Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 12:51:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124980.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_SRR3124980 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124980_1.fastq.gz SRR3124980_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 12:51:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124980.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,932,968
Mapped reads	5,801,136 / 97.78%
Unmapped reads	131,832 / 2.22%
Mapped paired reads	5,801,136 / 97.78%
Mapped reads, first in pair	2,907,943 / 49.01%
Mapped reads, second in pair	2,893,193 / 48.76%
Mapped reads, both in pair	5,768,568 / 97.23%
Mapped reads, singletons	32,568 / 0.55%
Secondary alignments	0
Supplementary alignments	58,267 / 0.98%
Read min/max/mean length	30 / 101 / 101.39
Duplicated reads (estimated)	878,324 / 14.8%
Duplication rate	10.43%
Clipped reads	3,276,396 / 55.22%

2.2. ACGT Content

Number/percentage of A's	142,186,610 / 28.92%
Number/percentage of C's	89,534,163 / 18.21%
Number/percentage of T's	149,011,780 / 30.31%
Number/percentage of G's	110,843,051 / 22.55%
Number/percentage of N's	5,358 / 0%

GC Percentage	40.76%

2.3. Coverage

Mean	0.1589
Standard Deviation	2.4728

2.4. Mapping Quality

Mean Mapping Quality	52.36

2.5. Insert size

Mean	83,350.54
Standard Deviation	2,717,580.77
P25/Median/P75	122 / 168 / 234

2.6. Mismatches and indels

General error rate	0.85%
Mismatches	3,978,784
Insertions	82,778
Mapped reads with at least one insertion	1.38%
Deletions	165,858
Mapped reads with at least one deletion	2.79%
Homopolymer indels	45.37%

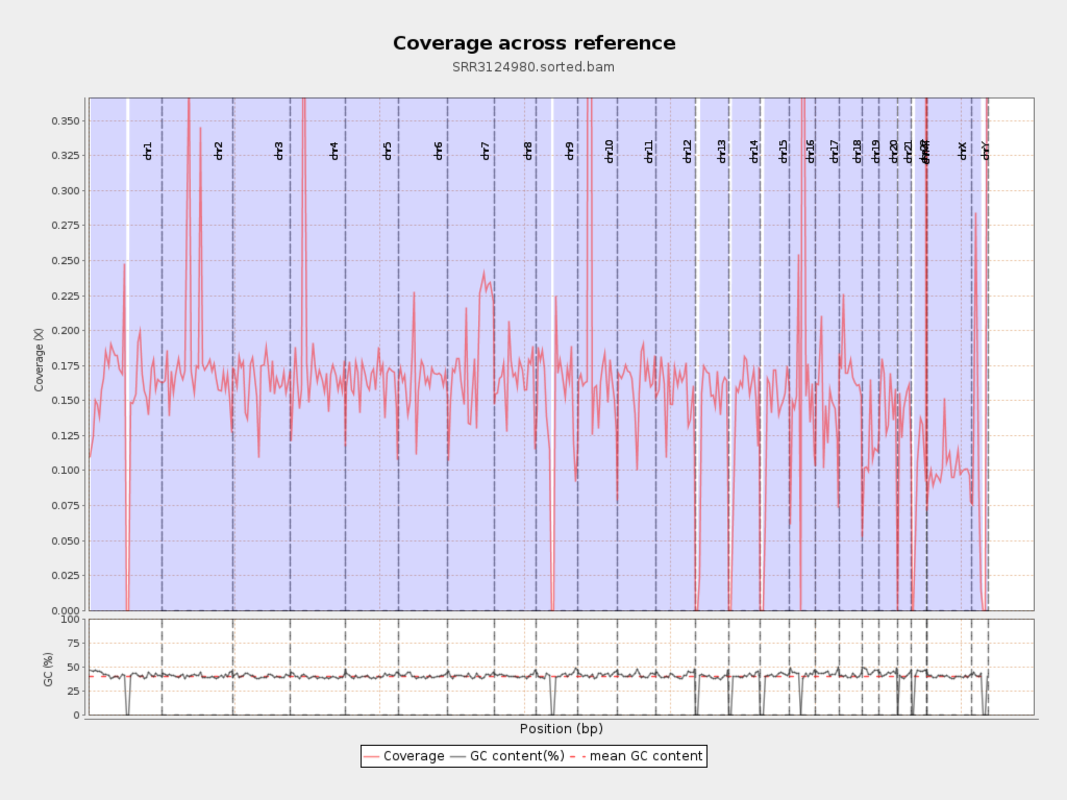
2.7. Chromosome stats

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

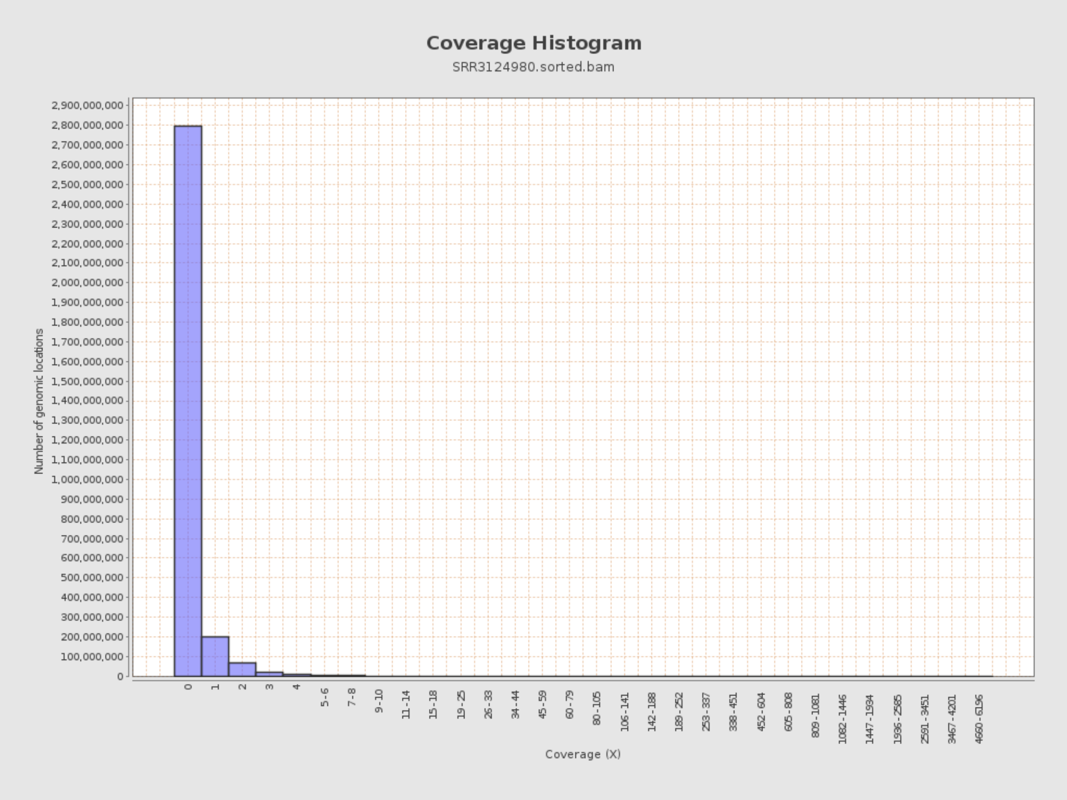
		bases	coverage	deviation
chr1	249250621	38827744	0.1558	1.5817
chr2	243199373	44539933	0.1831	2.6073
chr3	198022430	32568067	0.1645	0.6882
chr4	191154276	33975038	0.1777	1.9751
chr5	180915260	29758939	0.1645	0.637
chr6	171115067	28400106	0.166	0.9172
chr7	159138663	29324960	0.1843	1.3191
chr8	146364022	24369992	0.1665	0.7708
chr9	141213431	20464884	0.1449	1.9948
chr10	135534747	29512036	0.2177	9.0639
chr11	135006516	22025964	0.1631	1.0781
chr12	133851895	20946036	0.1565	0.5784
chr13	115169878	15285371	0.1327	0.5284
chr14	107349540	14280683	0.133	0.654
chr15	102531392	13158970	0.1283	0.5358
chr16	90354753	16746906	0.1853	3.8119
chr17	81195210	11663904	0.1437	1.5183
chr18	78077248	13532518	0.1733	2.2587
chr19	59128983	6639985	0.1123	0.9448
chr20	63025520	9410784	0.1493	0.7693
chr21	48129895	6297693	0.1308	0.944
chr22	51304566	4308952	0.084	0.5145
chrMT	16571	2160392	130.3719	74.5107
chrX	155270560	15643862	0.1008	0.6906

chrY	59373566	8051756	0.1356	3.5103

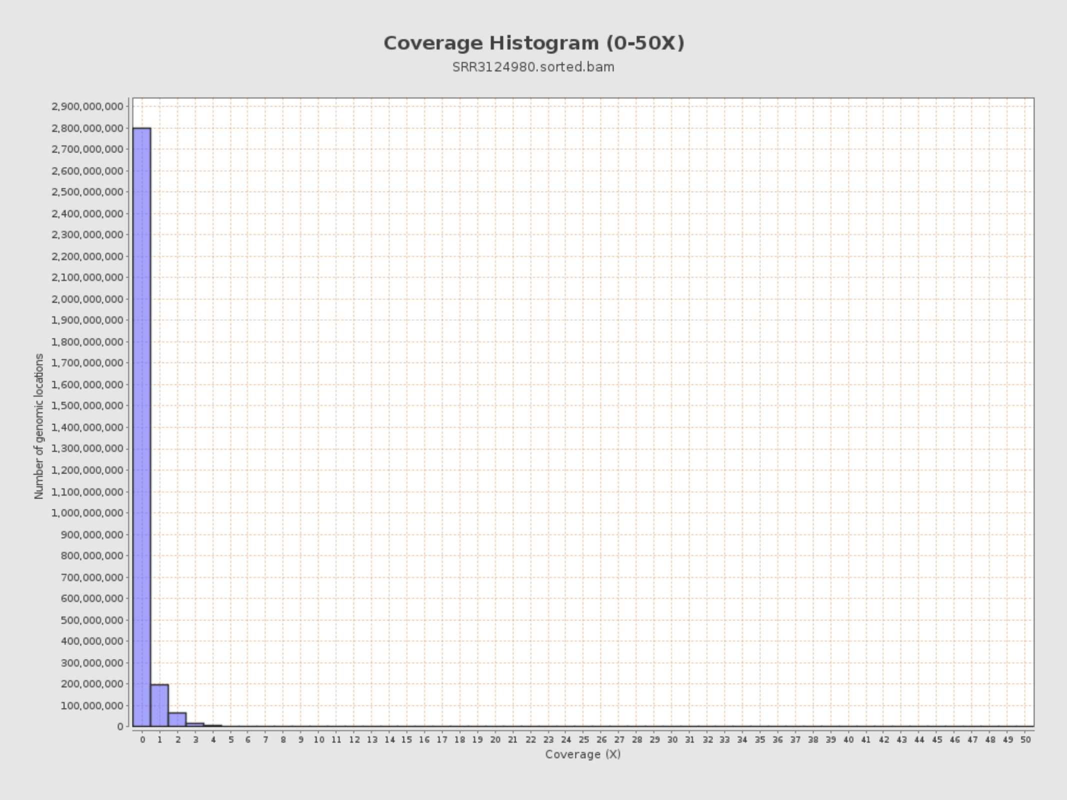
3. Results : Coverage across reference



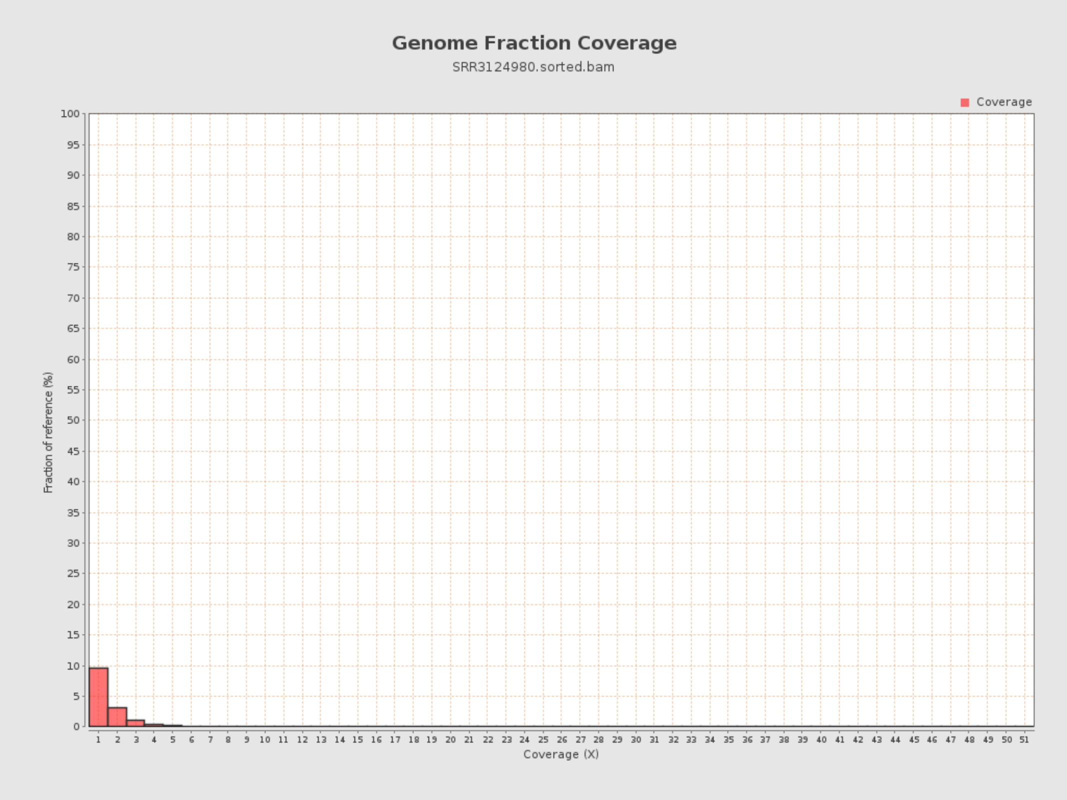
4. Results : Coverage Histogram



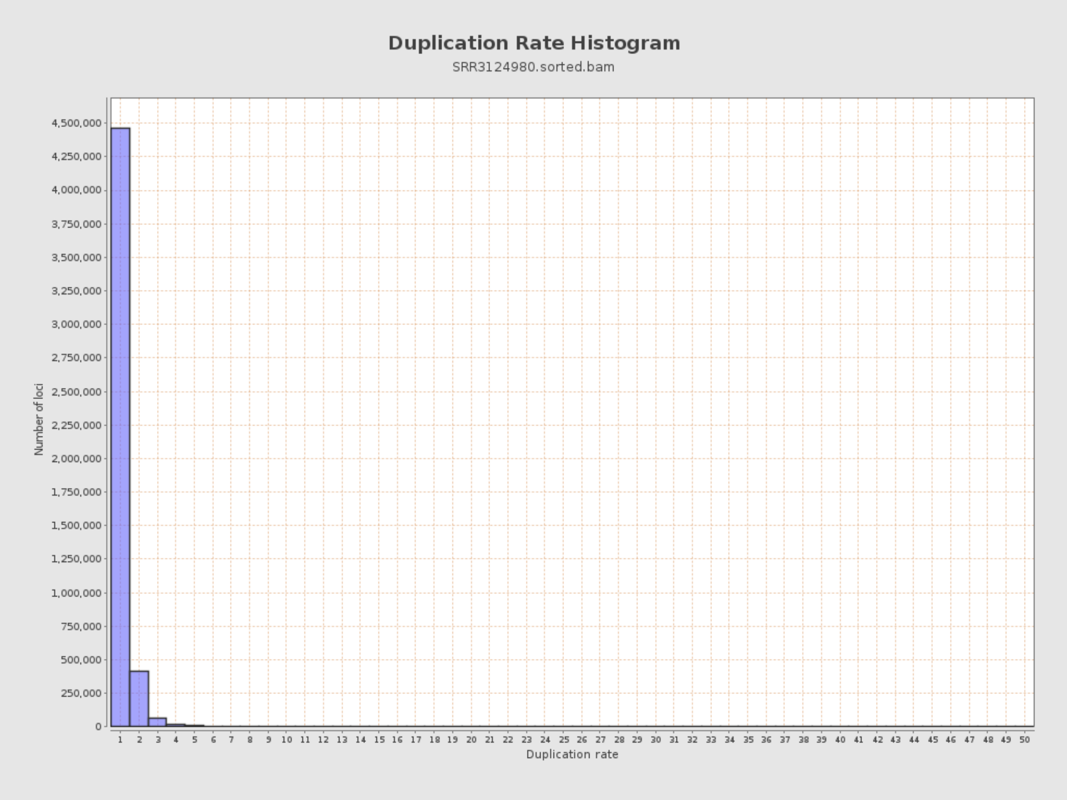
5. Results : Coverage Histogram (0-50X)



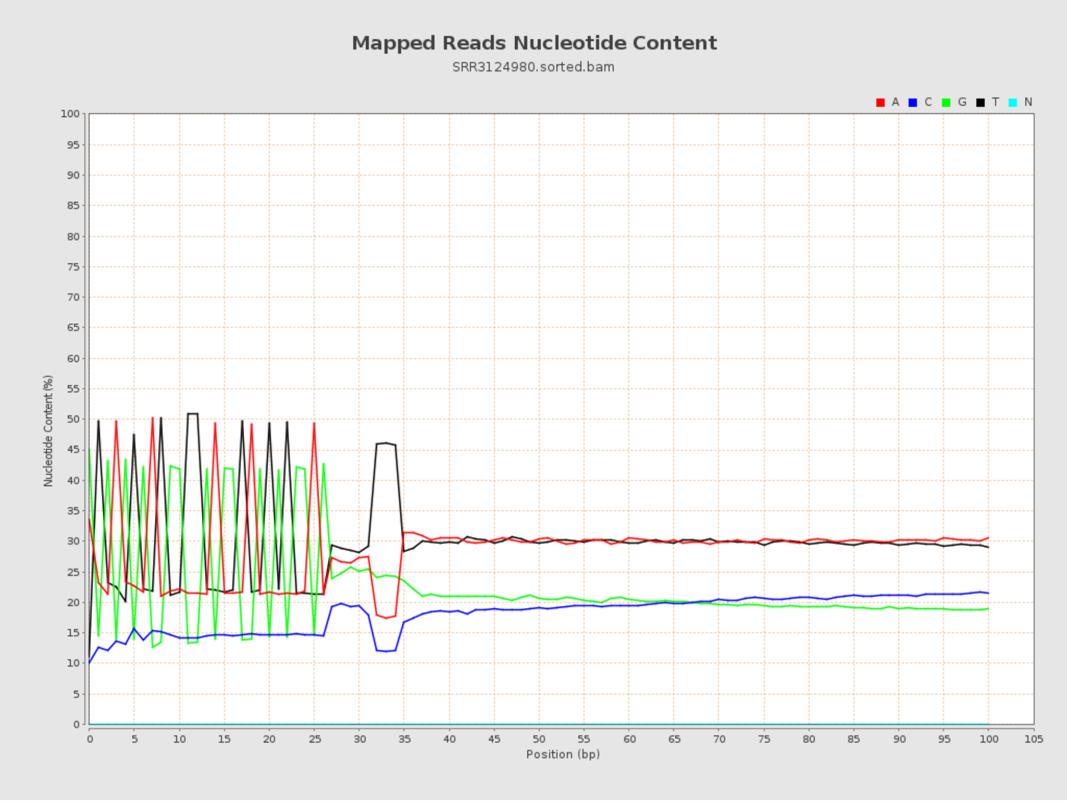
6. Results : Genome Fraction Coverage



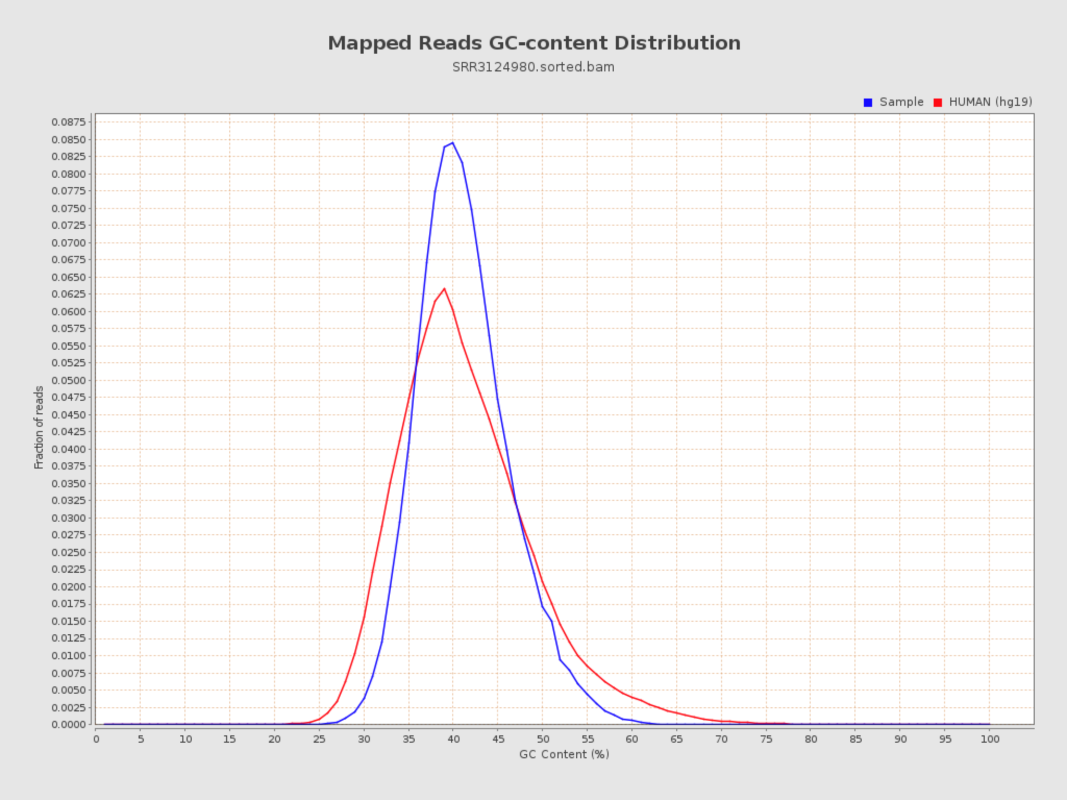
7. Results : Duplication Rate Histogram



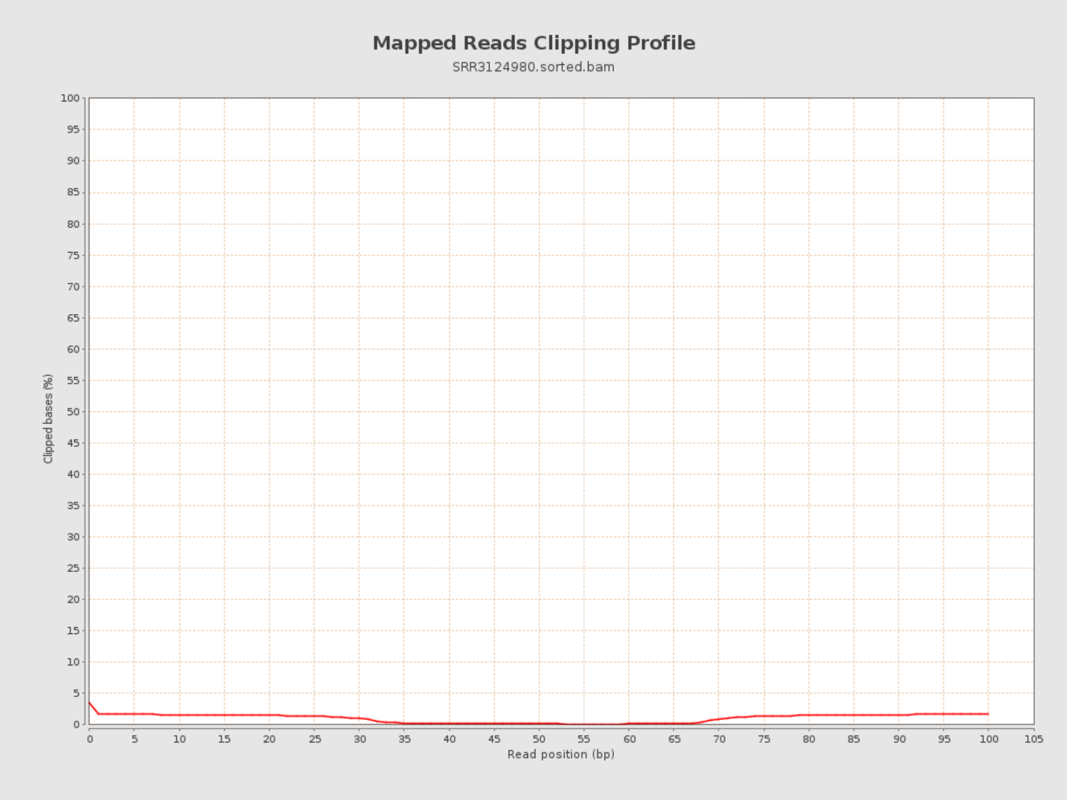
8. Results : Mapped Reads Nucleotide Content



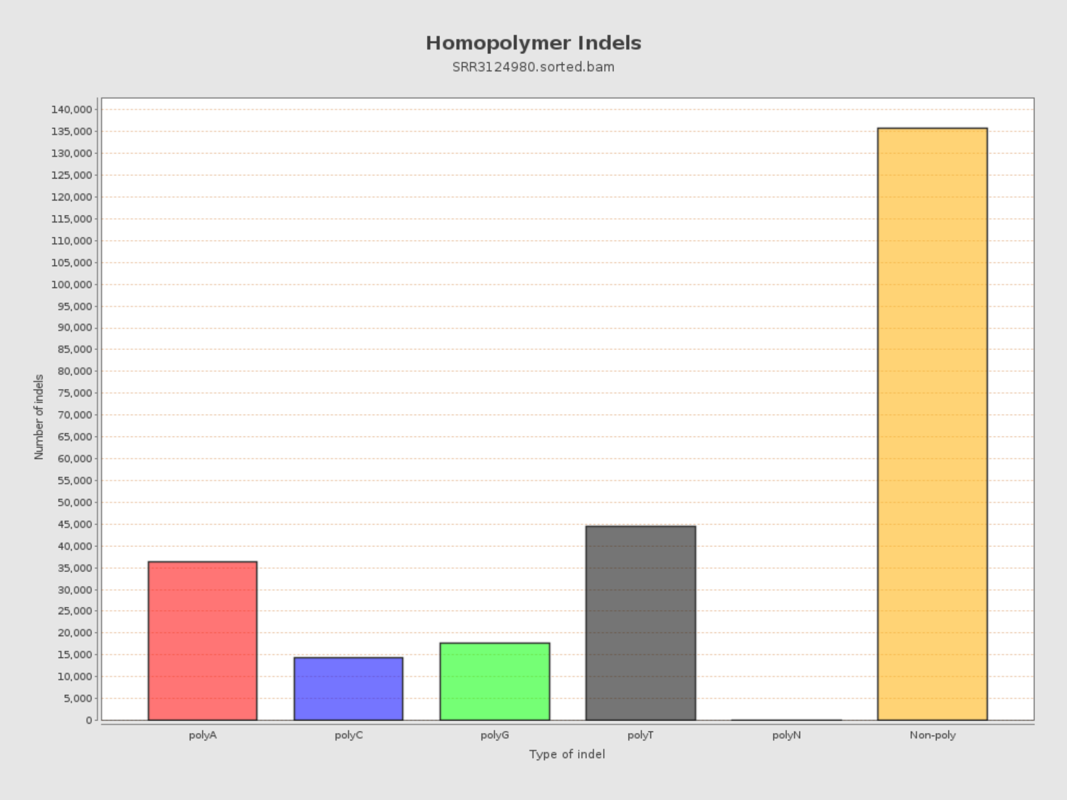
9. Results : Mapped Reads GC-content Distribution



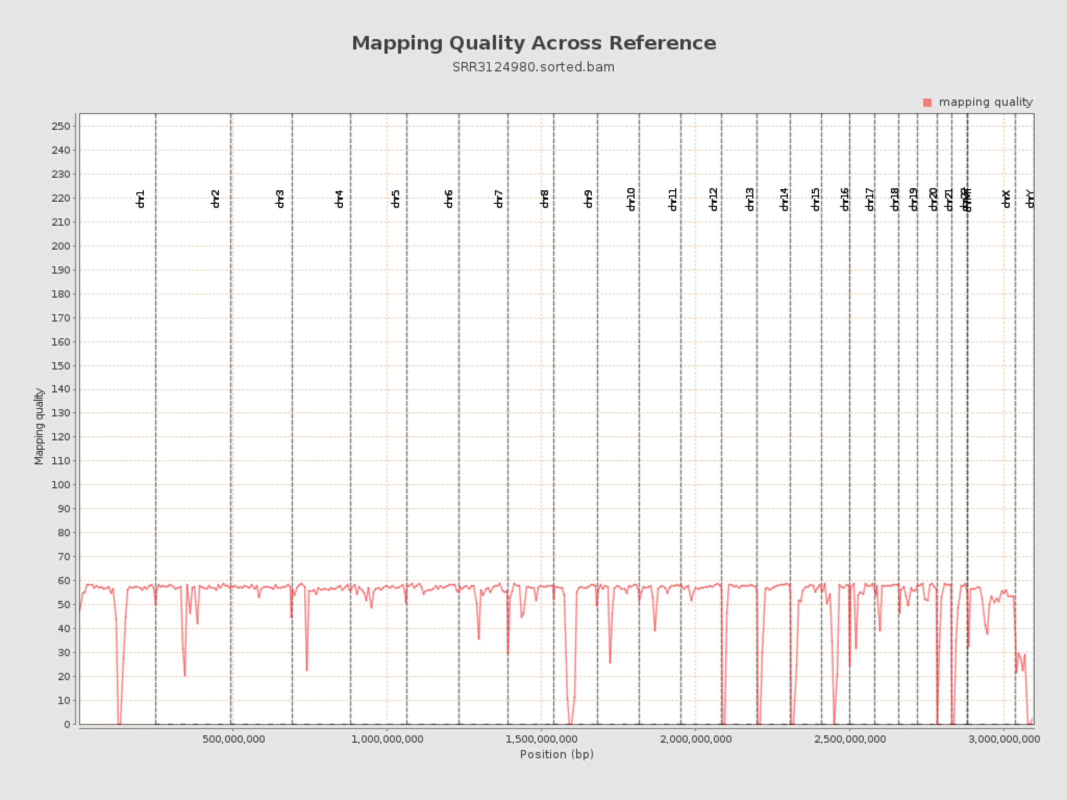
10. Results : Mapped Reads Clipping Profile



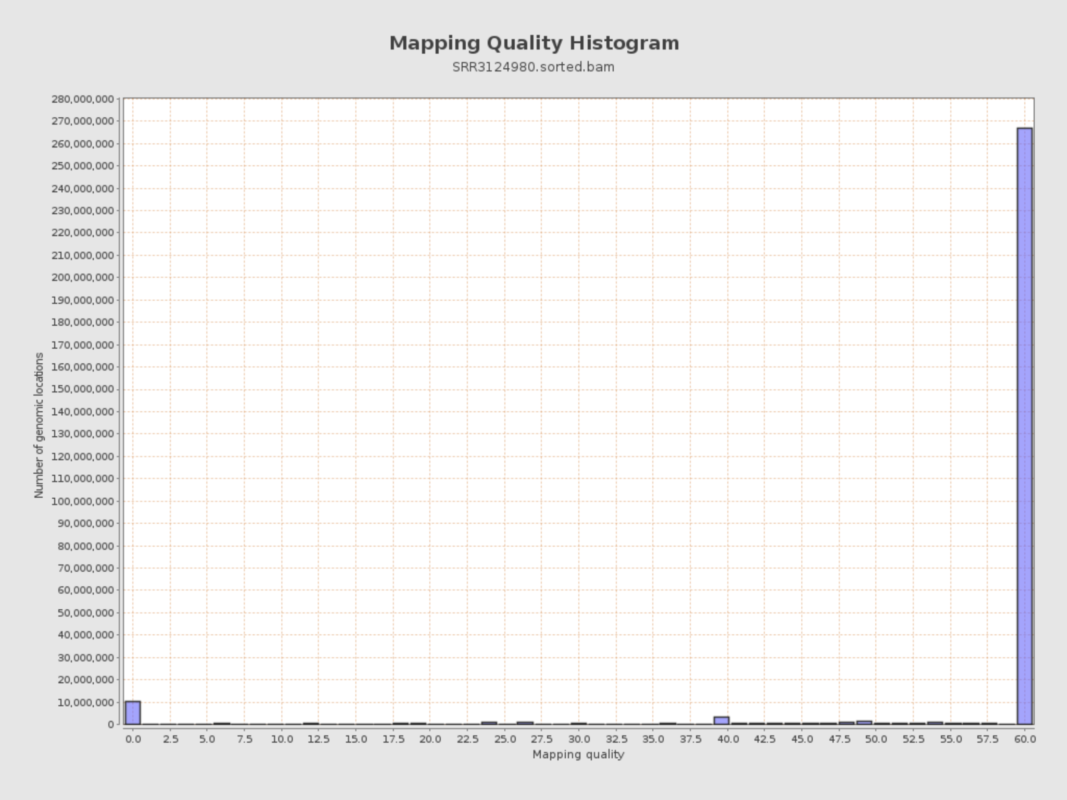
11. Results : Homopolymer Indels



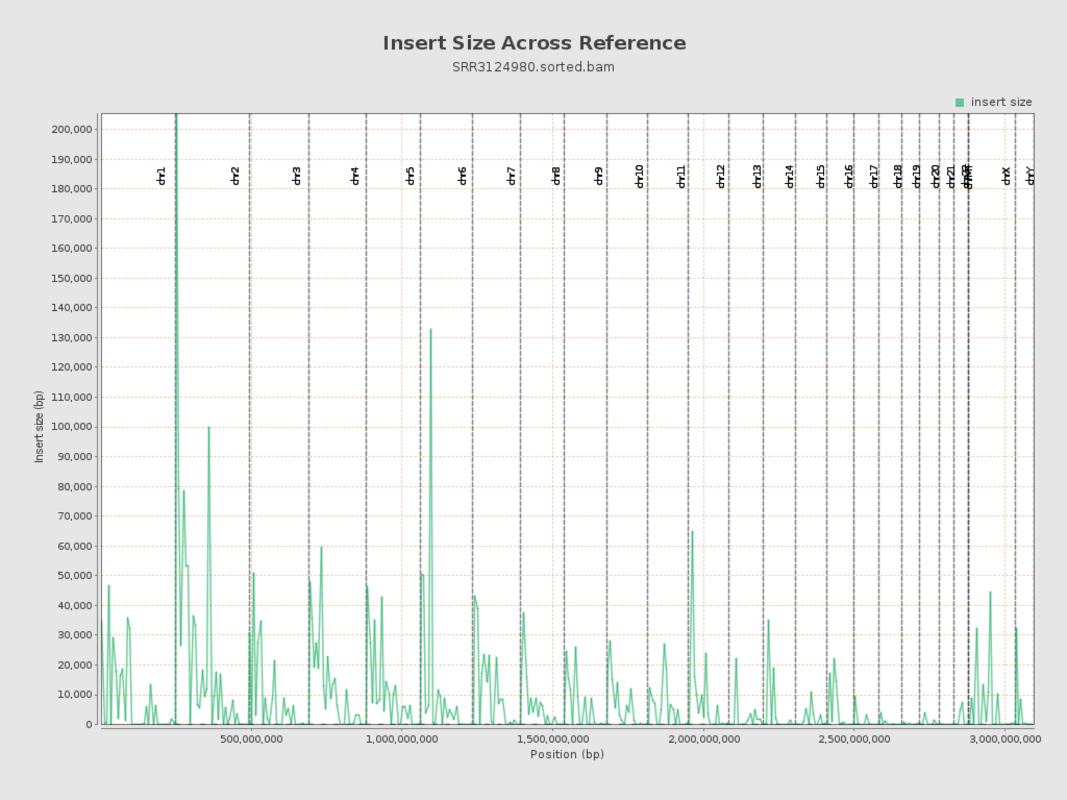
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram