Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/05 04:29:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10174069.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_SRR10174069 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10174069_1.fastq.gz SRR10174069_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Sep 05 04:29:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10174069.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,718,454
Mapped reads	3,637,138 / 97.81%
Unmapped reads	81,316 / 2.19%
Mapped paired reads	3,637,138 / 97.81%
Mapped reads, first in pair	1,820,009 / 48.95%
Mapped reads, second in pair	1,817,129 / 48.87%
Mapped reads, both in pair	3,586,306 / 96.45%
Mapped reads, singletons	50,832 / 1.37%
Secondary alignments	0
Supplementary alignments	328,069 / 8.82%
Read min/max/mean length	30 / 133 / 127.02
Duplicated reads (estimated)	2,661,671 / 71.58%
Duplication rate	62.92%
Clipped reads	1,352,099 / 36.36%

2.2. ACGT Content

Number/percentage of A's	130,517,166 / 30.42%
Number/percentage of C's	83,182,150 / 19.39%
Number/percentage of T's	129,925,171 / 30.28%
Number/percentage of G's	85,429,514 / 19.91%
Number/percentage of N's	5,239 / 0%

GC Percentage	39.3%

2.3. Coverage

Mean	0.1387
Standard Deviation	2.0685

2.4. Mapping Quality

Mean Mapping Quality	52.89

2.5. Insert size

Mean	623,846.45
Standard Deviation	7,350,253.36
P25/Median/P75	135 / 184 / 259

2.6. Mismatches and indels

General error rate	0.98%
Mismatches	4,104,604
Insertions	43,632
Mapped reads with at least one insertion	1.16%
Deletions	88,721
Mapped reads with at least one deletion	2.38%
Homopolymer indels	43.37%

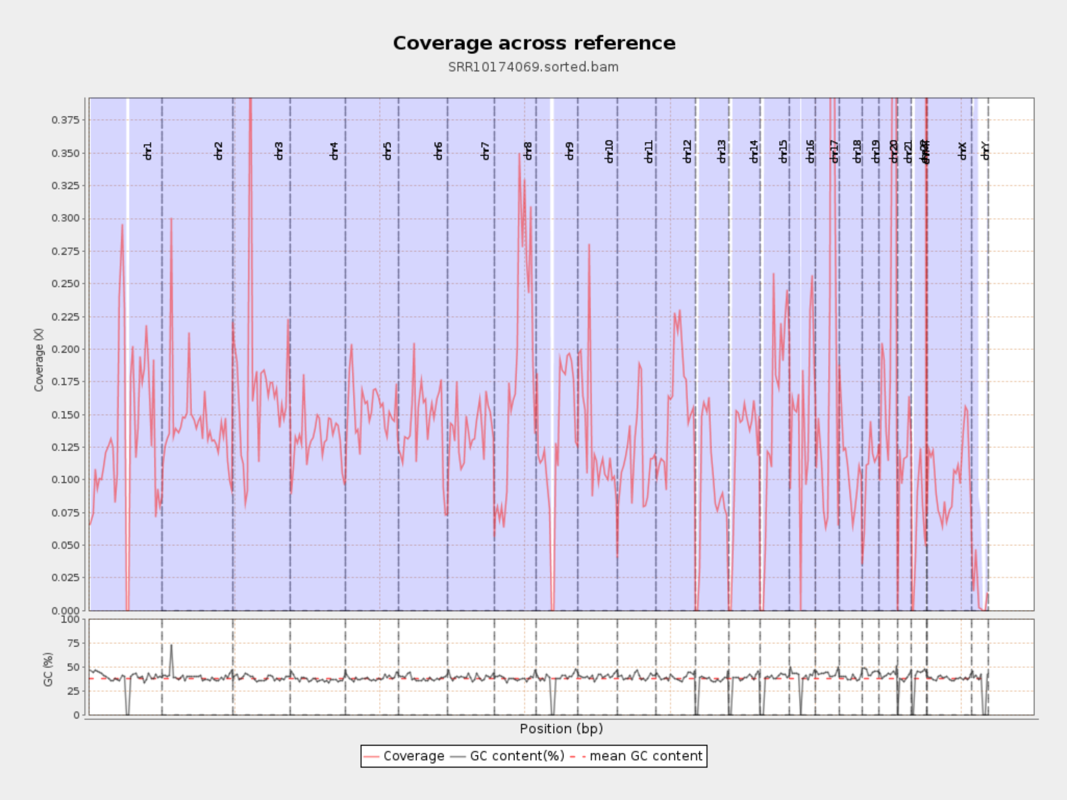
2.7. Chromosome stats

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

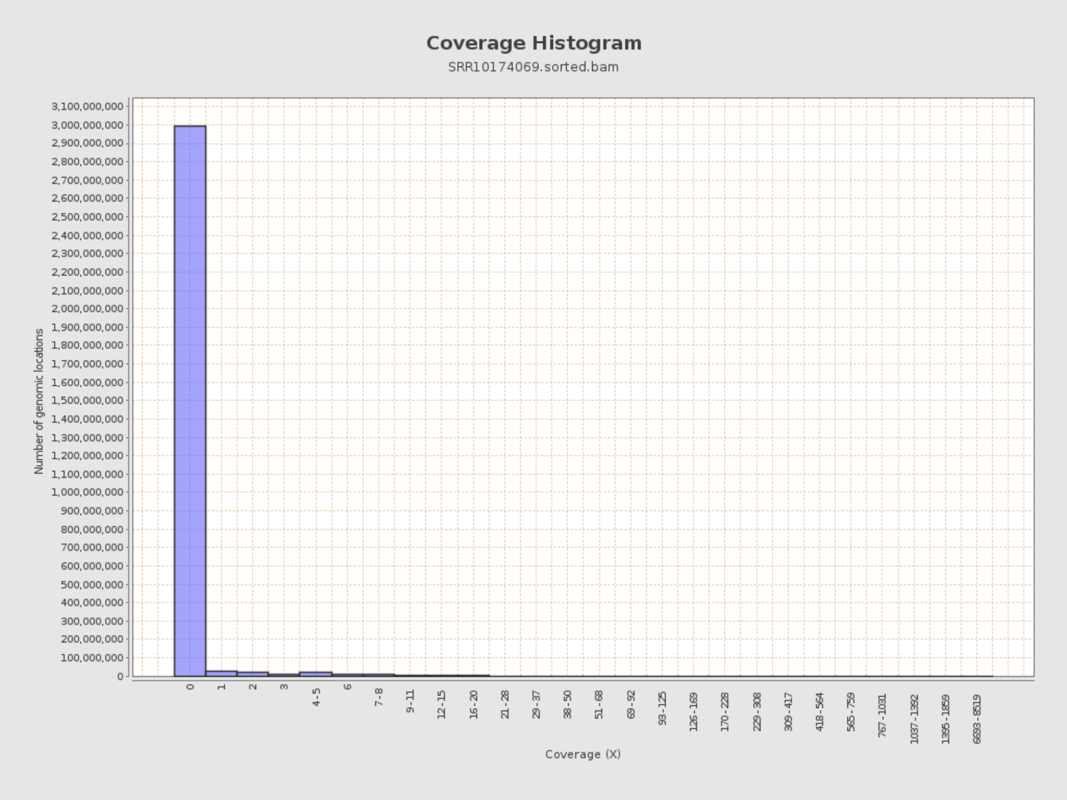
		bases	coverage	deviation
chr1	249250621	33189904	0.1332	1.438
chr2	243199373	34755214	0.1429	6.0148
chr3	198022430	34016368	0.1718	1.155
chr4	191154276	25009301	0.1308	1.1048
chr5	180915260	27974643	0.1546	1.0874
chr6	171115067	24273049	0.1419	1.1948
chr7	159138663	21959919	0.138	1.2837
chr8	146364022	26294090	0.1796	1.4692
chr9	141213431	18362820	0.13	1.1795
chr10	135534747	17781344	0.1312	2.1017
chr11	135006516	15822788	0.1172	0.9542
chr12	133851895	21216576	0.1585	1.1029
chr13	115169878	10608113	0.0921	0.8506
chr14	107349540	12976632	0.1209	0.9607
chr15	102531392	15211548	0.1484	1.0514
chr16	90354753	13659848	0.1512	1.3115
chr17	81195210	16804409	0.207	1.3382
chr18	78077248	8479758	0.1086	1.5652
chr19	59128983	6410980	0.1084	1.1065
chr20	63025520	18564574	0.2946	1.6042
chr21	48129895	5422970	0.1127	0.9587
chr22	51304566	3110166	0.0606	0.6354
chrMT	16571	961263	58.0088	47.3509
chrX	155270560	15686783	0.101	0.8763

chrY	59373566	731078	0.0123	0.4635

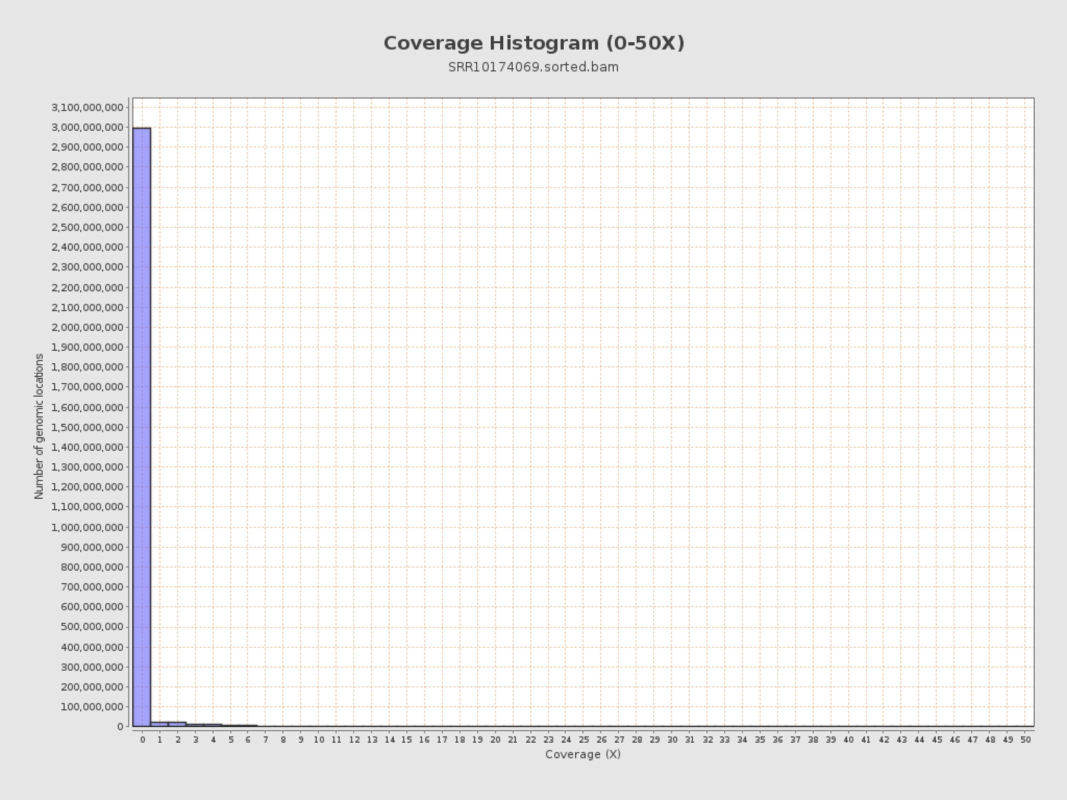
3. Results : Coverage across reference



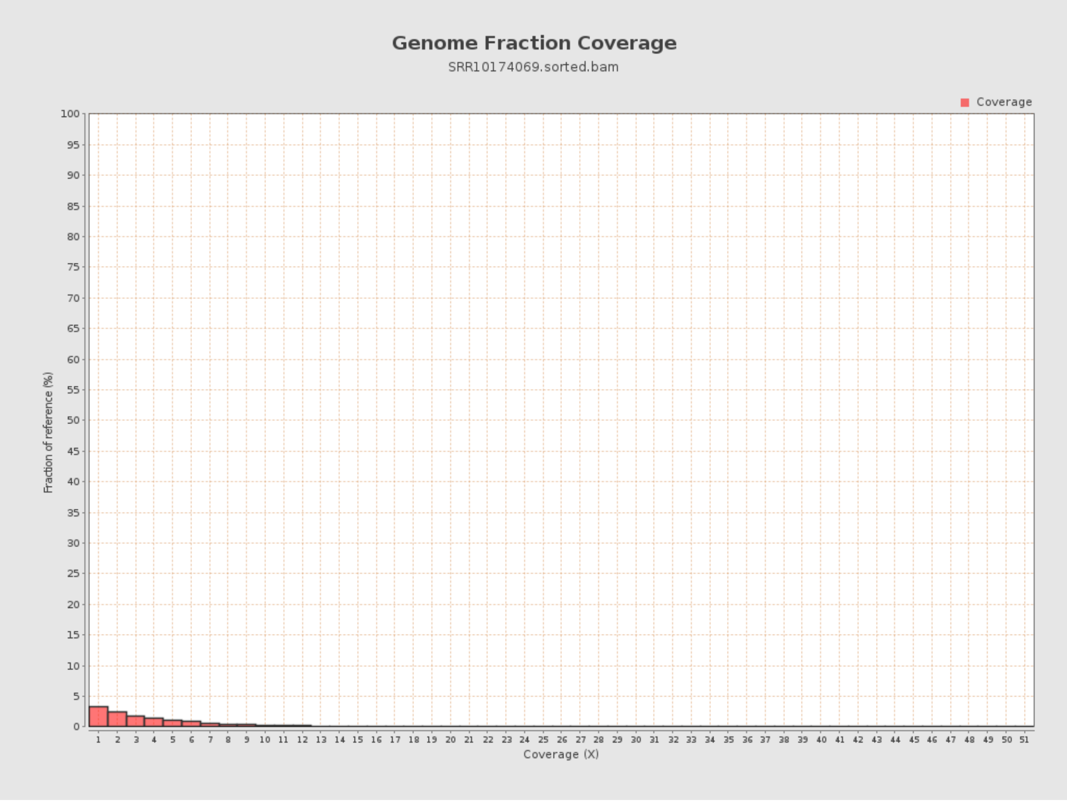
4. Results : Coverage Histogram



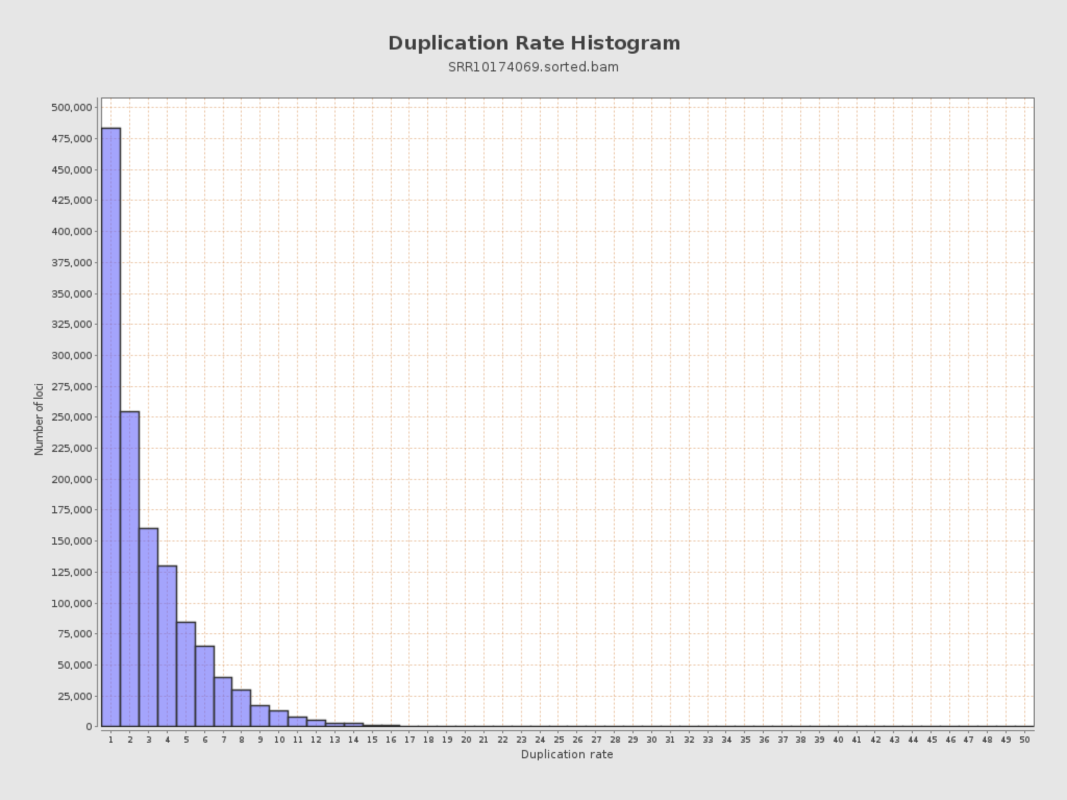
5. Results : Coverage Histogram (0-50X)



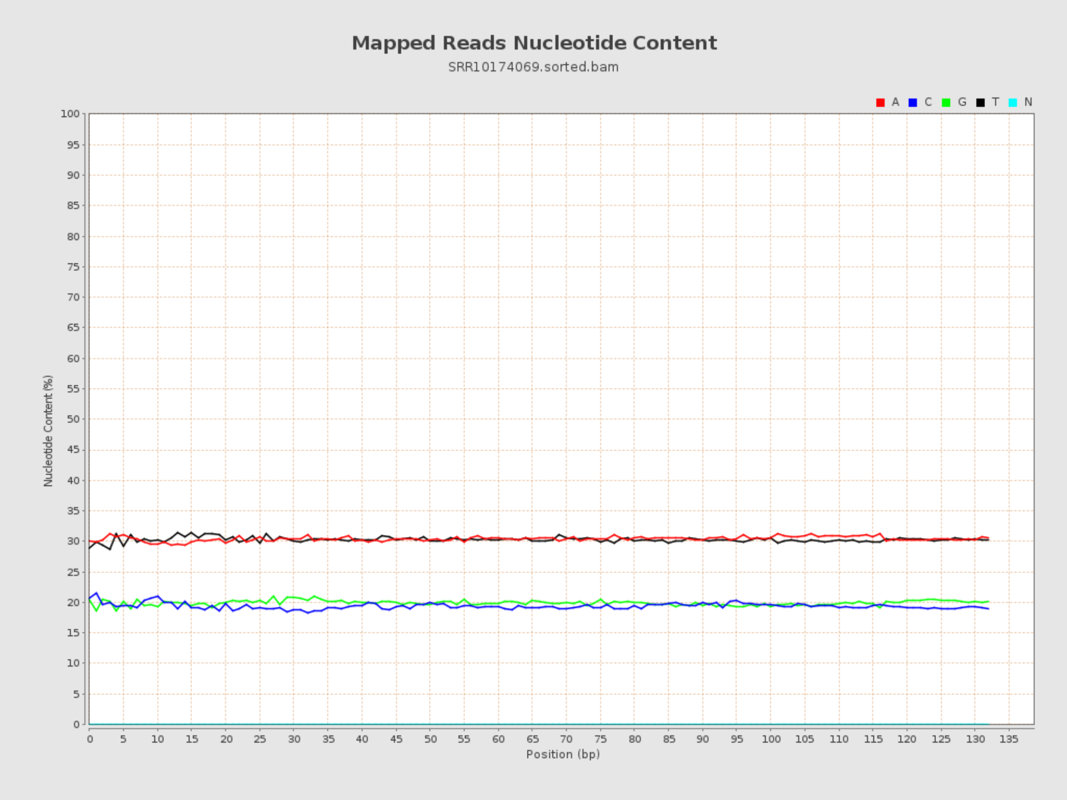
6. Results : Genome Fraction Coverage



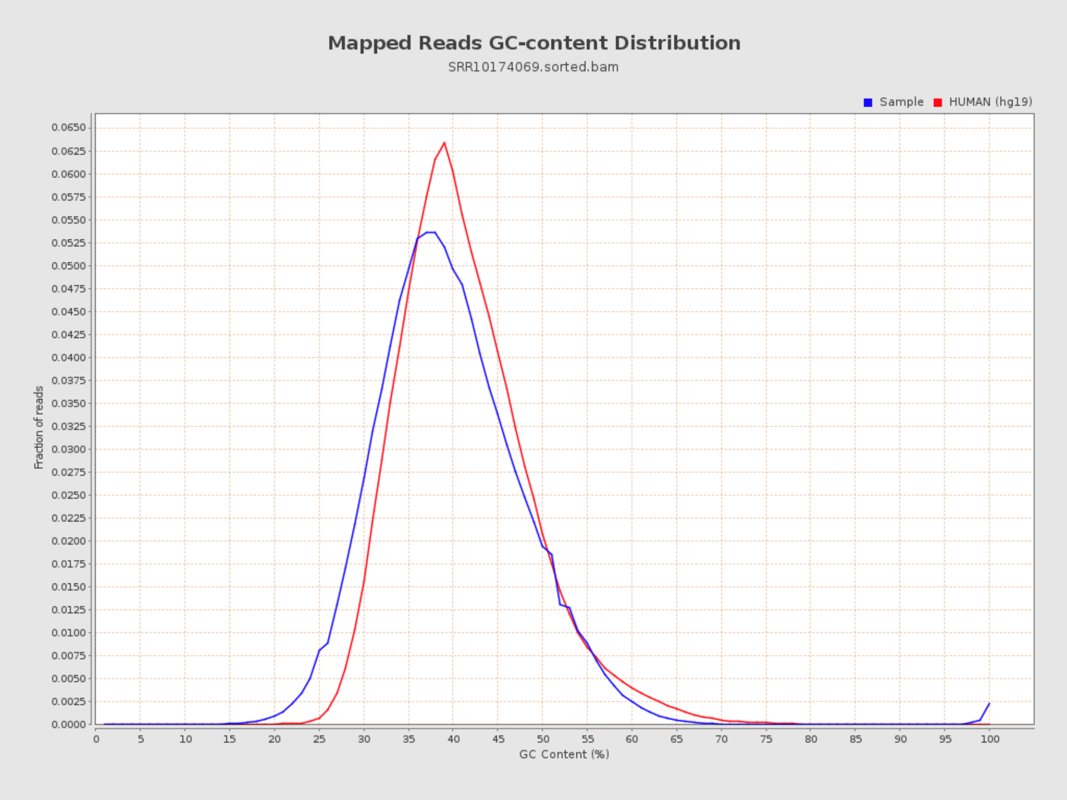
7. Results : Duplication Rate Histogram



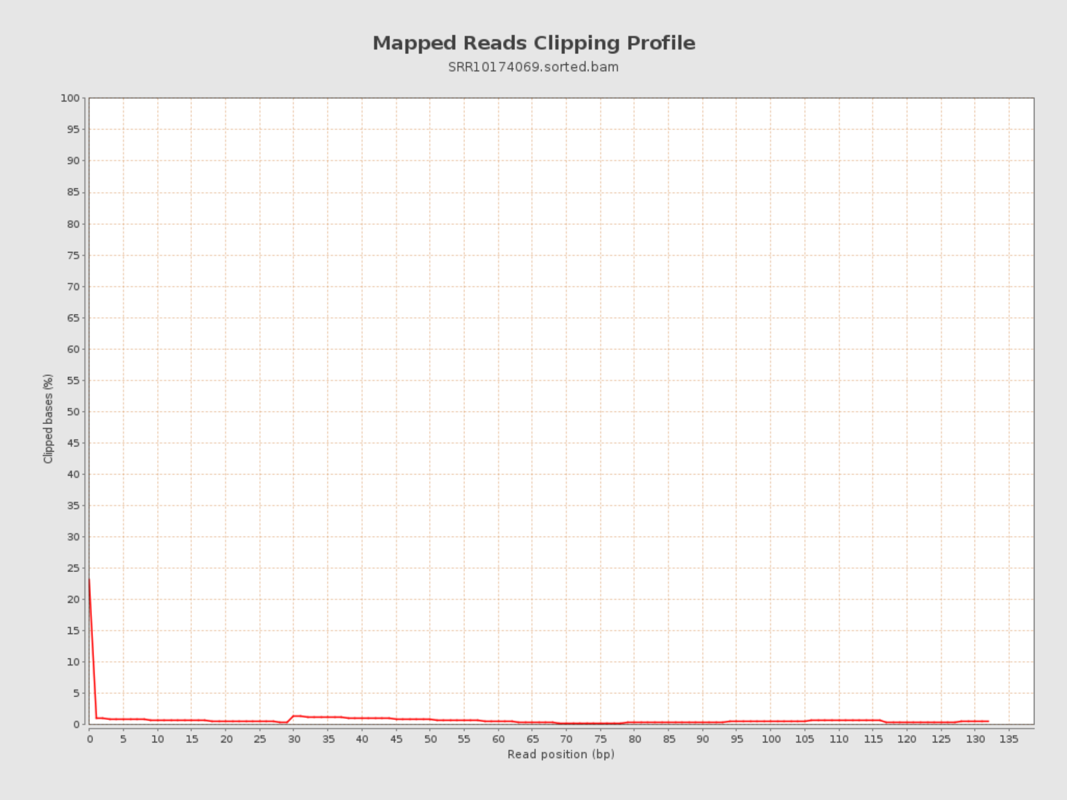
8. Results : Mapped Reads Nucleotide Content



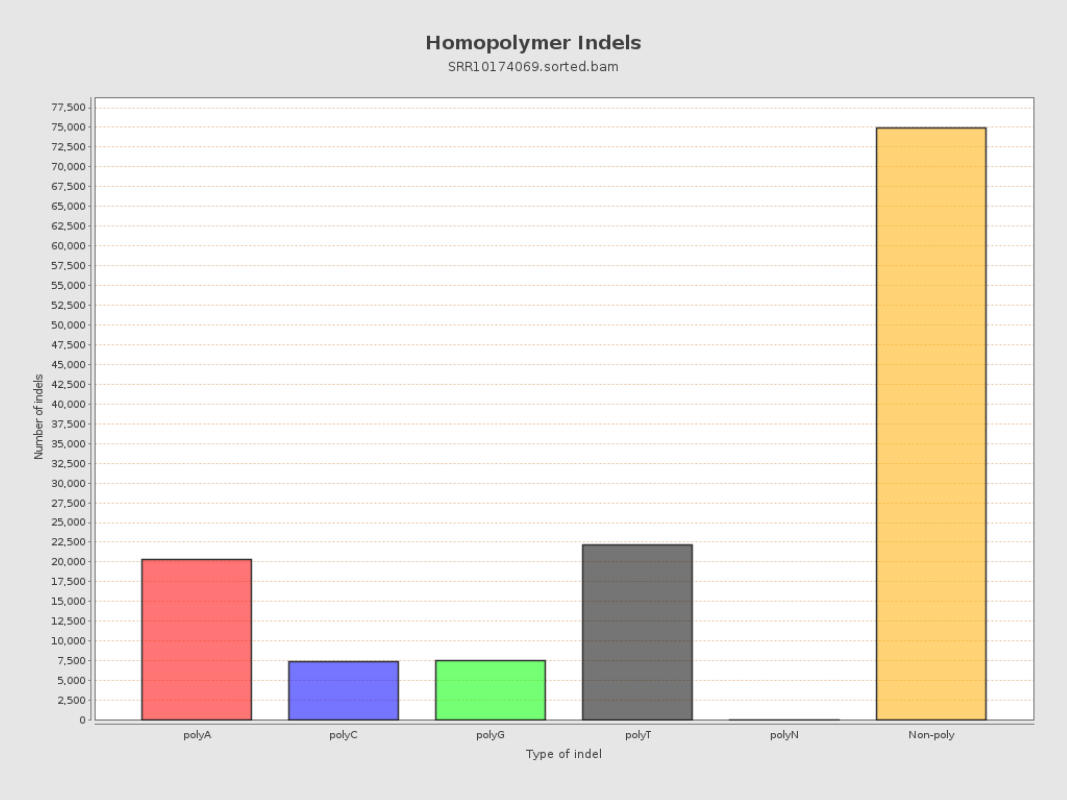
9. Results : Mapped Reads GC-content Distribution



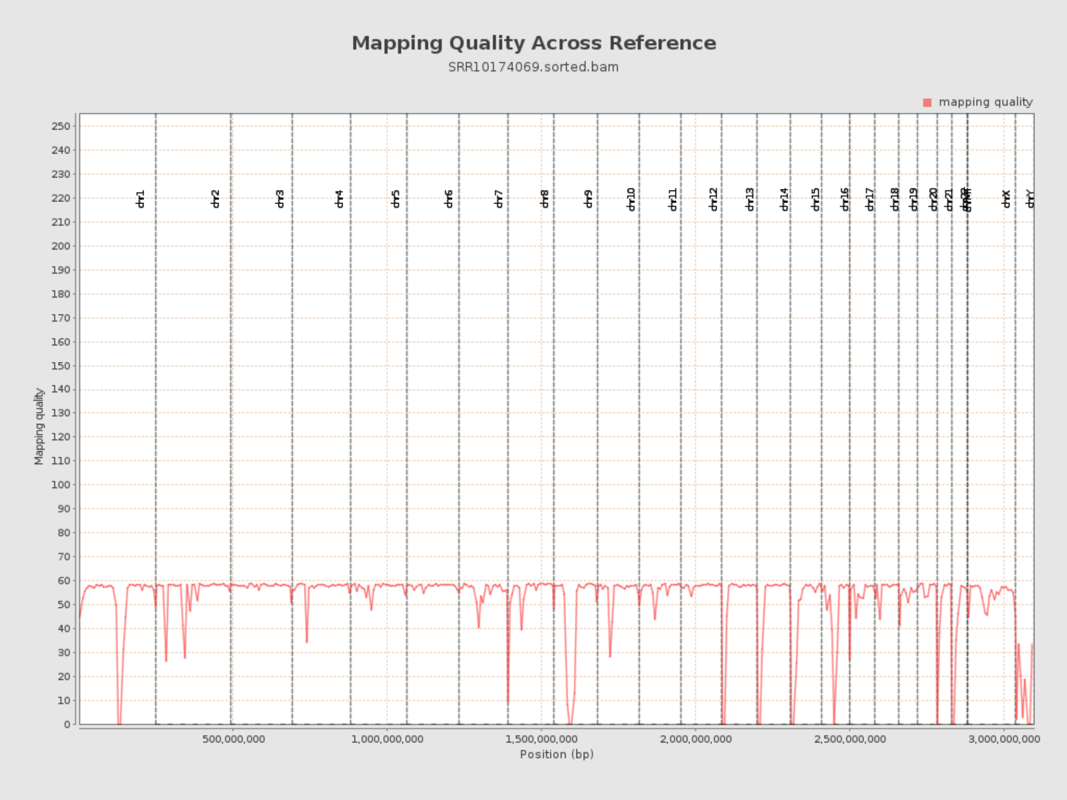
10. Results : Mapped Reads Clipping Profile



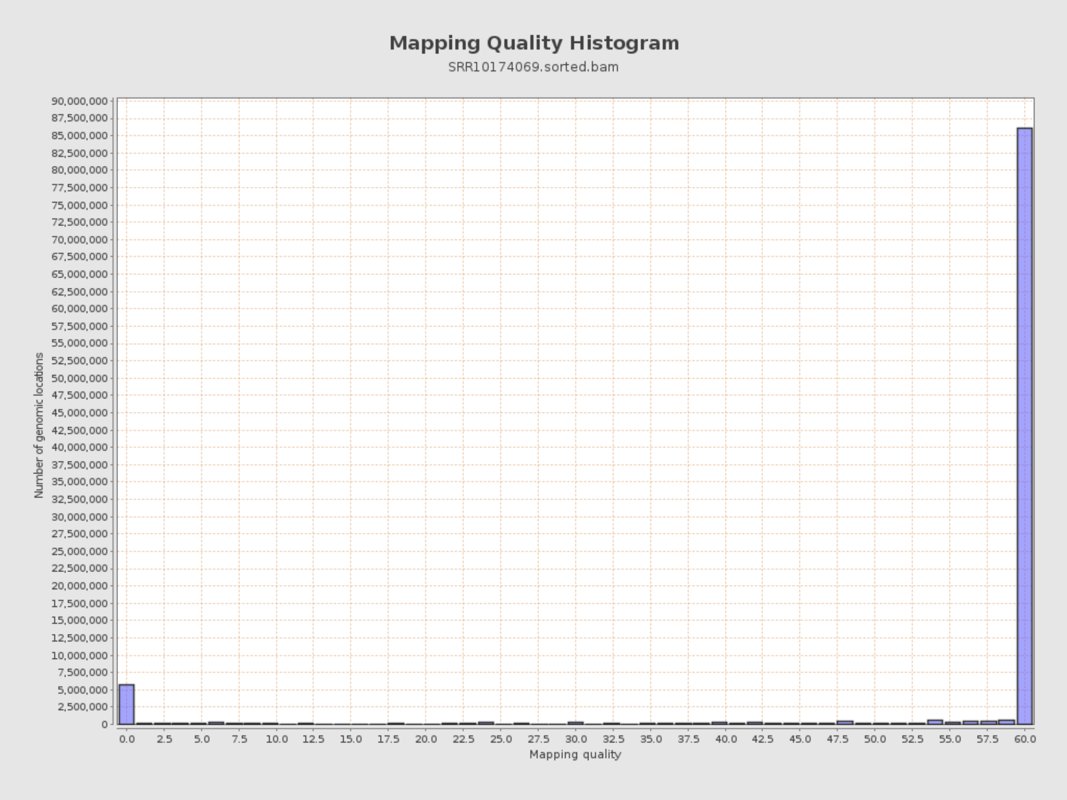
11. Results : Homopolymer Indels



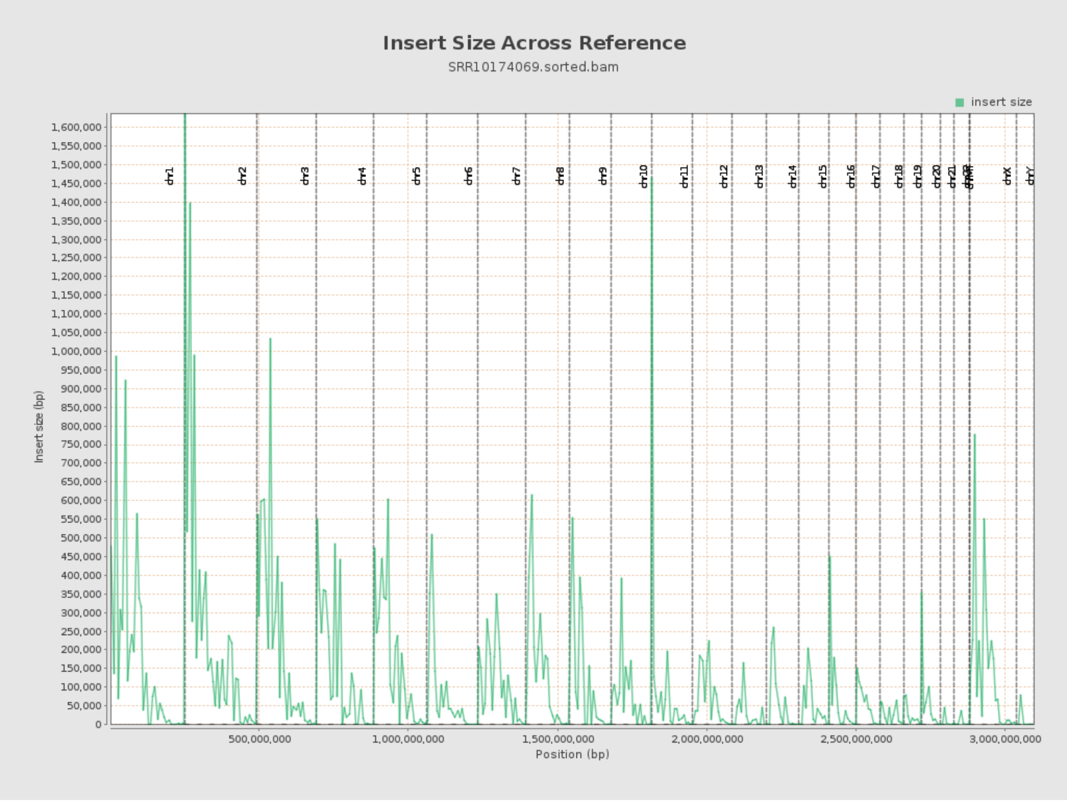
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram