Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 12:59:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124981.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_SRR3124981 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124981_1.fastq.gz SRR3124981_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 12:59:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124981.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,165,618
Mapped reads	4,947,923 / 95.79%
Unmapped reads	217,695 / 4.21%
Mapped paired reads	4,947,923 / 95.79%
Mapped reads, first in pair	2,516,608 / 48.72%
Mapped reads, second in pair	2,431,315 / 47.07%
Mapped reads, both in pair	4,833,888 / 93.58%
Mapped reads, singletons	114,035 / 2.21%
Secondary alignments	0
Supplementary alignments	19,402 / 0.38%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	371,612 / 7.19%
Duplication rate	4.34%
Clipped reads	2,590,695 / 50.15%

2.2. ACGT Content

Number/percentage of A's	84,303,499 / 27.97%
Number/percentage of C's	52,571,780 / 17.44%
Number/percentage of T's	92,612,712 / 30.73%
Number/percentage of G's	71,893,730 / 23.85%
Number/percentage of N's	0 / 0%

GC Percentage	41.3%

2.3. Coverage

Mean	0.0974
Standard Deviation	1.3126

2.4. Mapping Quality

Mean Mapping Quality	51.19

2.5. Insert size

Mean	90,181.03
Standard Deviation	2,833,861.51
P25/Median/P75	123 / 167 / 232

2.6. Mismatches and indels

General error rate	0.77%
Mismatches	2,249,027
Insertions	35,537
Mapped reads with at least one insertion	0.71%
Deletions	79,449
Mapped reads with at least one deletion	1.59%
Homopolymer indels	46.11%

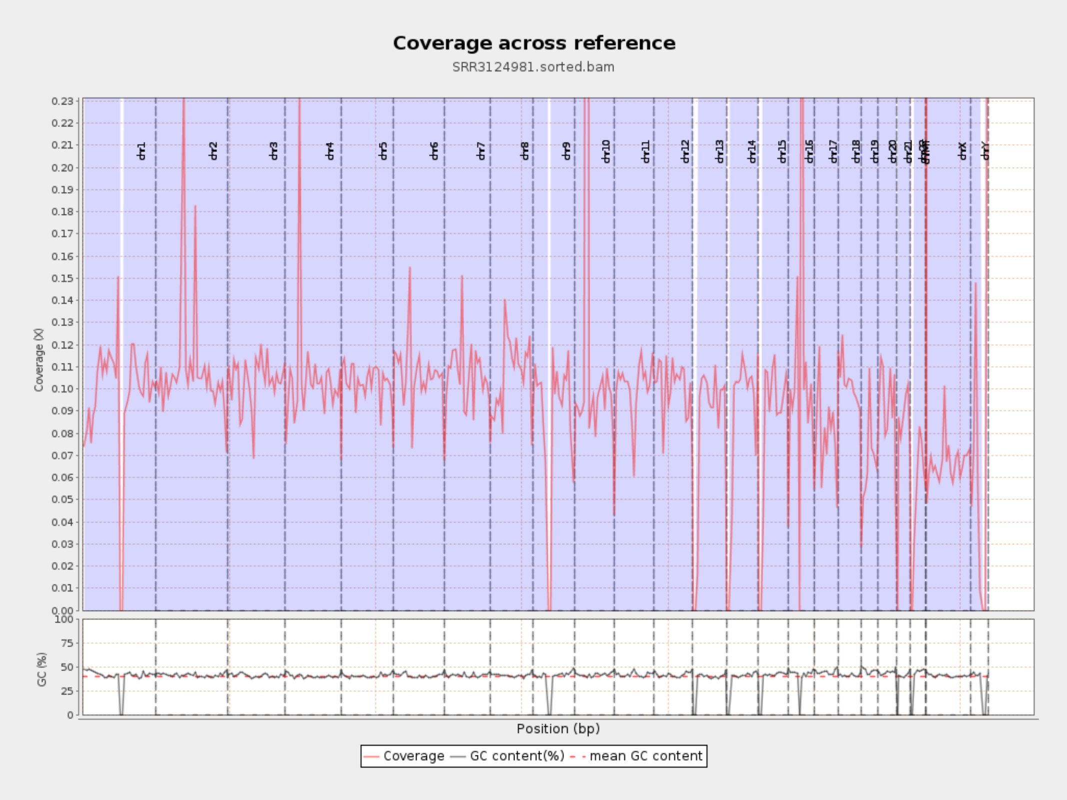
2.7. Chromosome stats

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

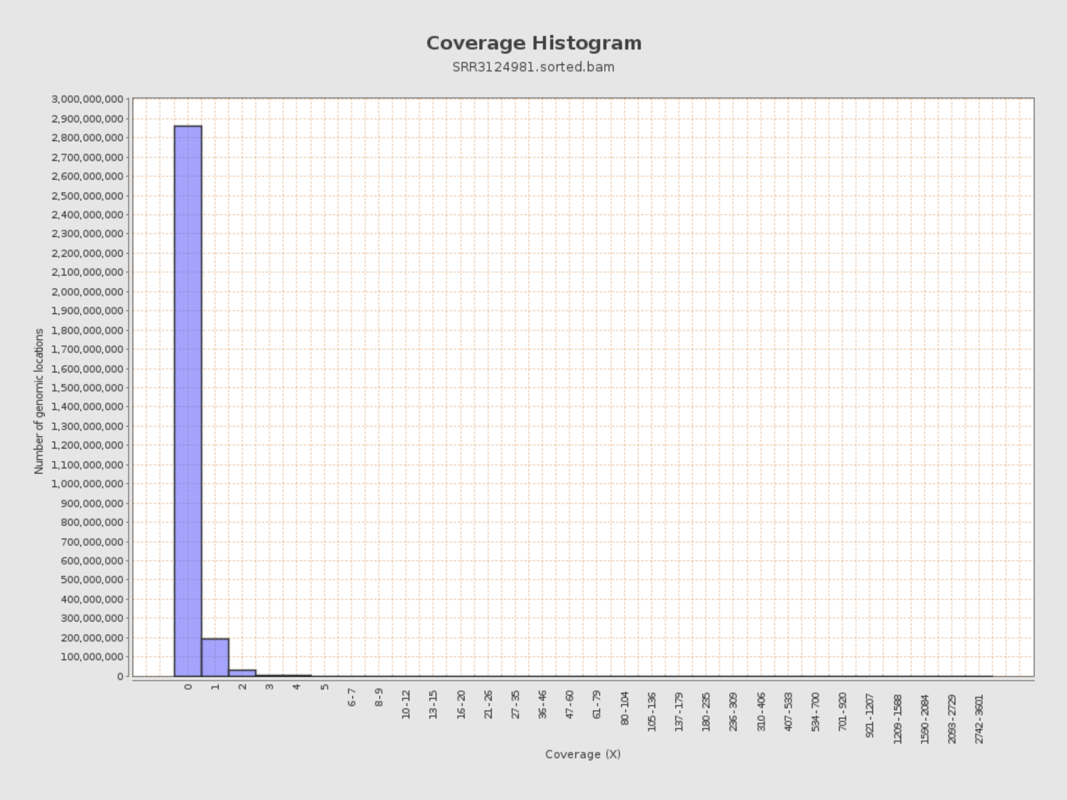
		bases	coverage	deviation
chr1	249250621	24255632	0.0973	0.9151
chr2	243199373	27113143	0.1115	1.3357
chr3	198022430	20539539	0.1037	0.4643
chr4	191154276	20246028	0.1059	0.7398
chr5	180915260	18624928	0.1029	0.4148
chr6	171115067	18471768	0.1079	0.6191
chr7	159138663	16954682	0.1065	0.981
chr8	146364022	15629966	0.1068	0.4822
chr9	141213431	12148142	0.086	0.864
chr10	135534747	17170281	0.1267	4.8261
chr11	135006516	13514429	0.1001	0.6083
chr12	133851895	13530967	0.1011	0.3893
chr13	115169878	9390871	0.0815	0.3353
chr14	107349540	9069032	0.0845	0.4393
chr15	102531392	8388517	0.0818	0.373
chr16	90354753	10431358	0.1154	2.1684
chr17	81195210	6604741	0.0813	0.7515
chr18	78077248	8047324	0.1031	1.2996
chr19	59128983	3996751	0.0676	0.7673
chr20	63025520	6004155	0.0953	0.592
chr21	48129895	3864223	0.0803	0.4876
chr22	51304566	2583701	0.0504	0.3345
chrMT	16571	160568	9.6897	6.6764
chrX	155270560	10397097	0.067	0.4548

chrY	59373566	4373276	0.0737	1.6789

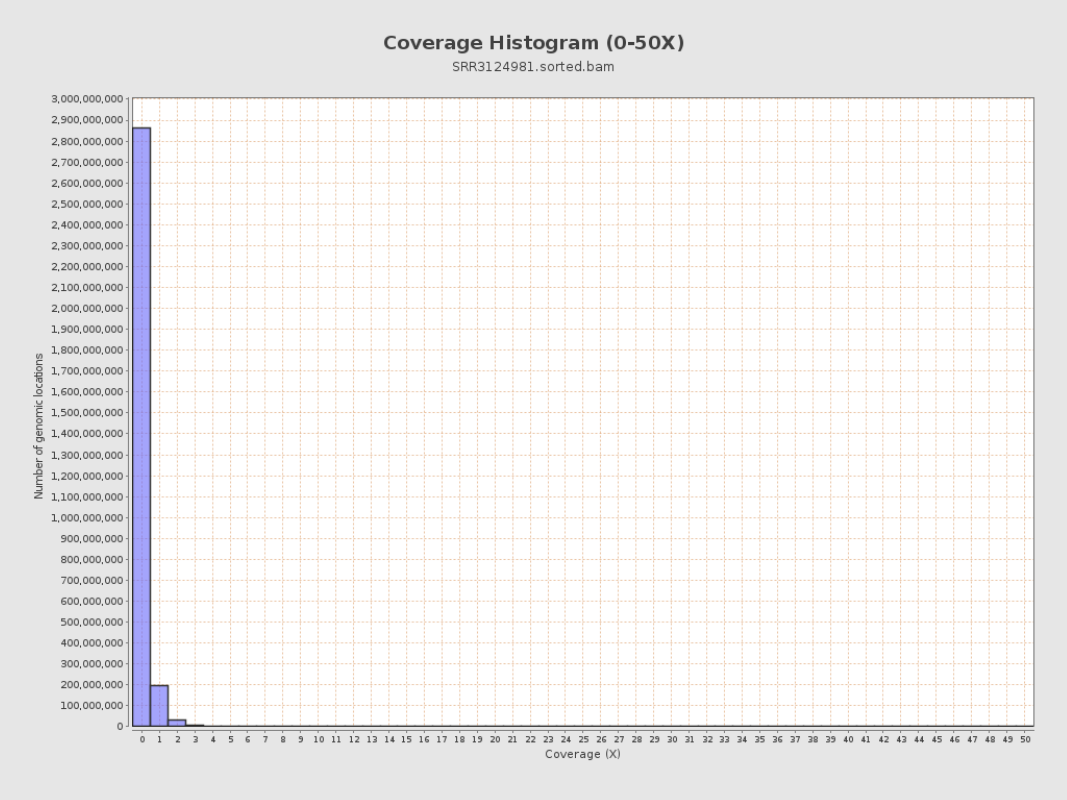
3. Results : Coverage across reference



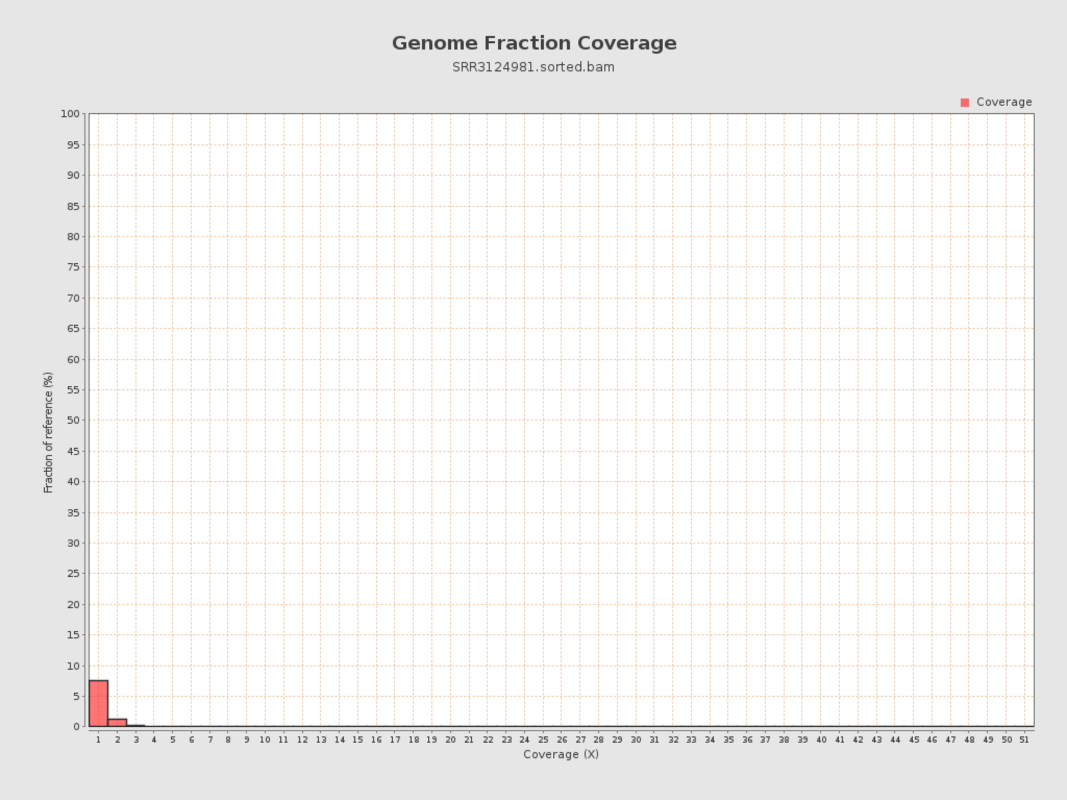
4. Results : Coverage Histogram



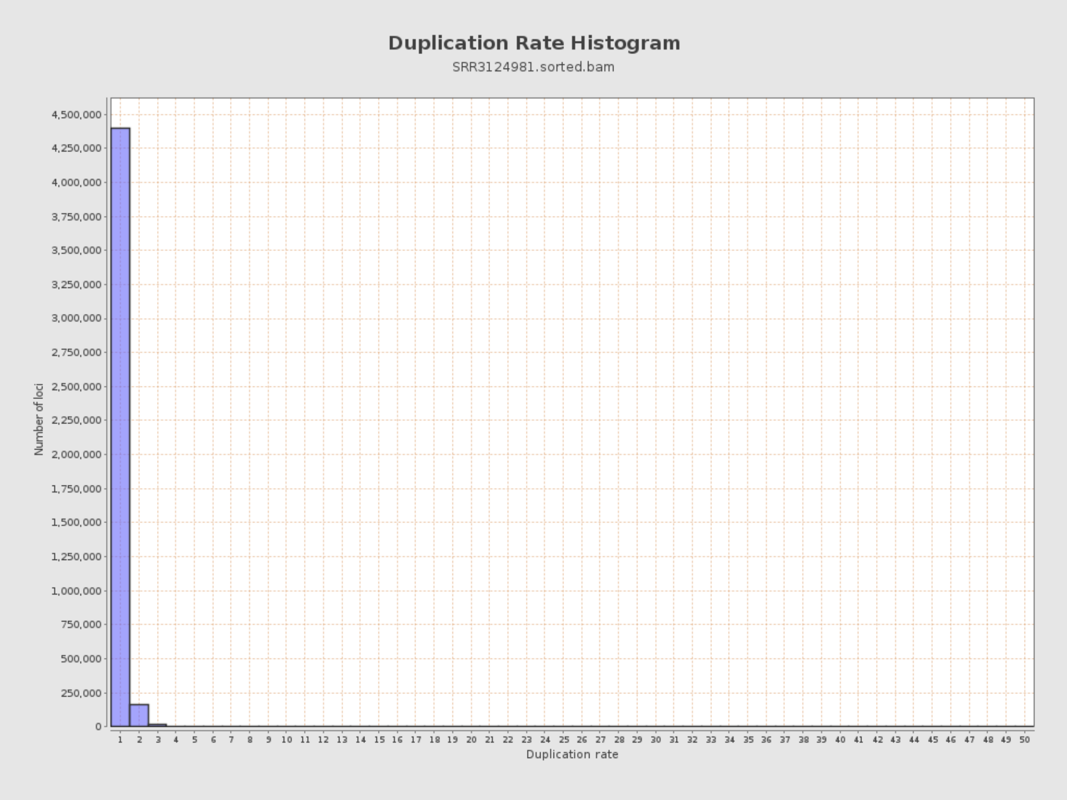
5. Results : Coverage Histogram (0-50X)



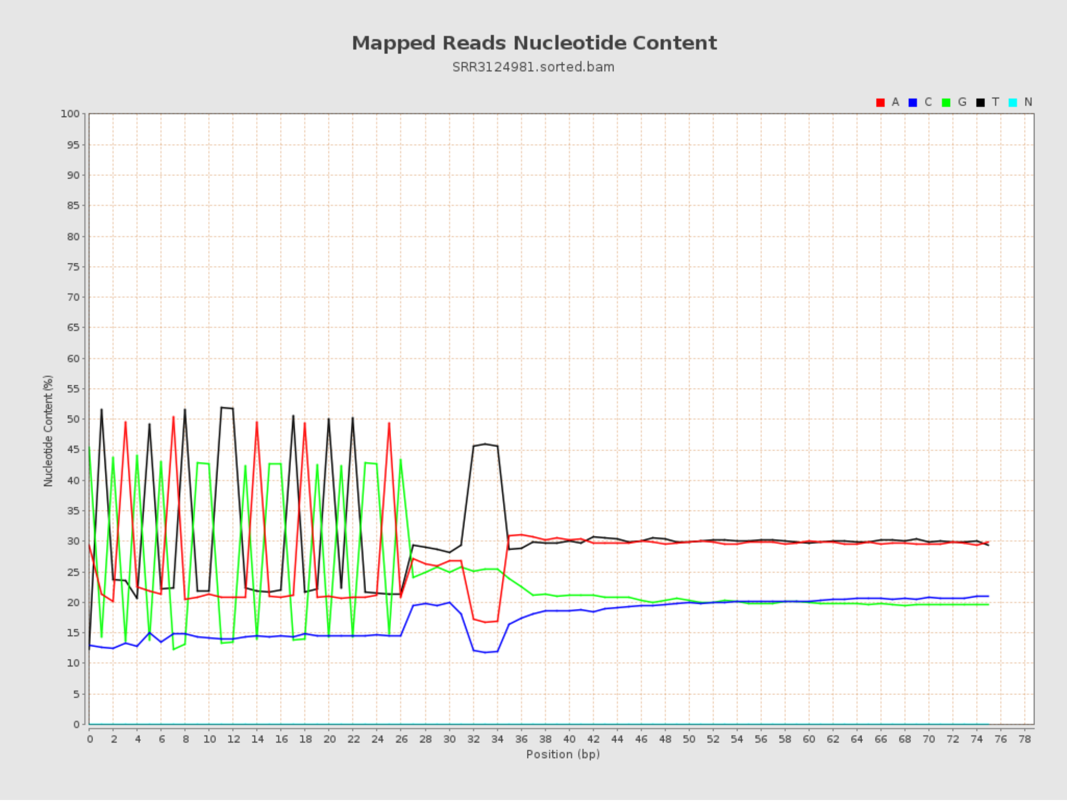
6. Results : Genome Fraction Coverage



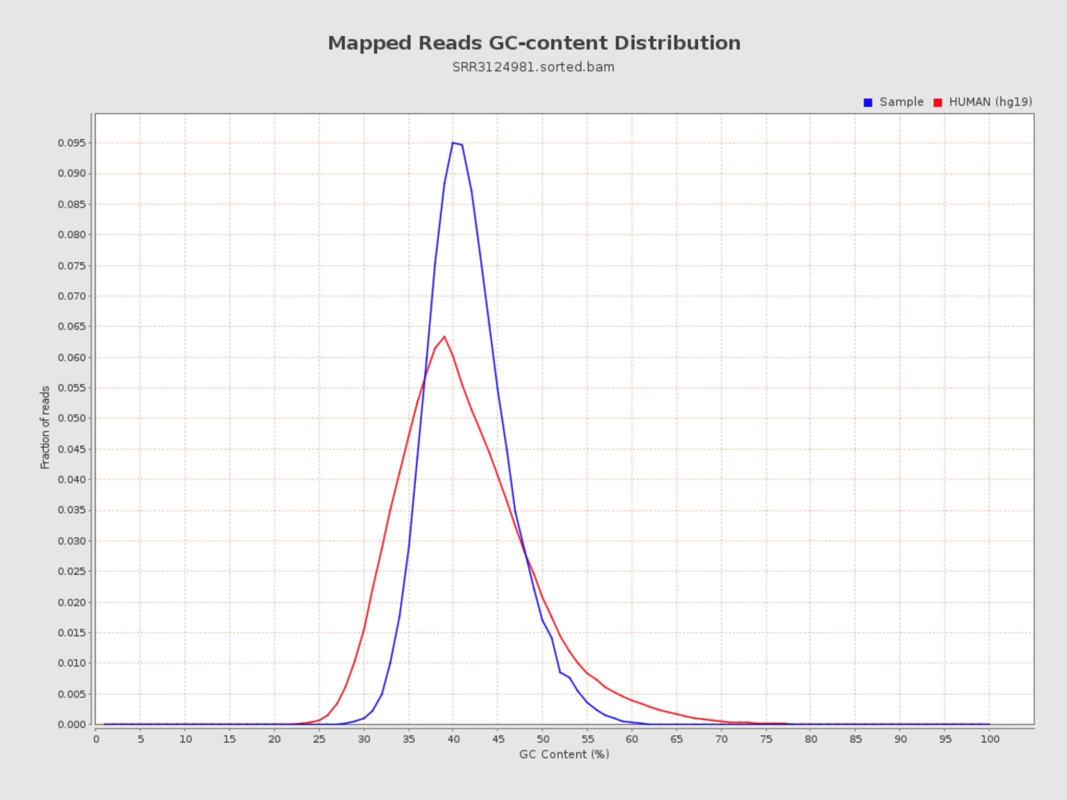
7. Results : Duplication Rate Histogram



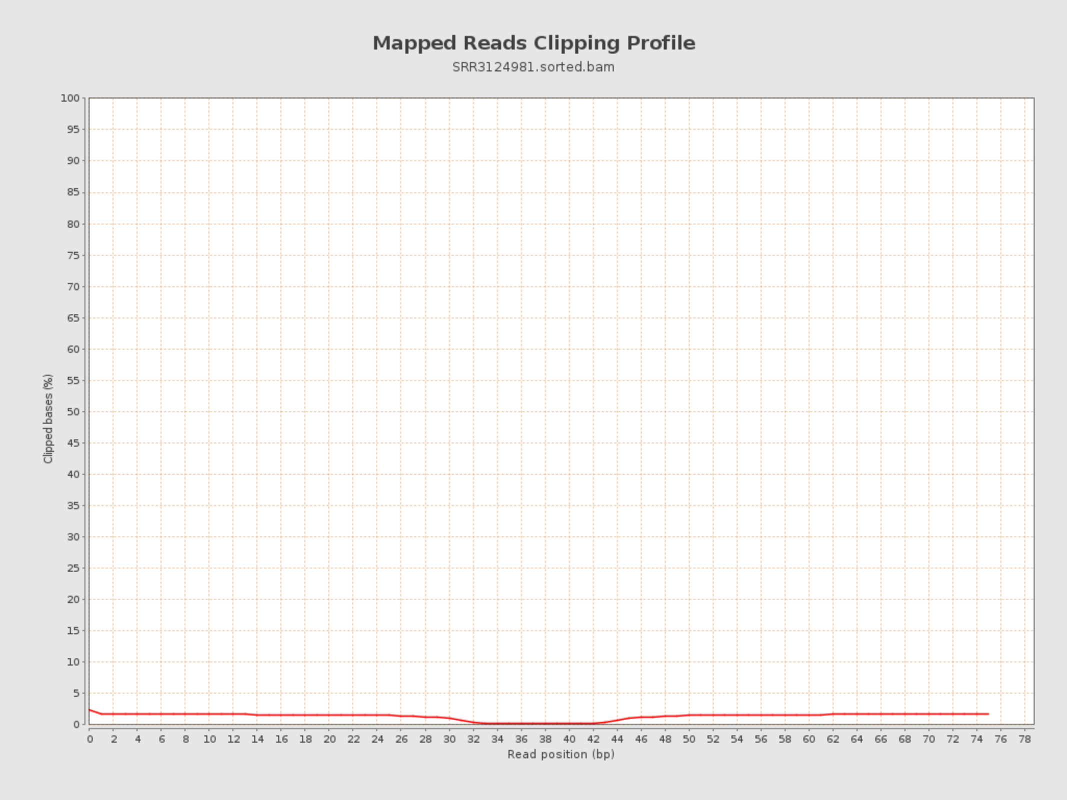
8. Results : Mapped Reads Nucleotide Content



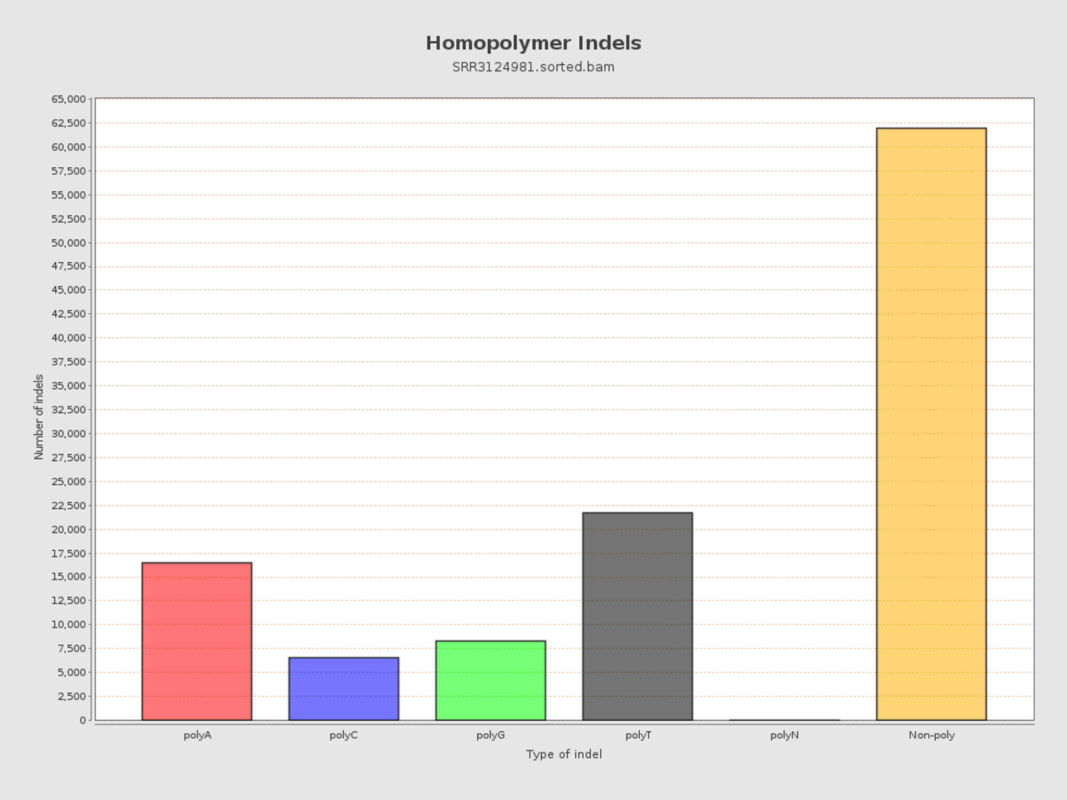
9. Results : Mapped Reads GC-content Distribution



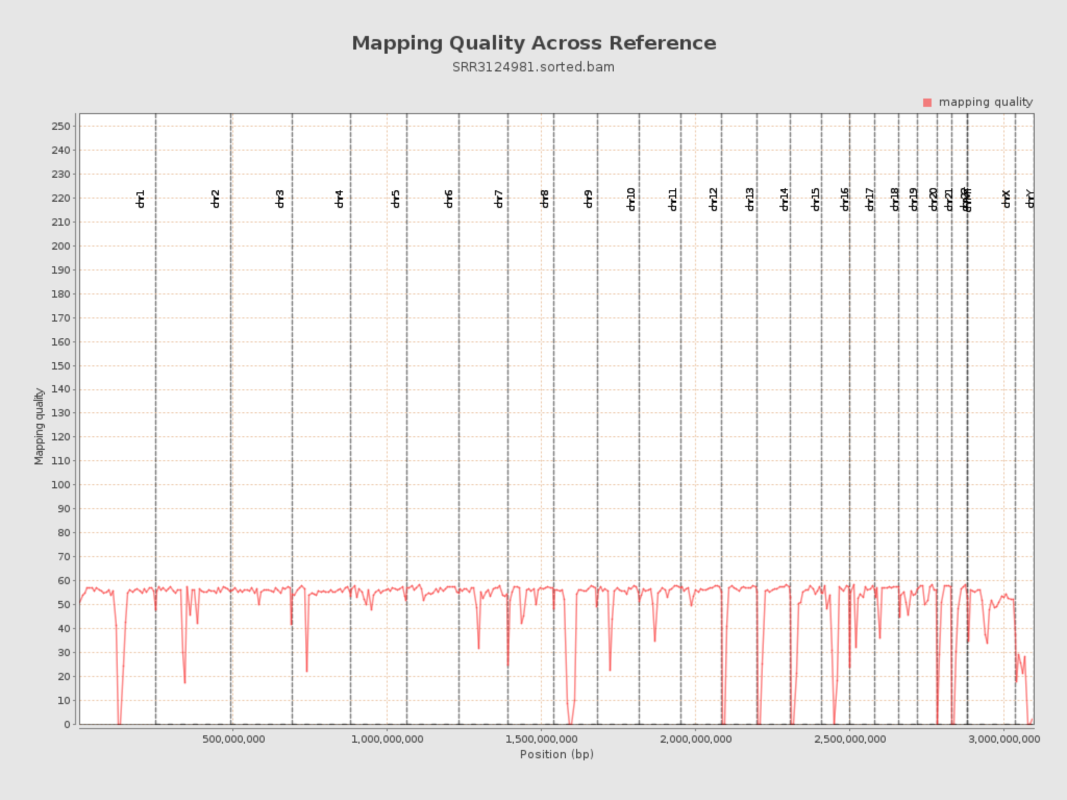
10. Results : Mapped Reads Clipping Profile



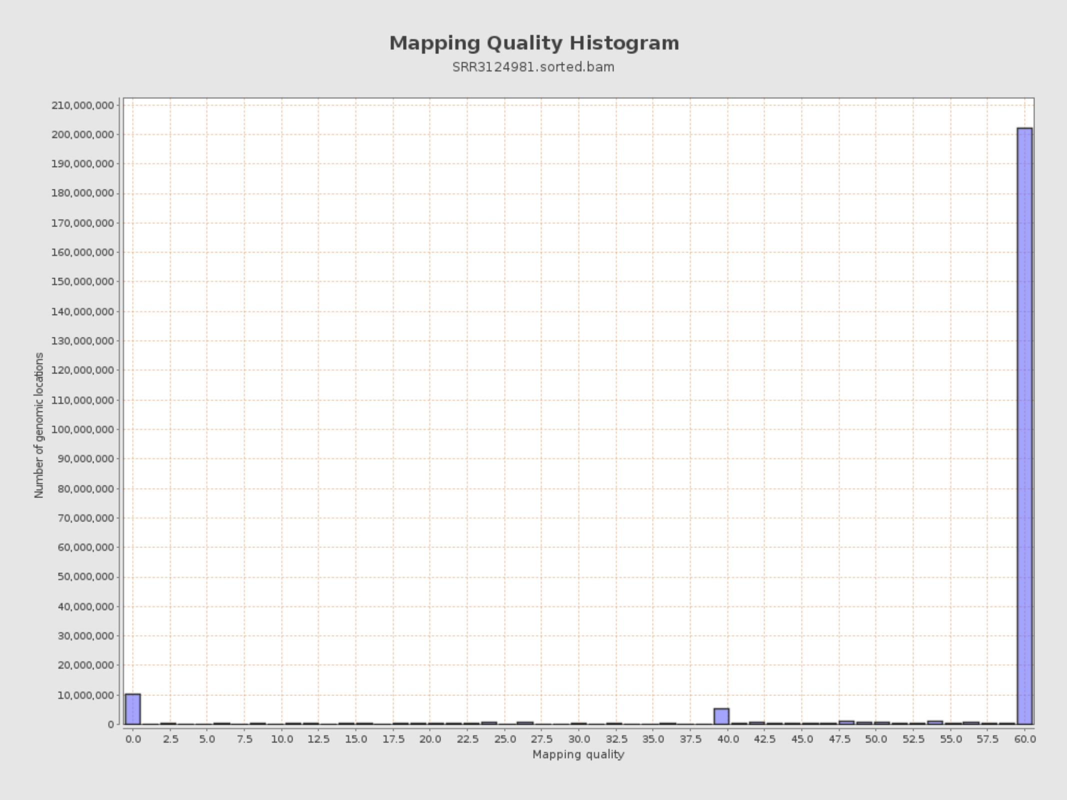
11. Results : Homopolymer Indels



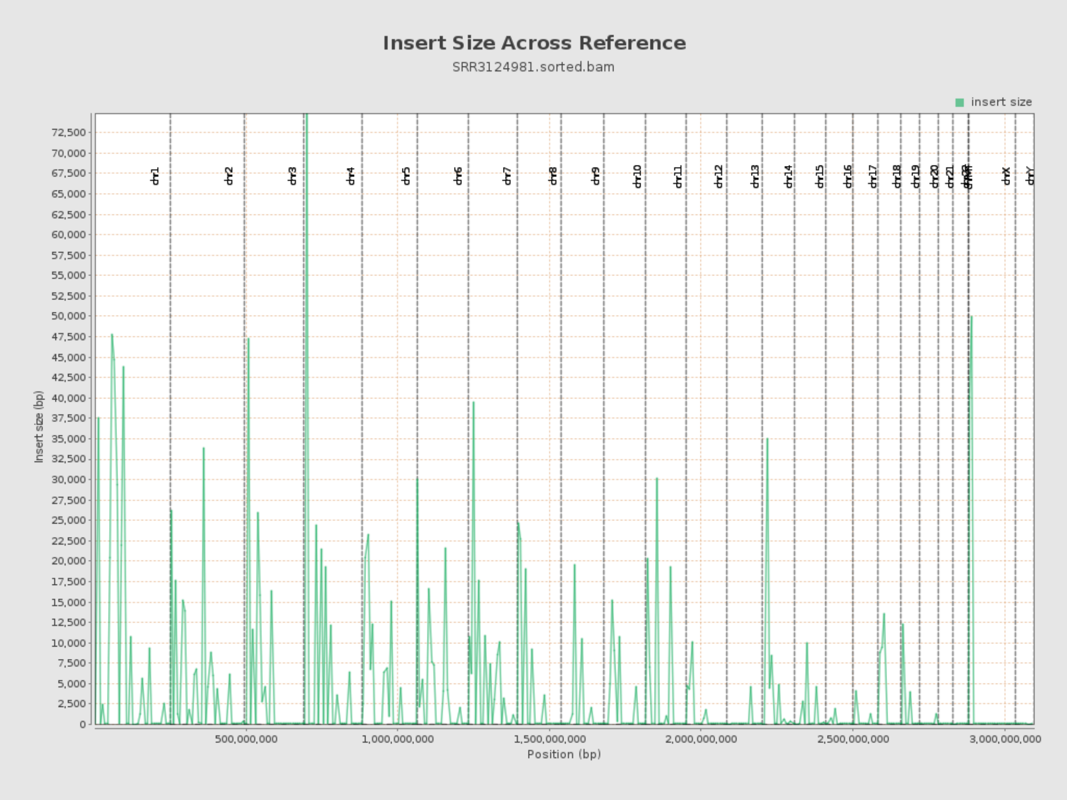
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram