Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 10:28:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124960.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_SRR3124960 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124960_1.fastq.gz SRR3124960_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 10:28:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124960.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,924,514
Mapped reads	4,665,144 / 94.73%
Unmapped reads	259,370 / 5.27%
Mapped paired reads	4,665,144 / 94.73%
Mapped reads, first in pair	2,367,077 / 48.07%
Mapped reads, second in pair	2,298,067 / 46.67%
Mapped reads, both in pair	4,571,454 / 92.83%
Mapped reads, singletons	93,690 / 1.9%
Secondary alignments	0
Supplementary alignments	21,408 / 0.43%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	293,329 / 5.96%
Duplication rate	3.82%
Clipped reads	2,449,072 / 49.73%

2.2. ACGT Content

Number/percentage of A's	79,504,197 / 27.79%
Number/percentage of C's	50,917,834 / 17.8%
Number/percentage of T's	86,300,512 / 30.17%
Number/percentage of G's	69,330,234 / 24.24%
Number/percentage of N's	0 / 0%

GC Percentage	42.04%

2.3. Coverage

Mean	0.0924
Standard Deviation	1.04

2.4. Mapping Quality

Mean Mapping Quality	51.42

2.5. Insert size

Mean	92,698.16
Standard Deviation	2,902,995.21
P25/Median/P75	119 / 165 / 231

2.6. Mismatches and indels

General error rate	0.72%
Mismatches	1,988,666
Insertions	34,154
Mapped reads with at least one insertion	0.72%
Deletions	74,914
Mapped reads with at least one deletion	1.59%
Homopolymer indels	46.35%

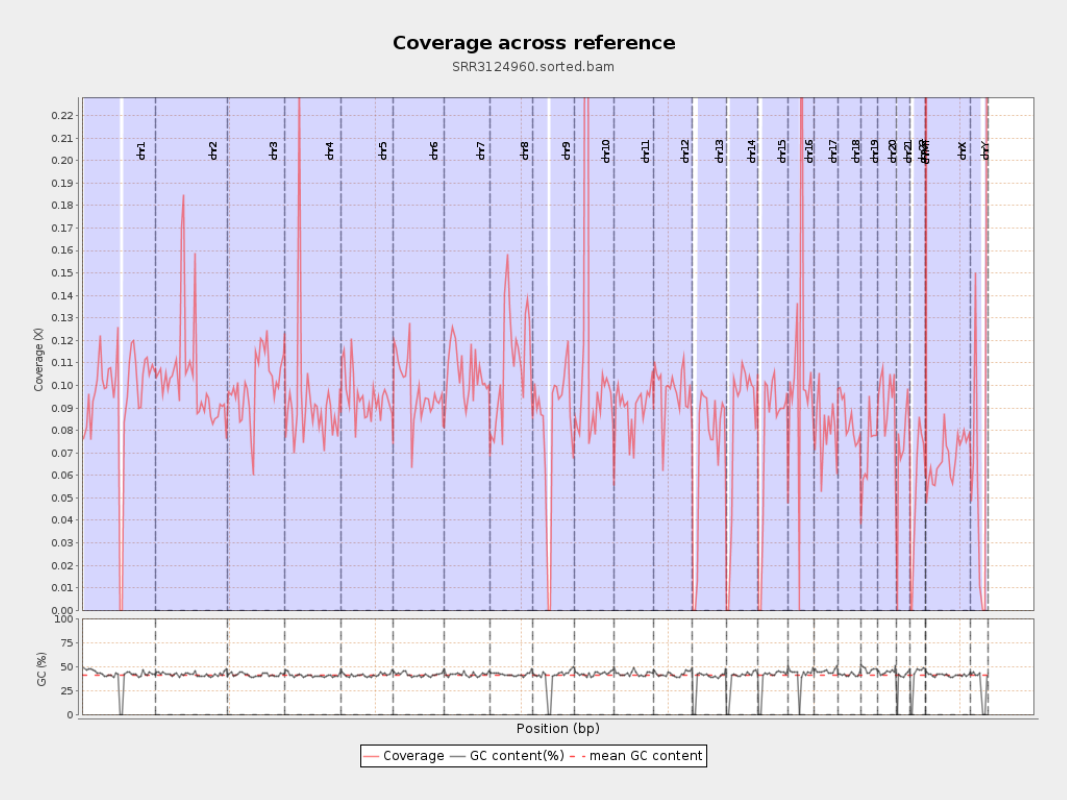
2.7. Chromosome stats

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

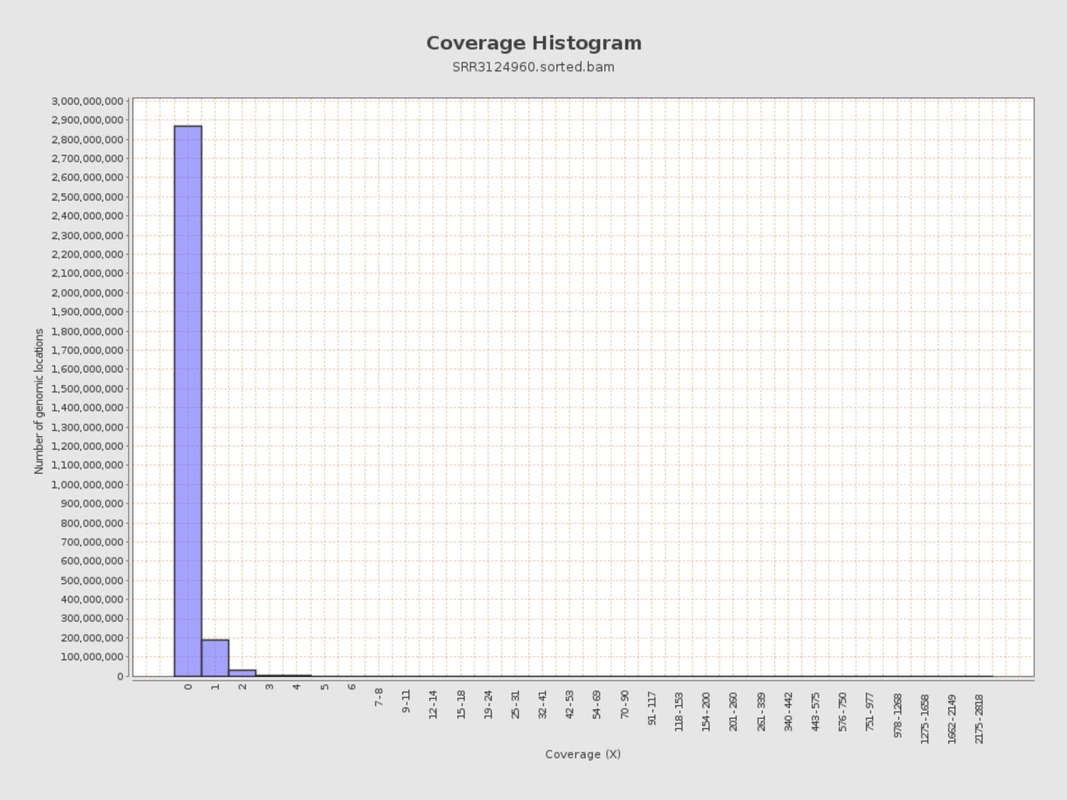
		bases	coverage	deviation
chr1	249250621	23806389	0.0955	0.6432
chr2	243199373	25271247	0.1039	1.122
chr3	198022430	19895338	0.1005	0.4301
chr4	191154276	17885910	0.0936	0.8049
chr5	180915260	17165483	0.0949	0.379
chr6	171115067	16735681	0.0978	0.4509
chr7	159138663	16719460	0.1051	0.6351
chr8	146364022	16147363	0.1103	0.4453
chr9	141213431	11728809	0.0831	0.6276
chr10	135534747	15939688	0.1176	3.7268
chr11	135006516	12168847	0.0901	0.4426
chr12	133851895	13111824	0.098	0.3736
chr13	115169878	8206052	0.0713	0.3081
chr14	107349540	8876230	0.0827	0.3915
chr15	102531392	7884388	0.0769	0.3406
chr16	90354753	9895977	0.1095	1.7235
chr17	81195210	6573713	0.081	0.5885
chr18	78077248	6613848	0.0847	0.8694
chr19	59128983	4210933	0.0712	0.5433
chr20	63025520	5975821	0.0948	0.4981
chr21	48129895	3457987	0.0718	0.504
chr22	51304566	2750062	0.0536	0.321
chrMT	16571	71576	4.3194	3.4789
chrX	155270560	10528863	0.0678	0.3857

chrY	59373566	4553025	0.0767	1.7022

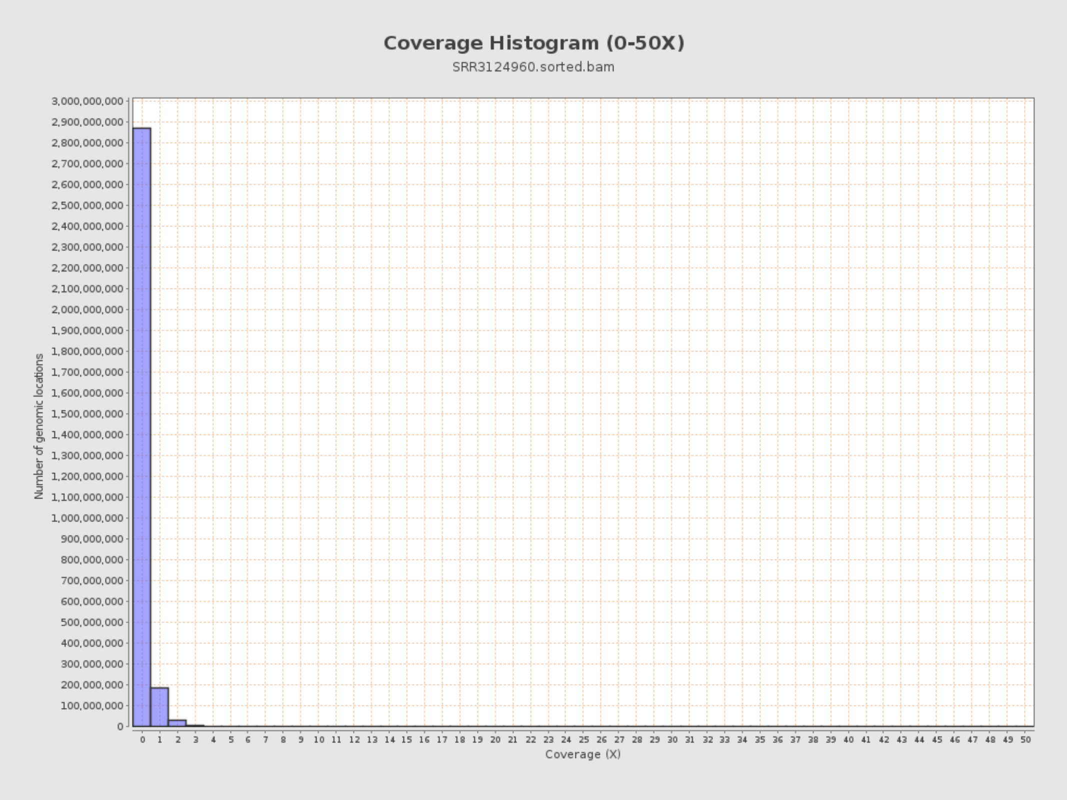
3. Results : Coverage across reference



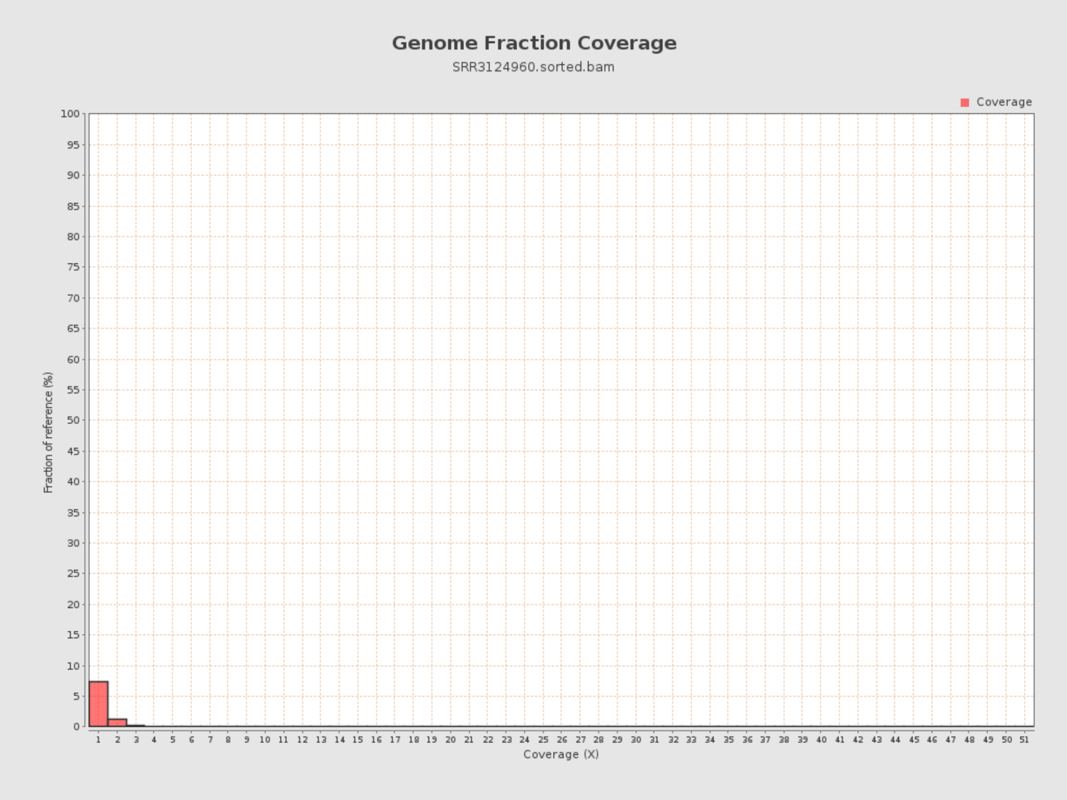
4. Results : Coverage Histogram



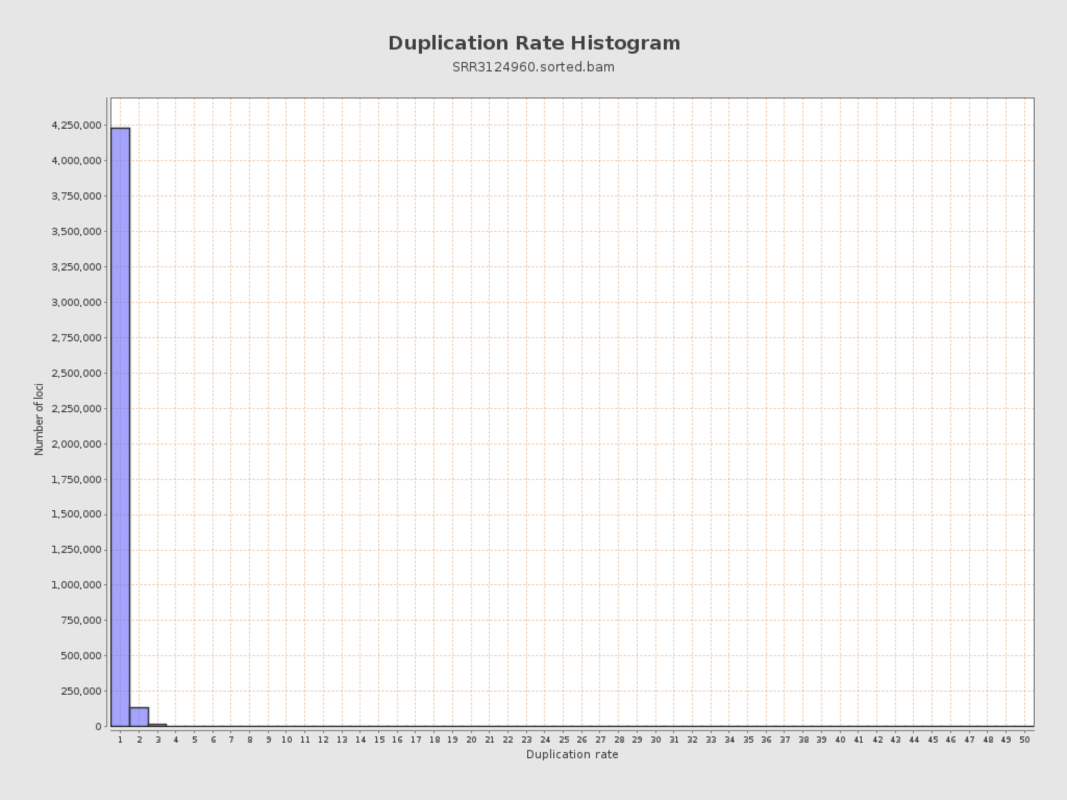
5. Results : Coverage Histogram (0-50X)



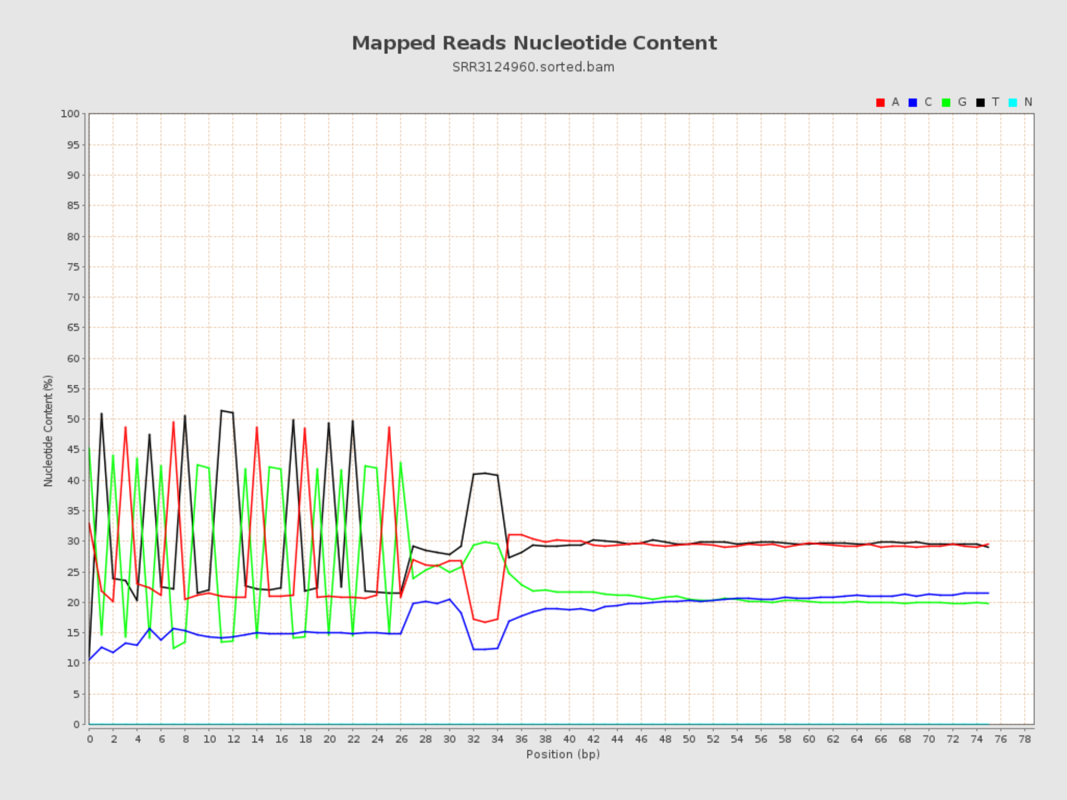
6. Results : Genome Fraction Coverage



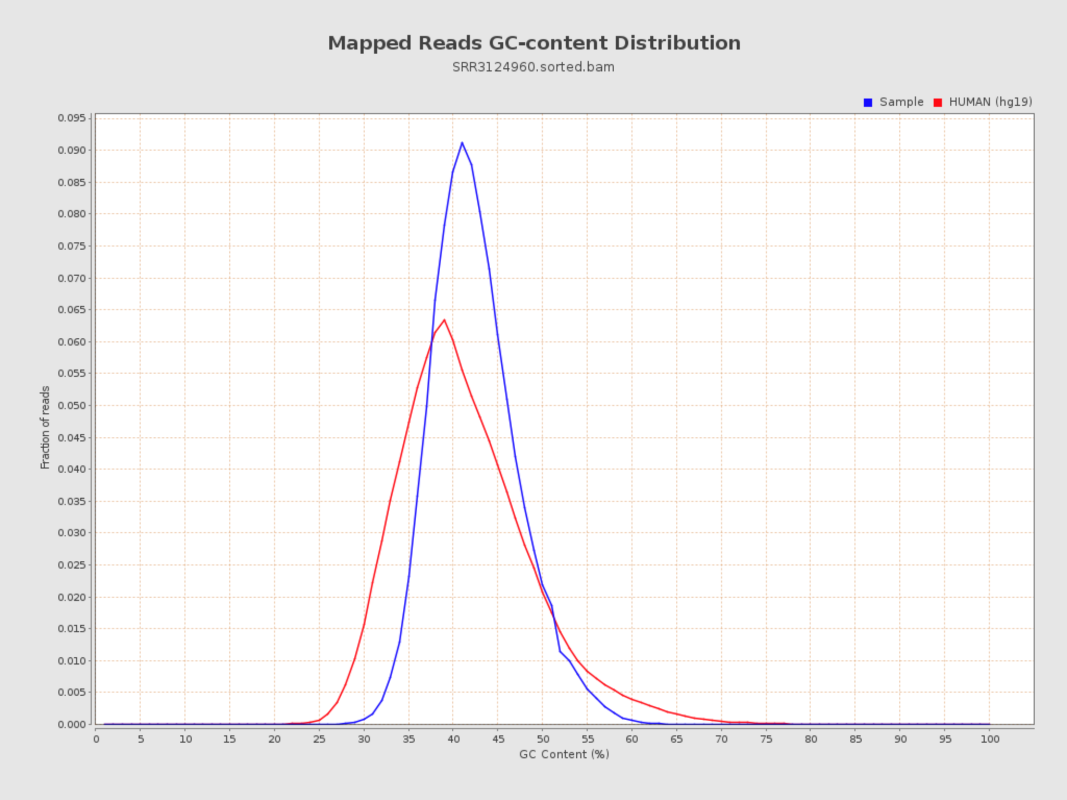
7. Results : Duplication Rate Histogram



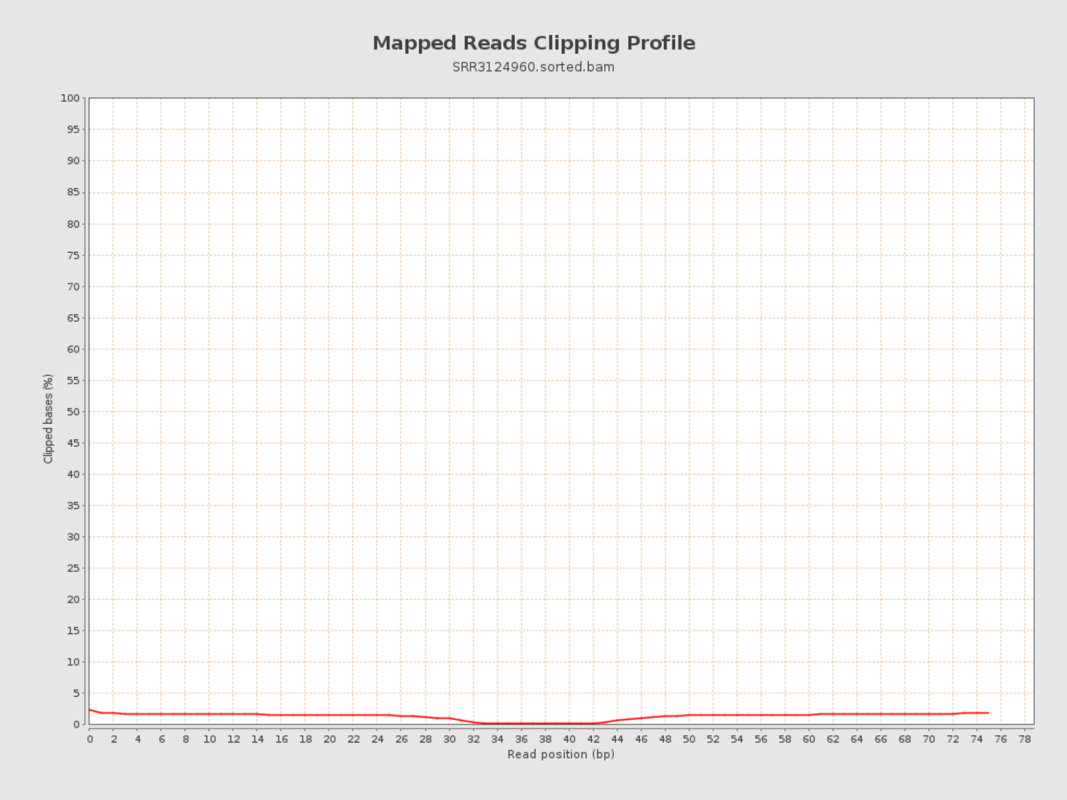
8. Results : Mapped Reads Nucleotide Content



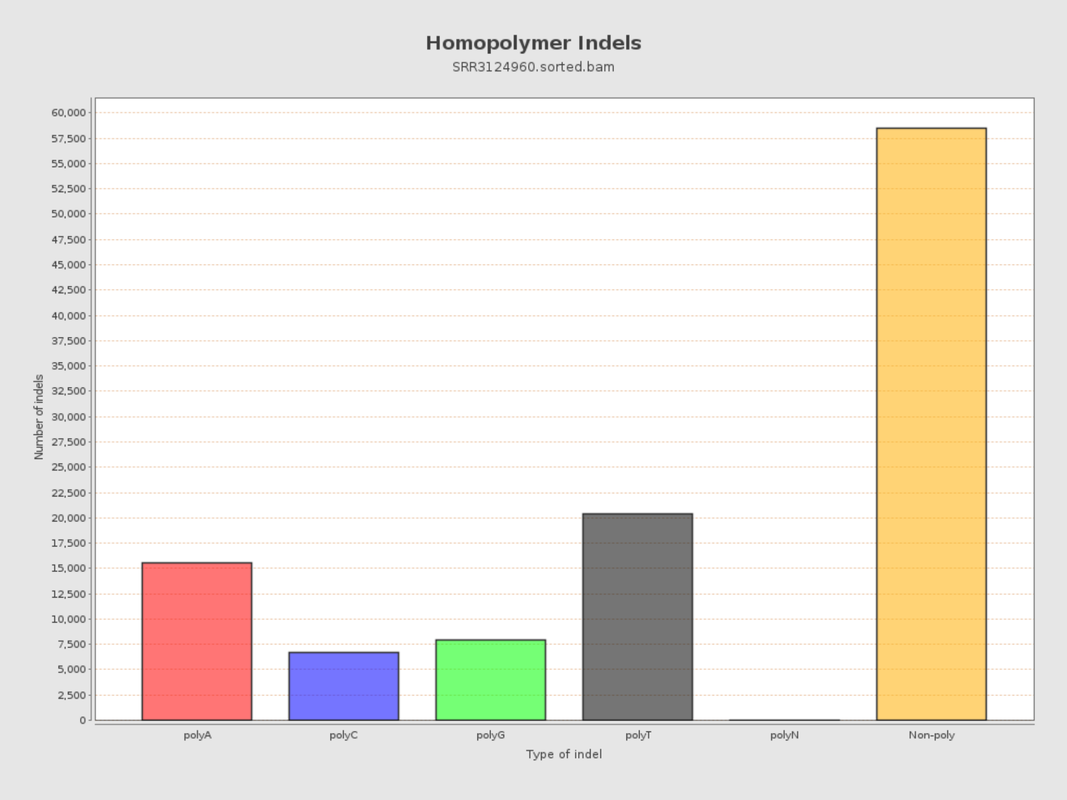
9. Results : Mapped Reads GC-content Distribution



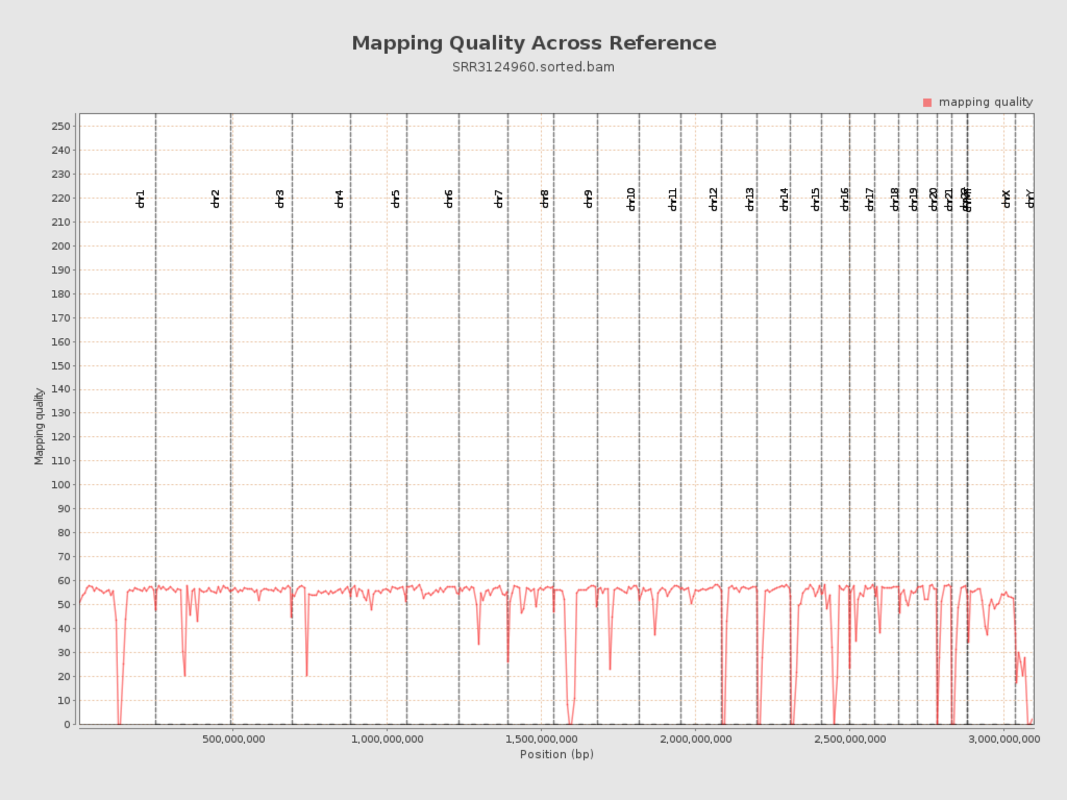
10. Results : Mapped Reads Clipping Profile



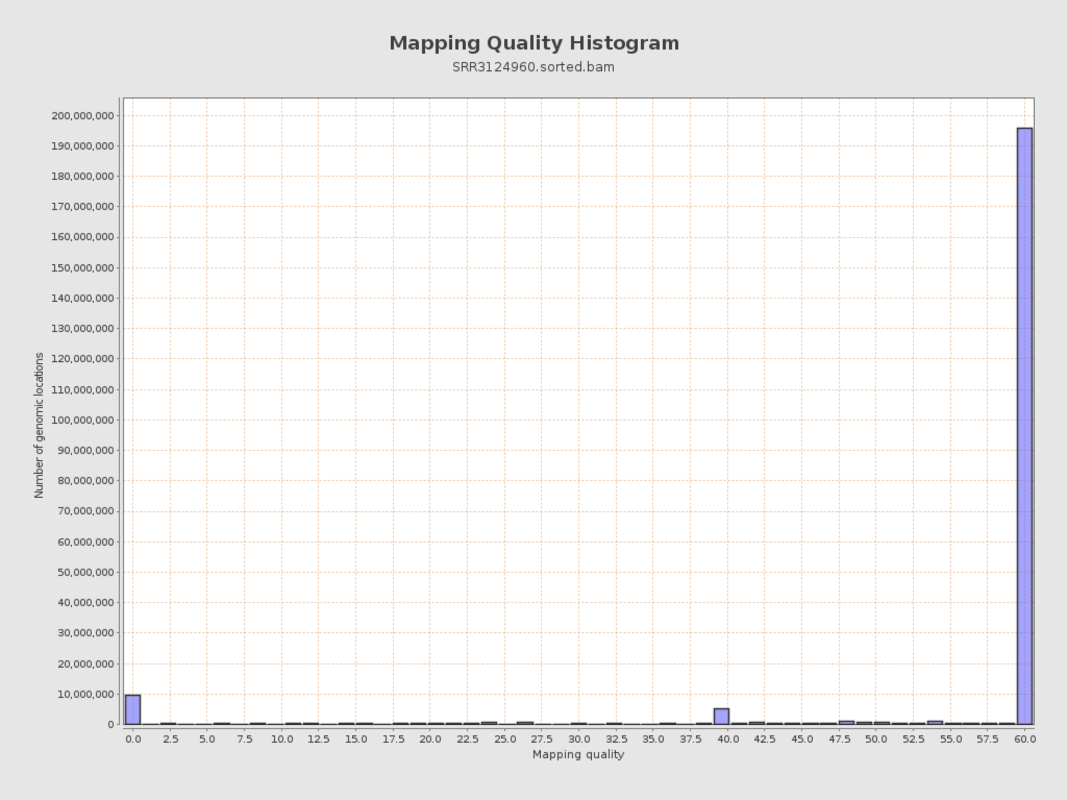
11. Results : Homopolymer Indels



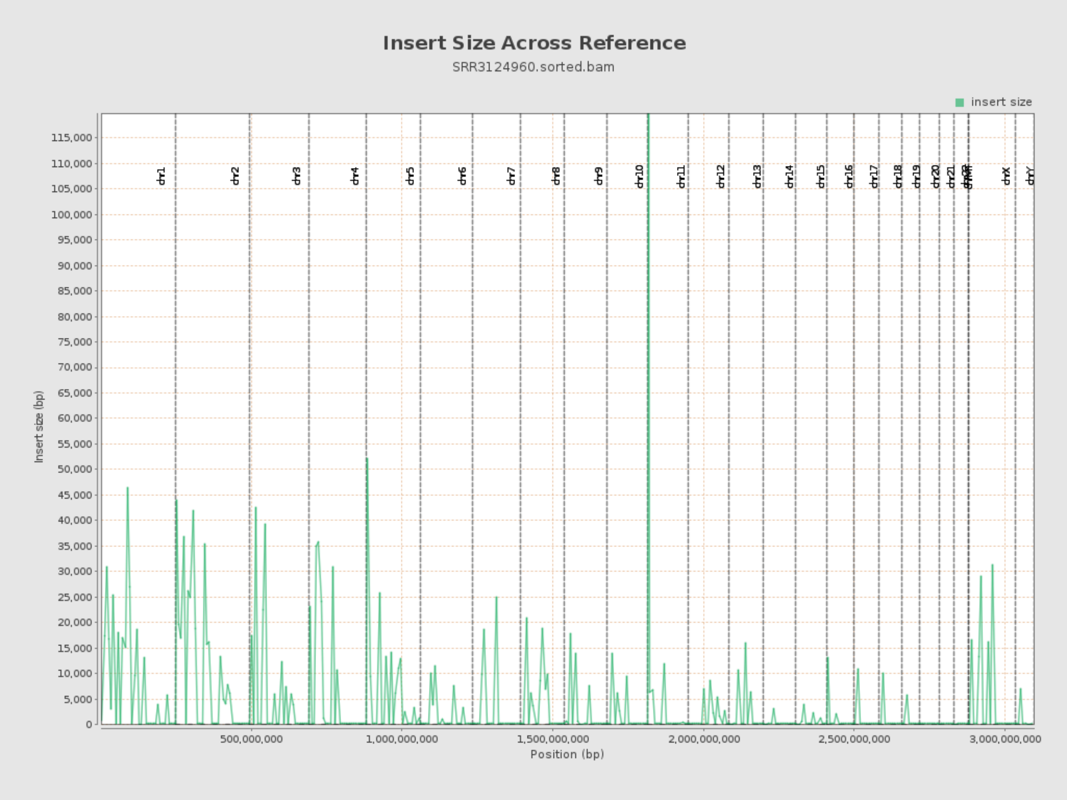
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram