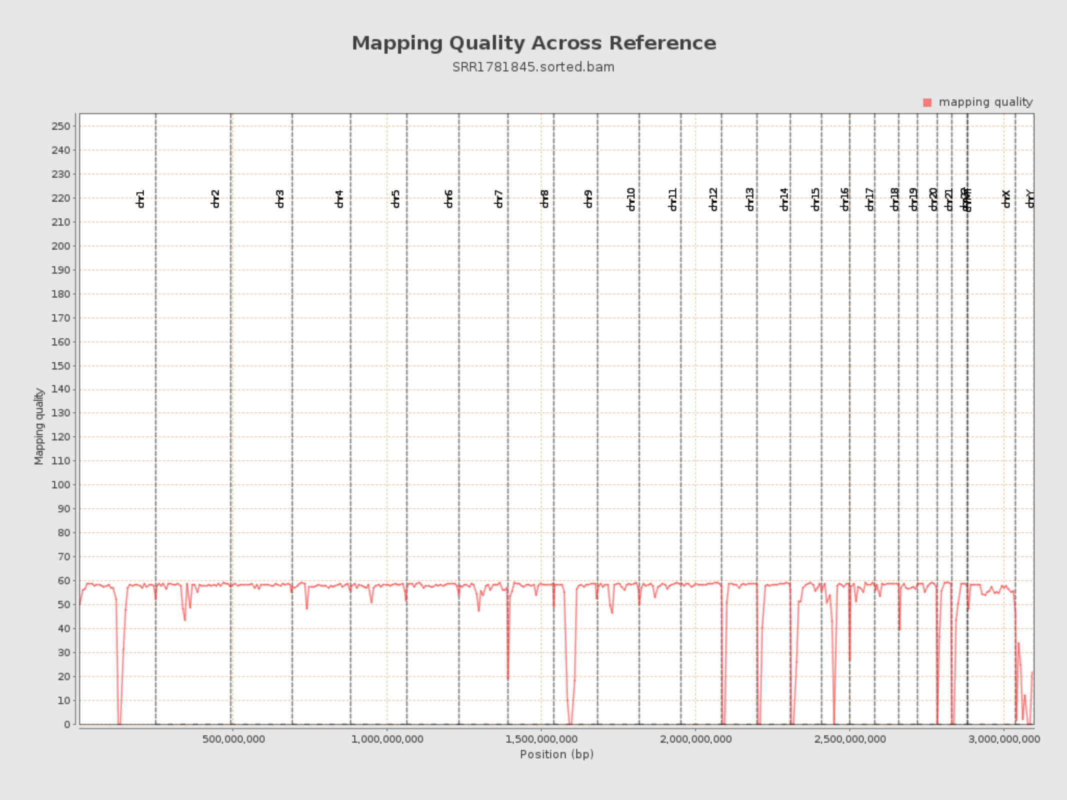
10. Results : Mapped Reads Clipping Profile



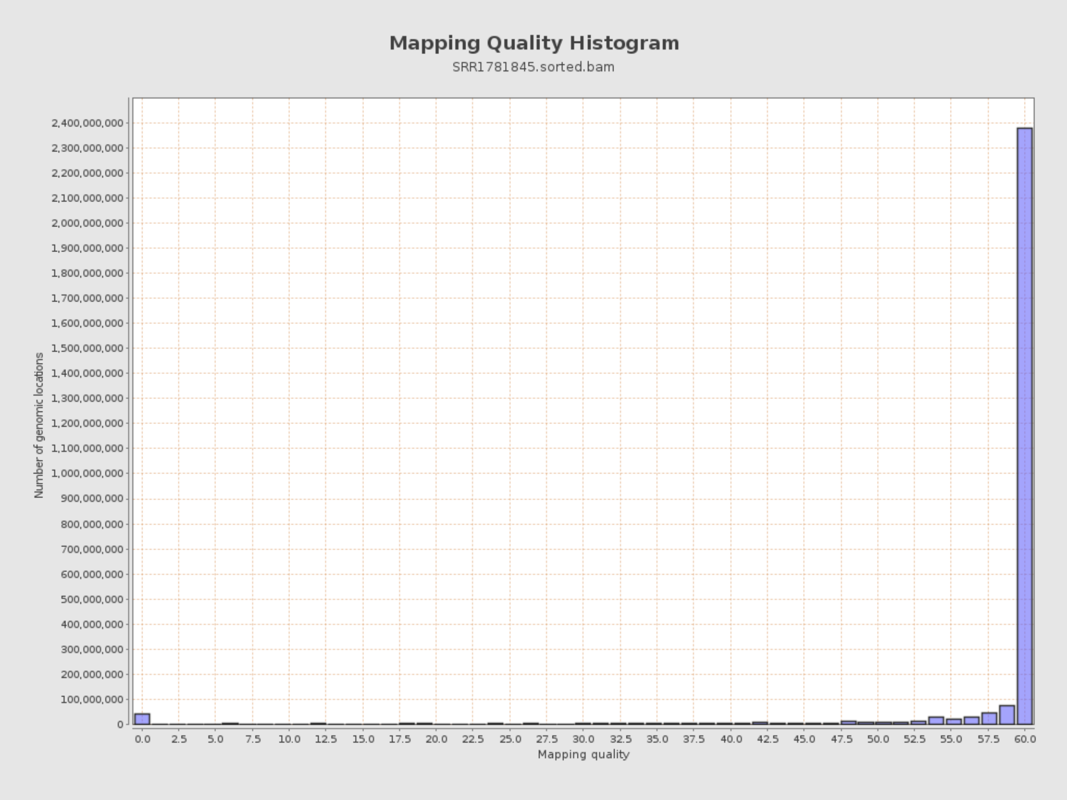
11. Results : Homopolymer Indels



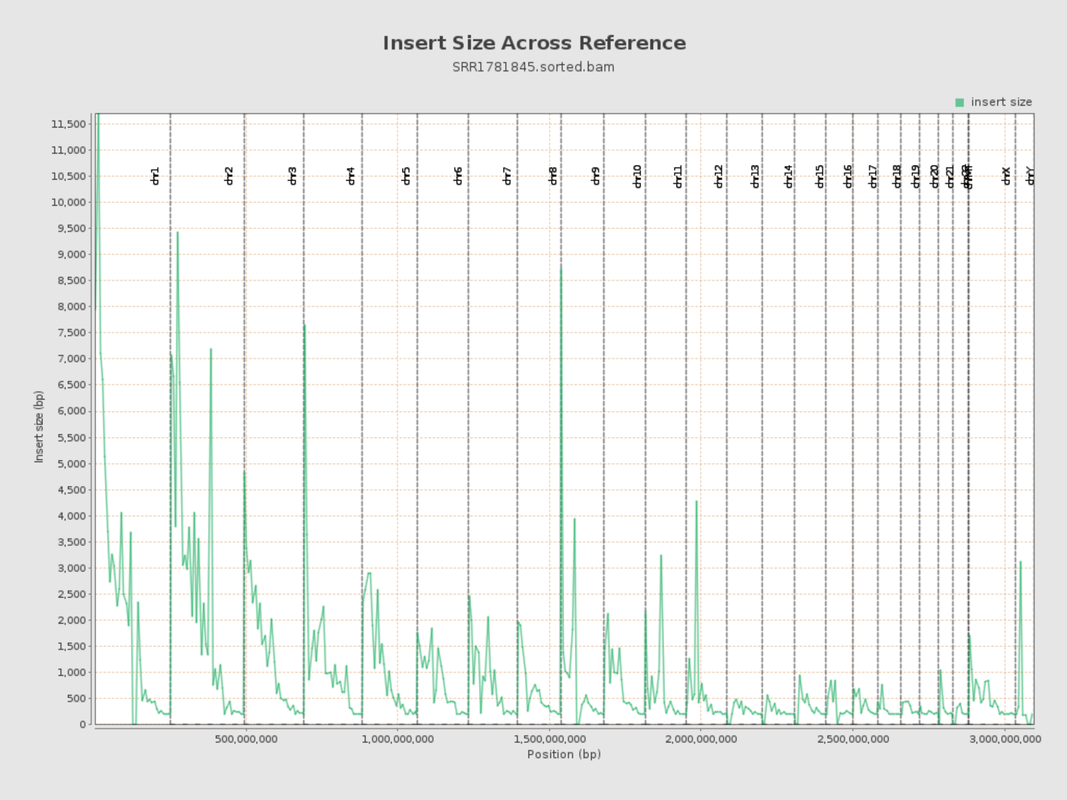
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram