Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 00:56:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124884.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_SRR3124884 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124884_1.fastq.gz SRR3124884_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 00:56:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124884.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,579,268
Mapped reads	5,421,286 / 97.17%
Unmapped reads	157,982 / 2.83%
Mapped paired reads	5,421,286 / 97.17%
Mapped reads, first in pair	2,757,142 / 49.42%
Mapped reads, second in pair	2,664,144 / 47.75%
Mapped reads, both in pair	5,315,040 / 95.26%
Mapped reads, singletons	106,246 / 1.9%
Secondary alignments	0
Supplementary alignments	5,559 / 0.1%
Read min/max/mean length	30 / 76 / 76.04
Duplicated reads (estimated)	273,383 / 4.9%
Duplication rate	3.75%
Clipped reads	2,407,142 / 43.14%

2.2. ACGT Content

Number/percentage of A's	92,635,597 / 27.32%
Number/percentage of C's	61,424,327 / 18.11%
Number/percentage of T's	100,880,202 / 29.75%
Number/percentage of G's	84,150,821 / 24.82%
Number/percentage of N's	2,707 / 0%

GC Percentage	42.93%

2.3. Coverage

Mean	0.1096
Standard Deviation	0.7025

2.4. Mapping Quality

Mean Mapping Quality	51.94

2.5. Insert size

Mean	27,840.44
Standard Deviation	1,598,669.93
P25/Median/P75	156 / 211 / 289

2.6. Mismatches and indels

General error rate	0.63%
Mismatches	2,073,935
Insertions	33,044
Mapped reads with at least one insertion	0.6%
Deletions	87,287
Mapped reads with at least one deletion	1.59%
Homopolymer indels	50%

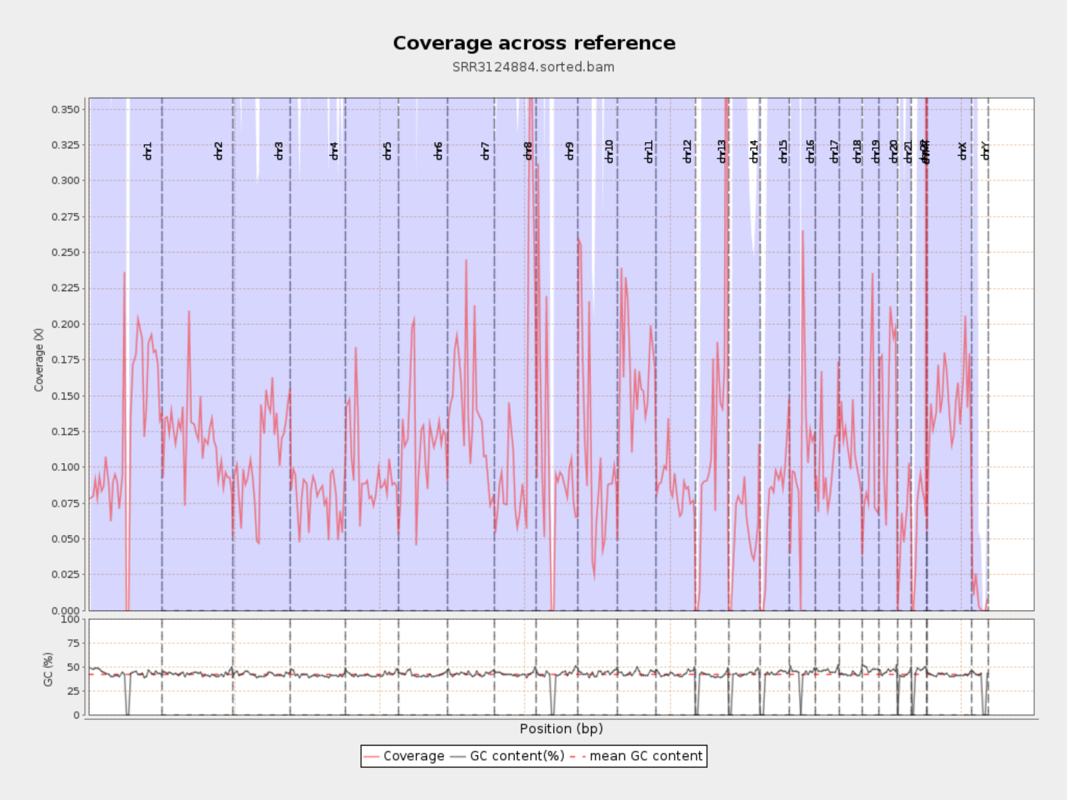
2.7. Chromosome stats

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

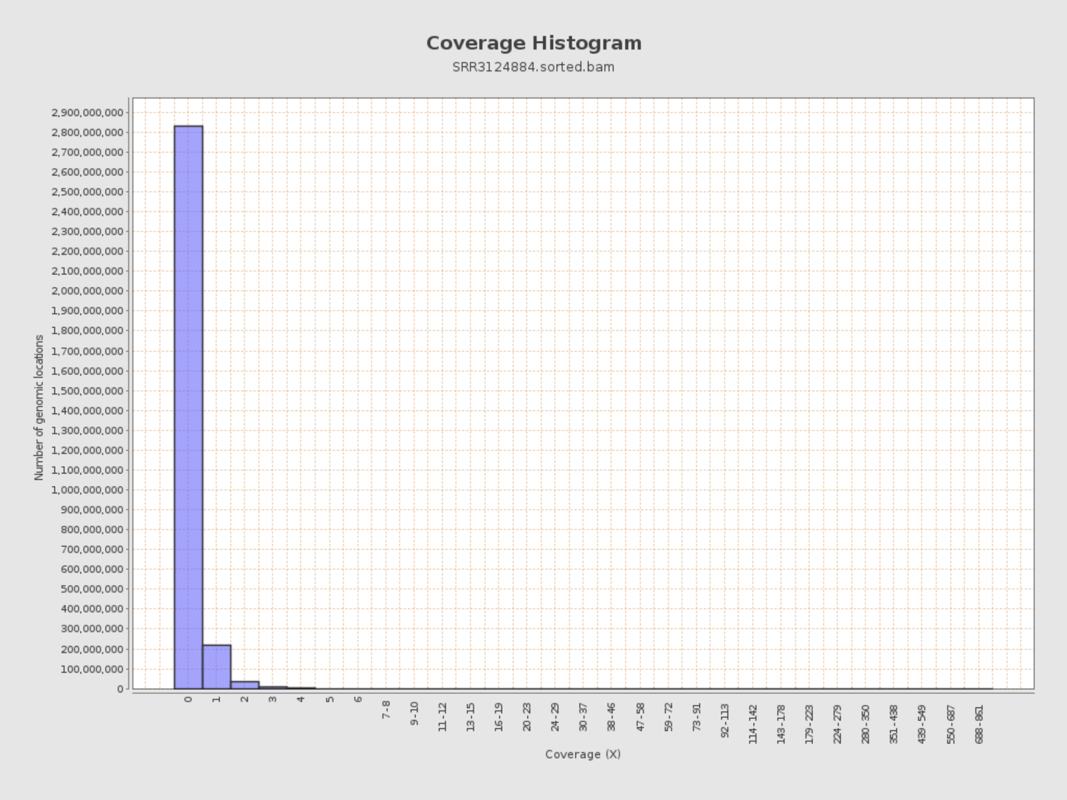
		bases	coverage	deviation
chr1	249250621	30500647	0.1224	0.9673
chr2	243199373	29212773	0.1201	0.765
chr3	198022430	21525050	0.1087	0.3885
chr4	191154276	15016051	0.0786	0.3793
chr5	180915260	17755585	0.0981	0.3659
chr6	171115067	20444665	0.1195	0.653
chr7	159138663	22356205	0.1405	1.0934
chr8	146364022	19120582	0.1306	0.5187
chr9	141213431	14134863	0.1001	0.6085
chr10	135534747	14637847	0.108	1.3426
chr11	135006516	22229609	0.1647	0.6497
chr12	133851895	11571651	0.0865	0.3437
chr13	115169878	15627836	0.1357	0.5677
chr14	107349540	5703676	0.0531	0.3038
chr15	102531392	7610113	0.0742	0.3326
chr16	90354753	9814216	0.1086	1.0799
chr17	81195210	8347773	0.1028	0.6884
chr18	78077248	8961412	0.1148	0.9862
chr19	59128983	6308297	0.1067	0.7978
chr20	63025520	9613181	0.1525	0.4737
chr21	48129895	2813517	0.0585	0.2994
chr22	51304566	2891237	0.0564	0.2733
chrMT	16571	44890	2.7089	2.7897
chrX	155270560	22497541	0.1449	0.5782

chrY	59373566	482666	0.0081	0.3099

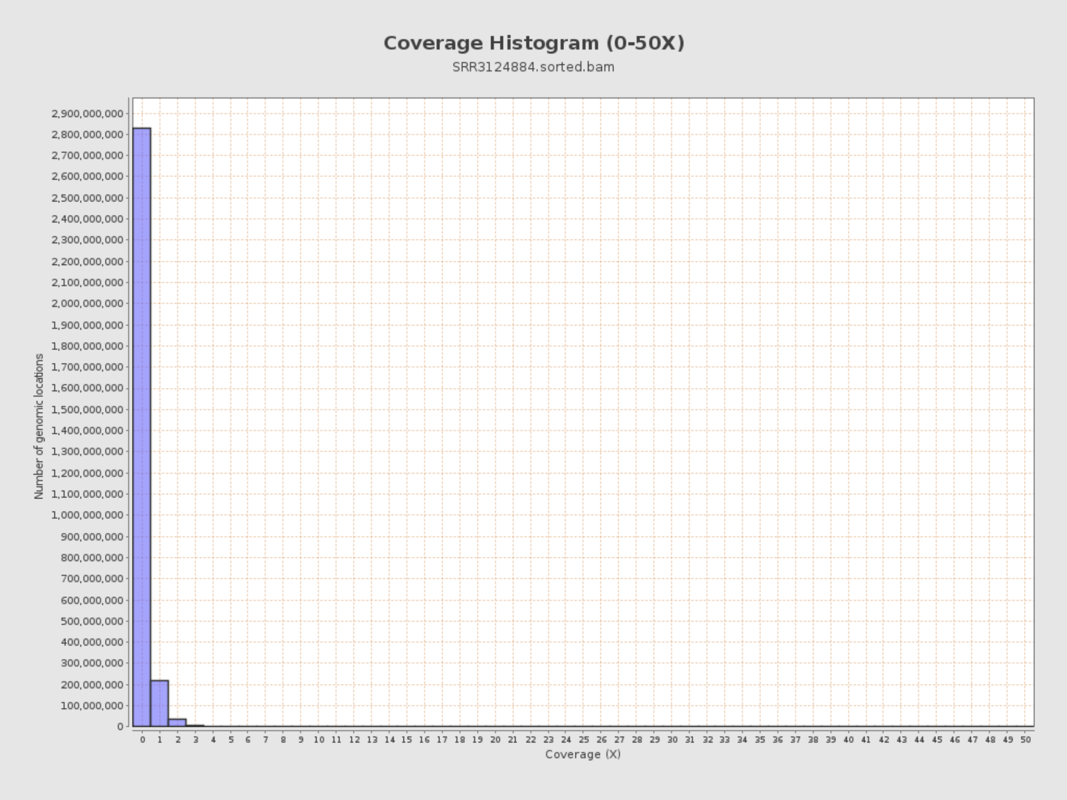
3. Results : Coverage across reference



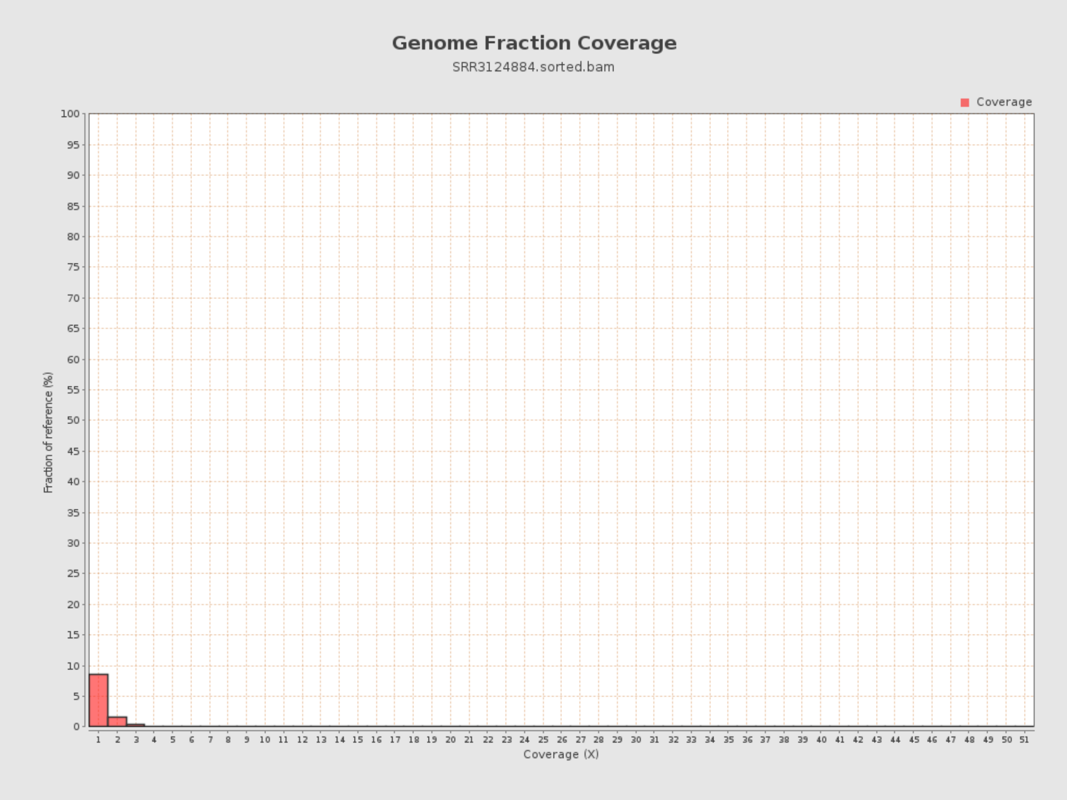
4. Results : Coverage Histogram



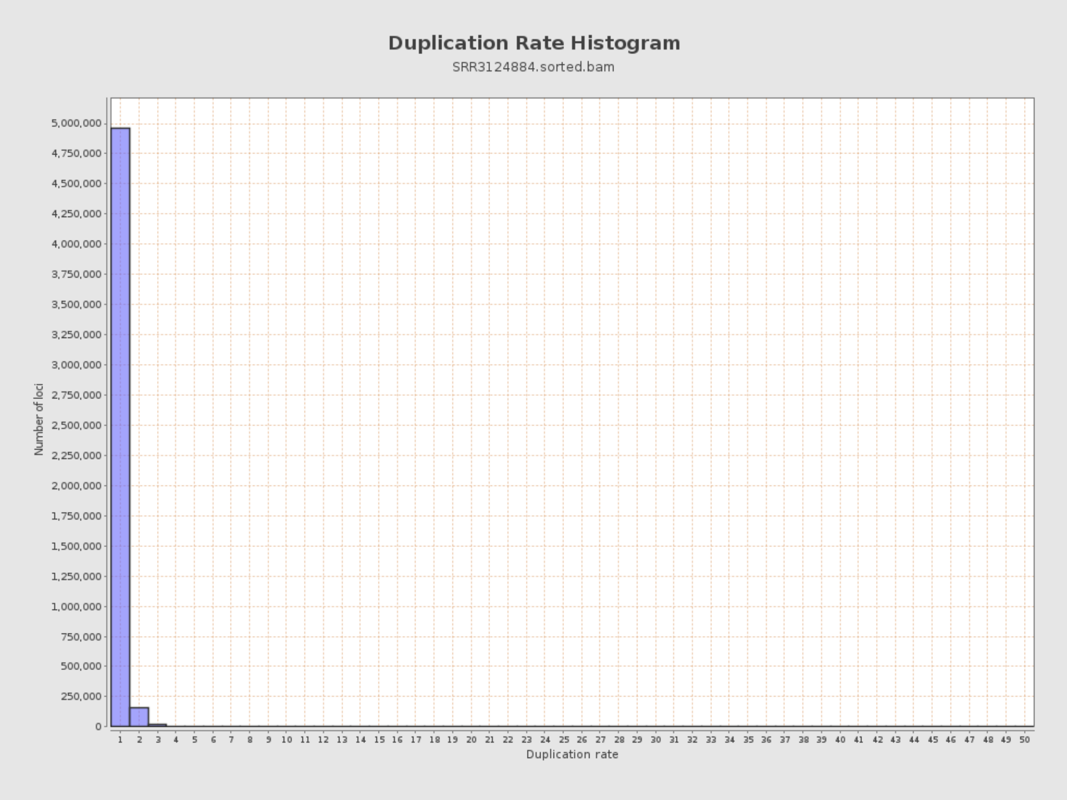
5. Results : Coverage Histogram (0-50X)



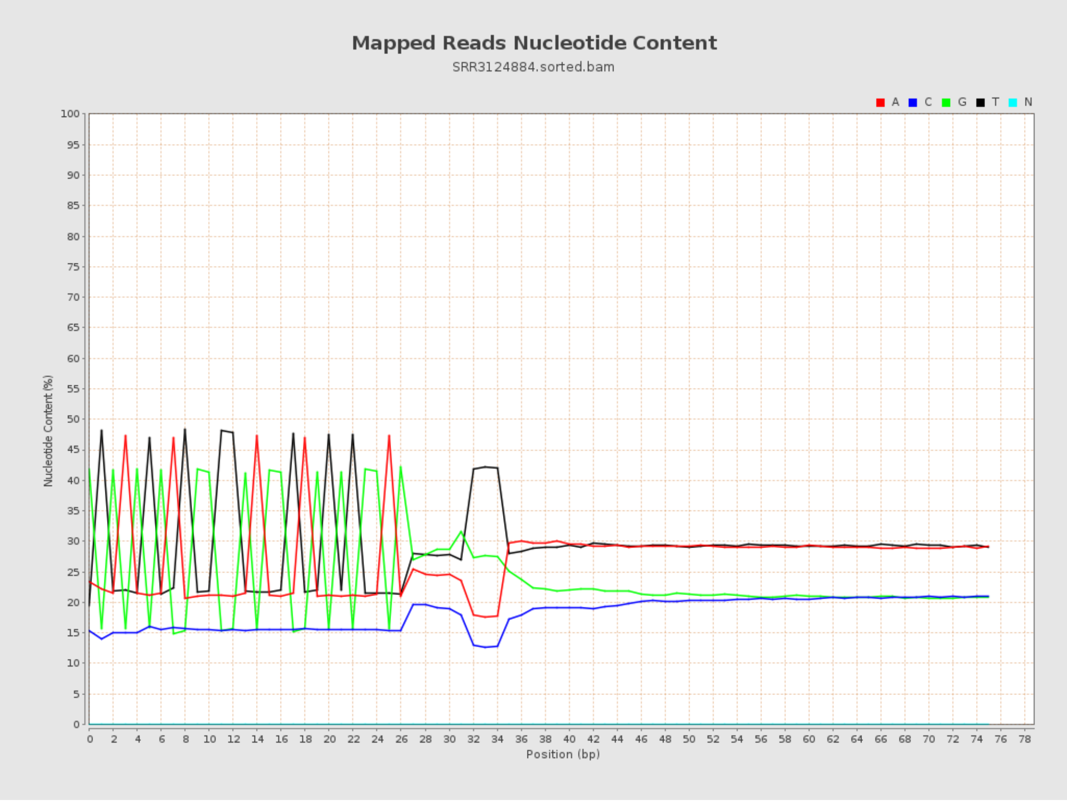
6. Results : Genome Fraction Coverage



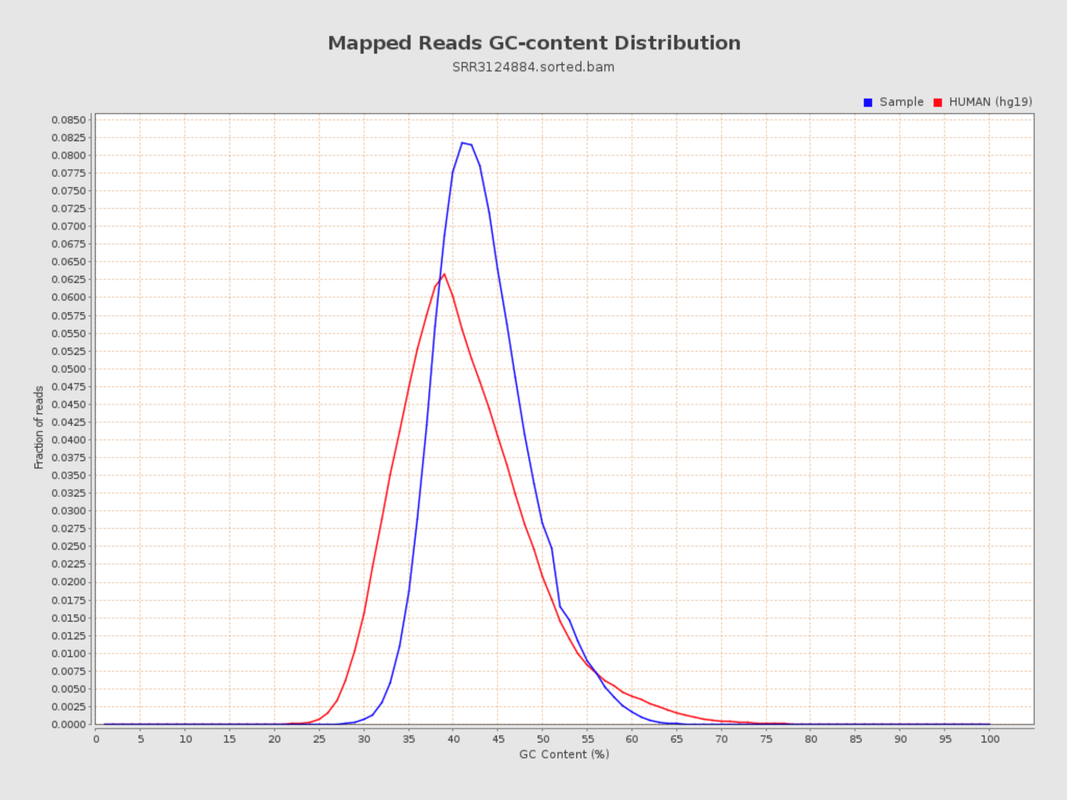
7. Results : Duplication Rate Histogram



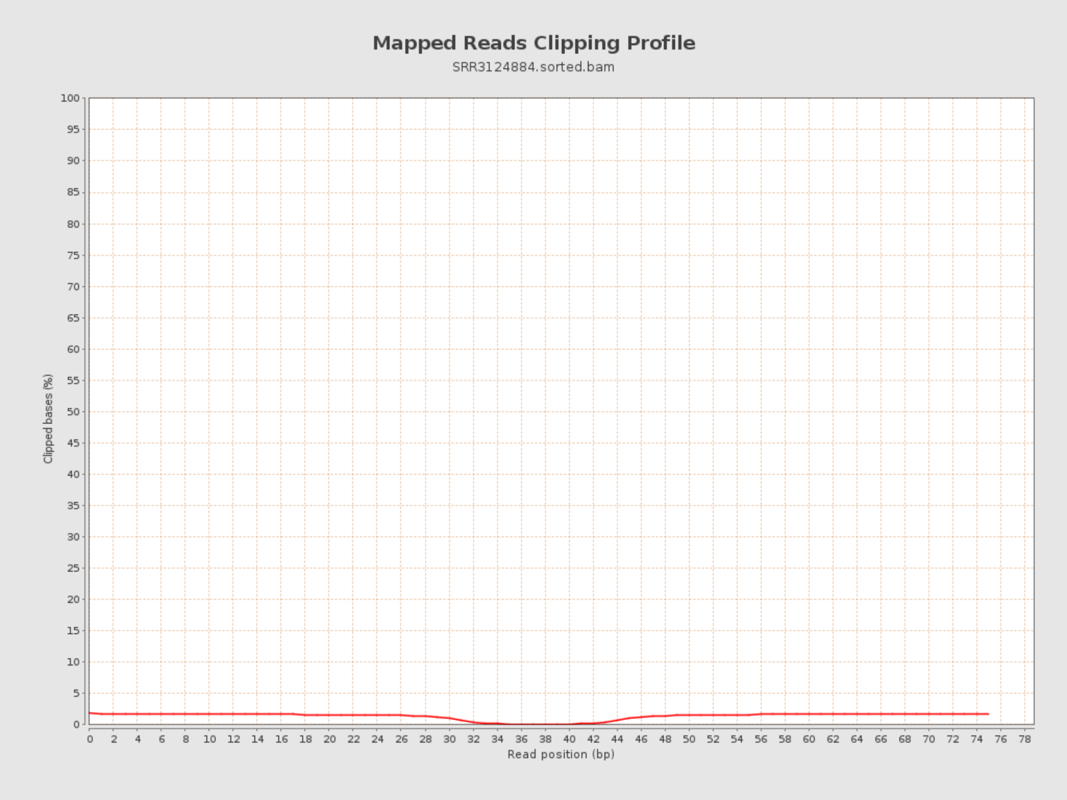
8. Results : Mapped Reads Nucleotide Content



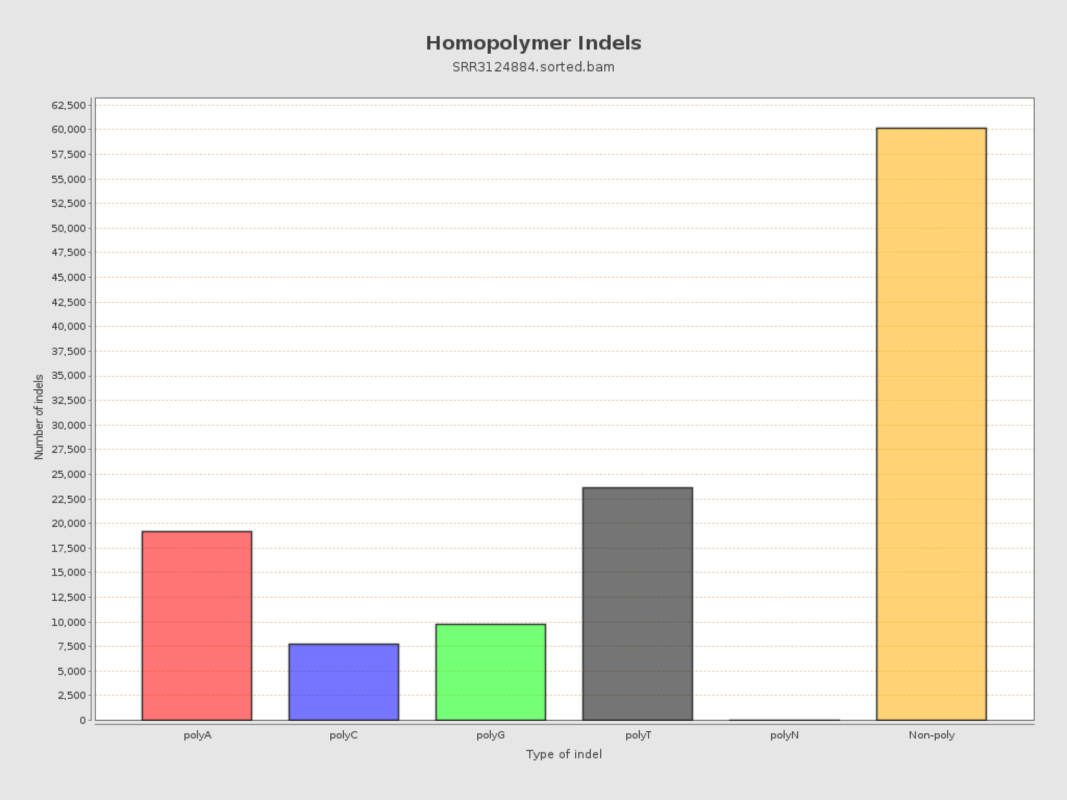
9. Results : Mapped Reads GC-content Distribution



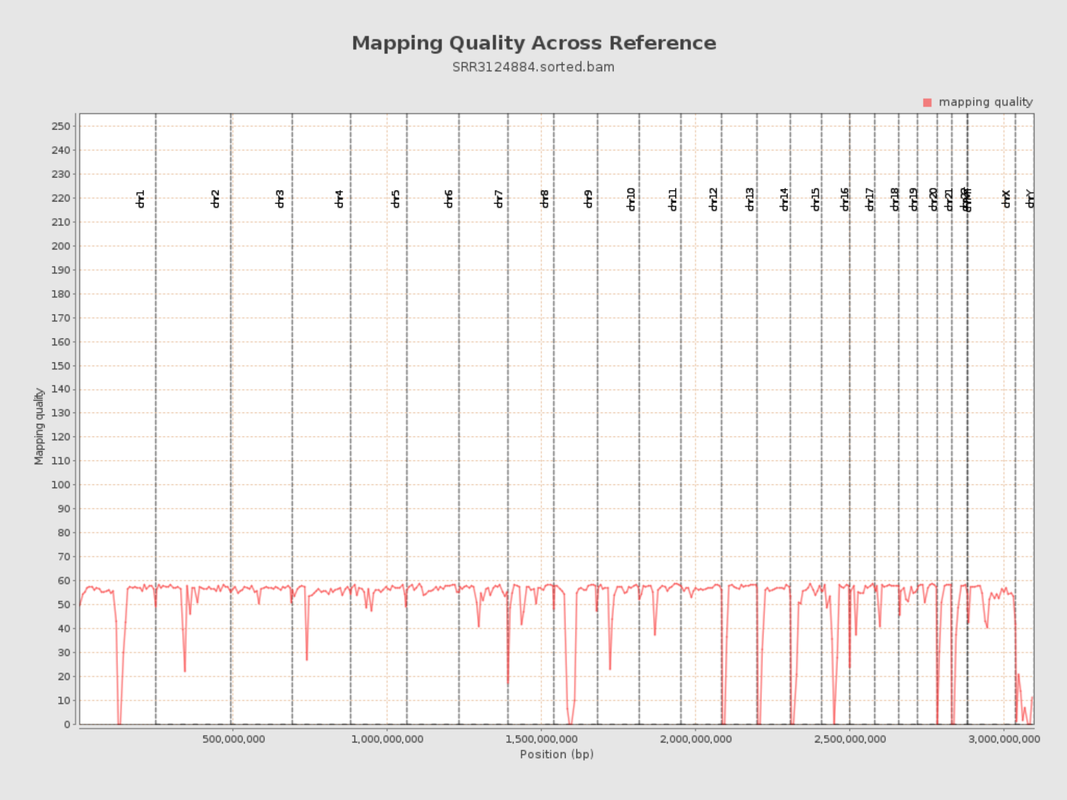
10. Results : Mapped Reads Clipping Profile



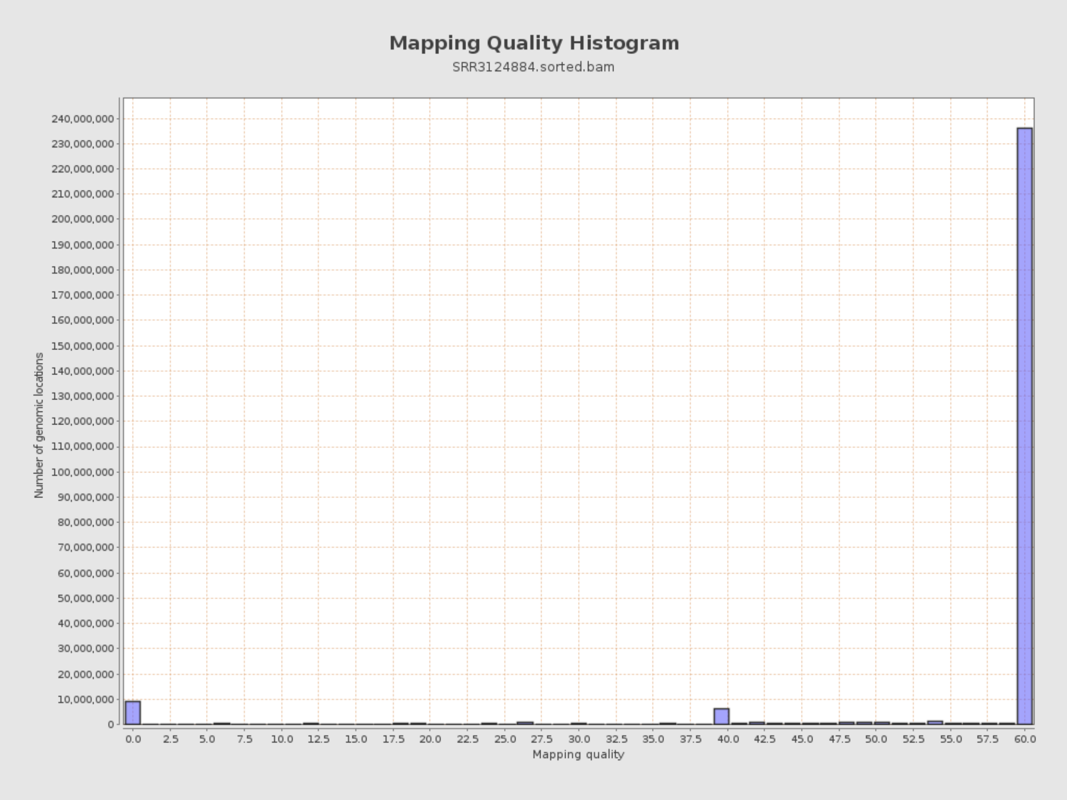
11. Results : Homopolymer Indels



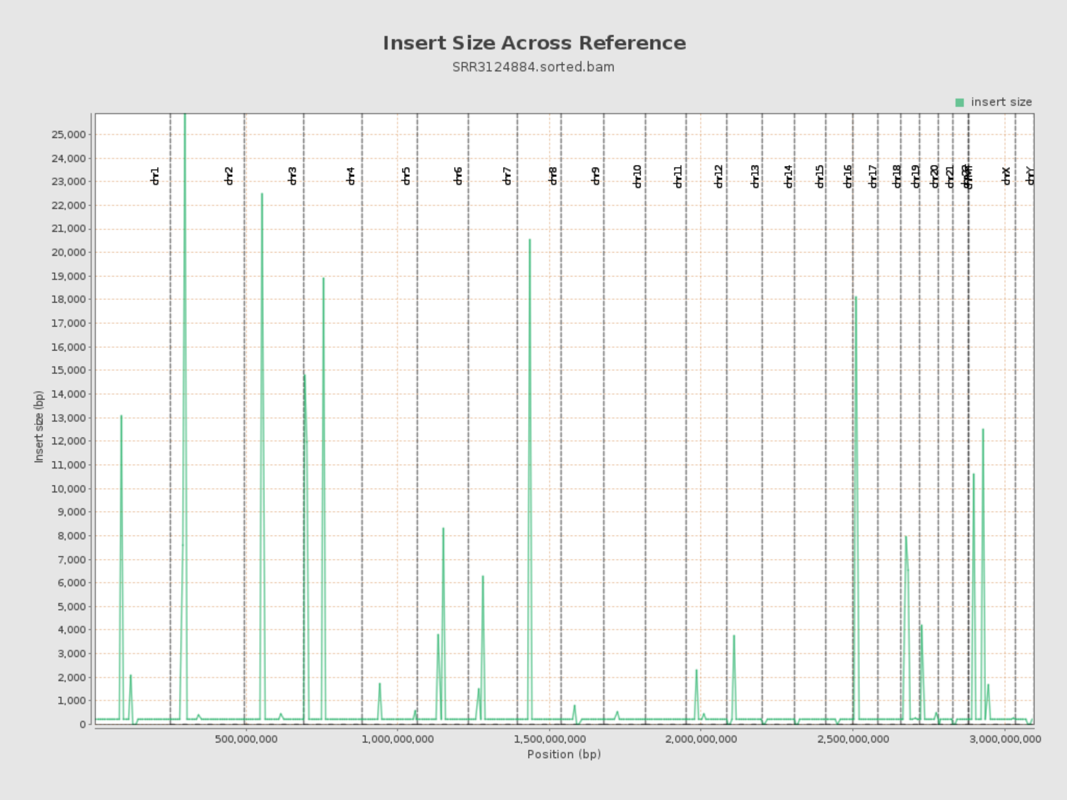
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram