Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 11:16:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124967.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_SRR3124967 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124967_1.fastq.gz SRR3124967_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 11:16:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124967.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,893,060
Mapped reads	5,734,020 / 97.3%
Unmapped reads	159,040 / 2.7%
Mapped paired reads	5,734,020 / 97.3%
Mapped reads, first in pair	2,873,012 / 48.75%
Mapped reads, second in pair	2,861,008 / 48.55%
Mapped reads, both in pair	5,702,606 / 96.77%
Mapped reads, singletons	31,414 / 0.53%
Secondary alignments	0
Supplementary alignments	57,284 / 0.97%
Read min/max/mean length	30 / 101 / 101.39
Duplicated reads (estimated)	767,797 / 13.03%
Duplication rate	9.63%
Clipped reads	3,368,502 / 57.16%

2.2. ACGT Content

Number/percentage of A's	139,798,139 / 29.01%
Number/percentage of C's	87,684,459 / 18.2%
Number/percentage of T's	146,579,592 / 30.42%
Number/percentage of G's	107,772,874 / 22.37%
Number/percentage of N's	4,823 / 0%

GC Percentage	40.56%

2.3. Coverage

Mean	0.1557
Standard Deviation	2.2235

2.4. Mapping Quality

Mean Mapping Quality	52.32

2.5. Insert size

Mean	81,513.45
Standard Deviation	2,673,167.47
P25/Median/P75	115 / 161 / 229

2.6. Mismatches and indels

General error rate	0.81%
Mismatches	3,707,292
Insertions	75,994
Mapped reads with at least one insertion	1.28%
Deletions	152,856
Mapped reads with at least one deletion	2.61%
Homopolymer indels	45.65%

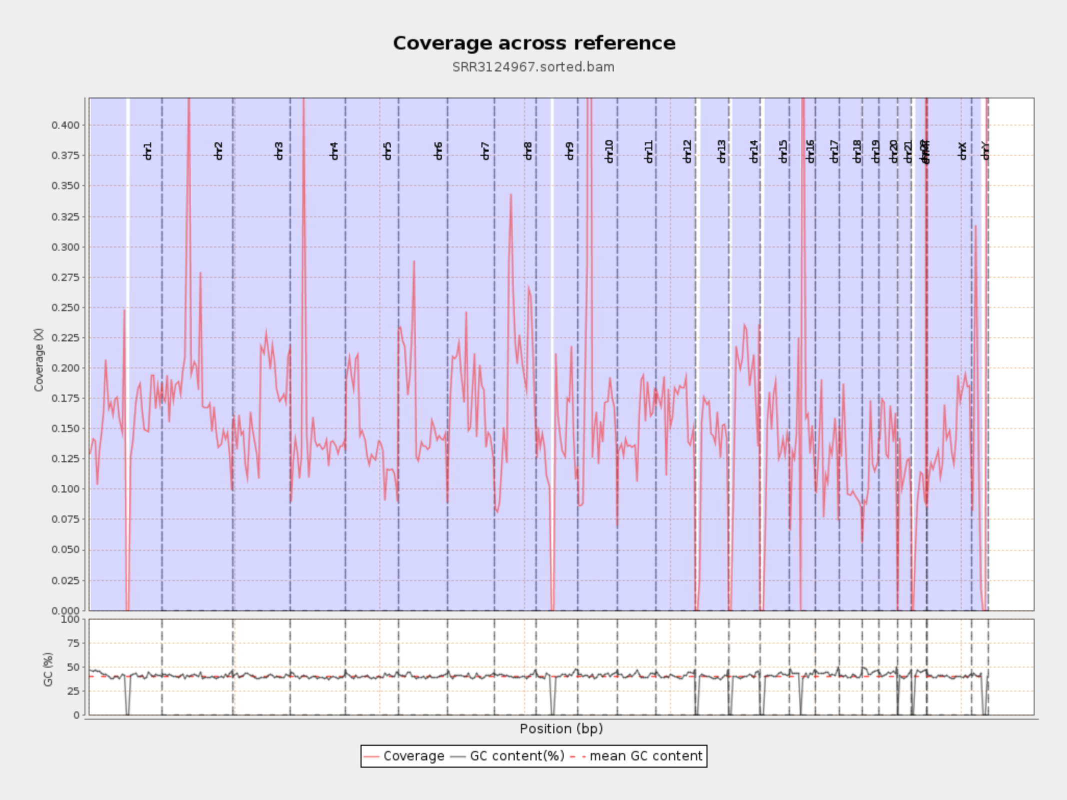
2.7. Chromosome stats

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

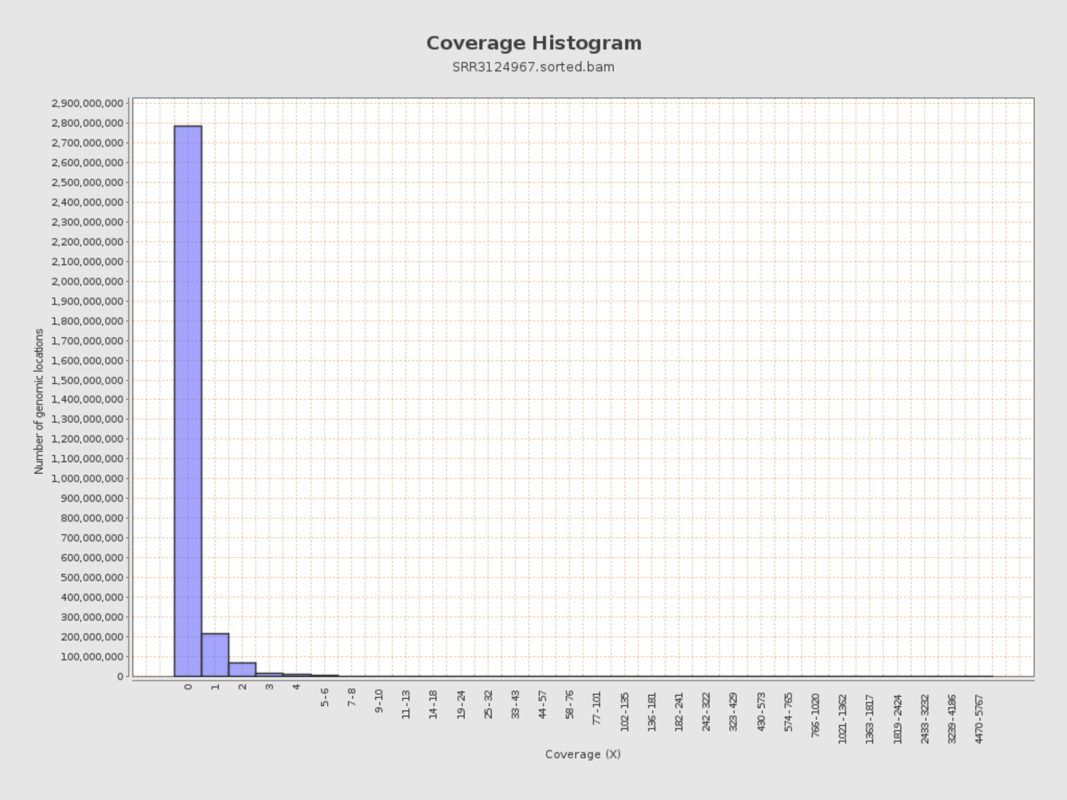
		bases	coverage	deviation
chr1	249250621	38188119	0.1532	1.7868
chr2	243199373	45309833	0.1863	2.3206
chr3	198022430	33726946	0.1703	0.6543
chr4	191154276	27613860	0.1445	1.7139
chr5	180915260	25967449	0.1435	0.5526
chr6	171115067	28761767	0.1681	1.0435
chr7	159138663	28440702	0.1787	1.5323
chr8	146364022	28282928	0.1932	0.8428
chr9	141213431	18620660	0.1319	1.732
chr10	135534747	27976797	0.2064	8.0094
chr11	135006516	20312696	0.1505	0.9278
chr12	133851895	22302244	0.1666	0.5624
chr13	115169878	14620731	0.1269	0.478
chr14	107349540	17893491	0.1667	0.644
chr15	102531392	12700748	0.1239	0.5065
chr16	90354753	15333357	0.1697	3.1242
chr17	81195210	10013106	0.1233	1.4246
chr18	78077248	8847247	0.1133	1.9398
chr19	59128983	6738131	0.114	1.1266
chr20	63025520	9337550	0.1482	0.6877
chr21	48129895	5088994	0.1057	0.9549
chr22	51304566	3708286	0.0723	0.4267
chrMT	16571	210101	12.6788	8.3825
chrX	155270560	22537351	0.1451	0.7434

chrY	59373566	9594712	0.1616	3.8281

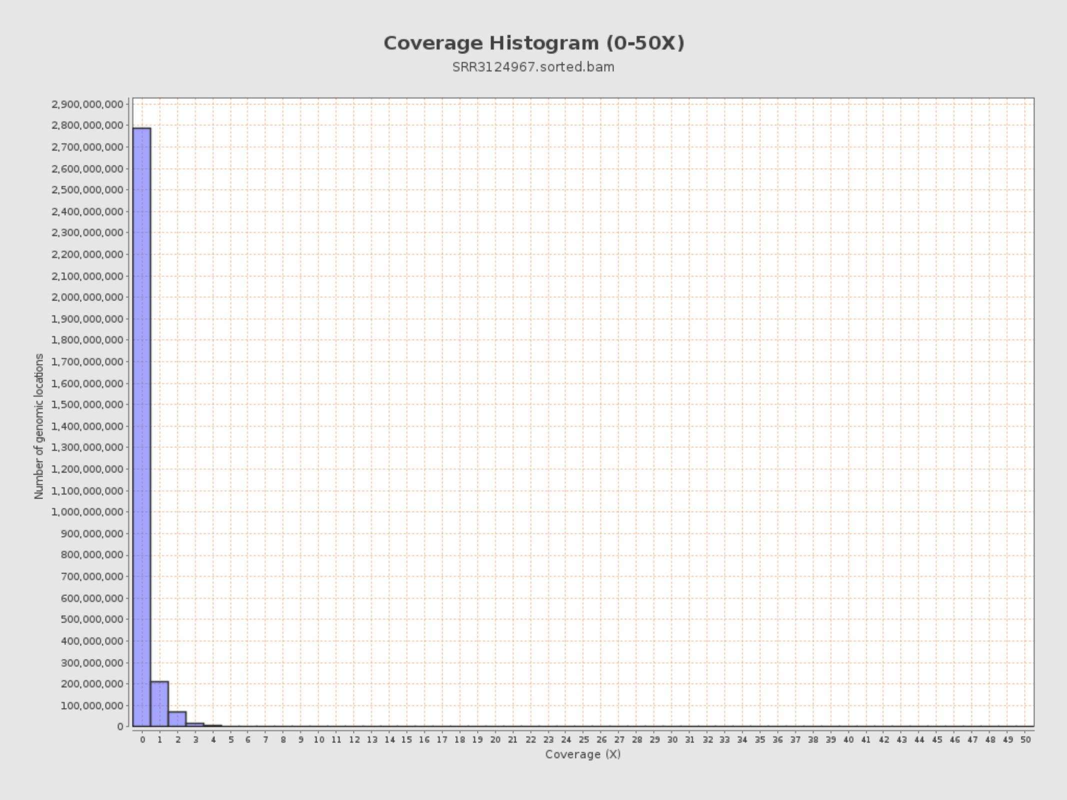
3. Results : Coverage across reference



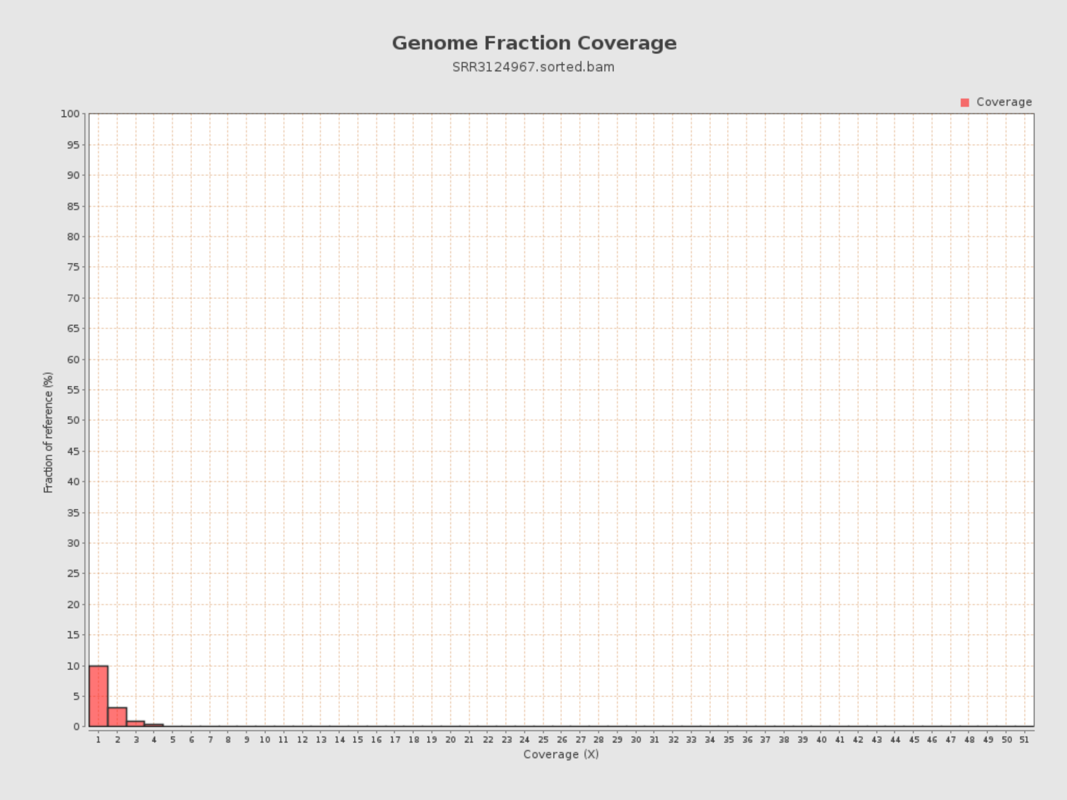
4. Results : Coverage Histogram



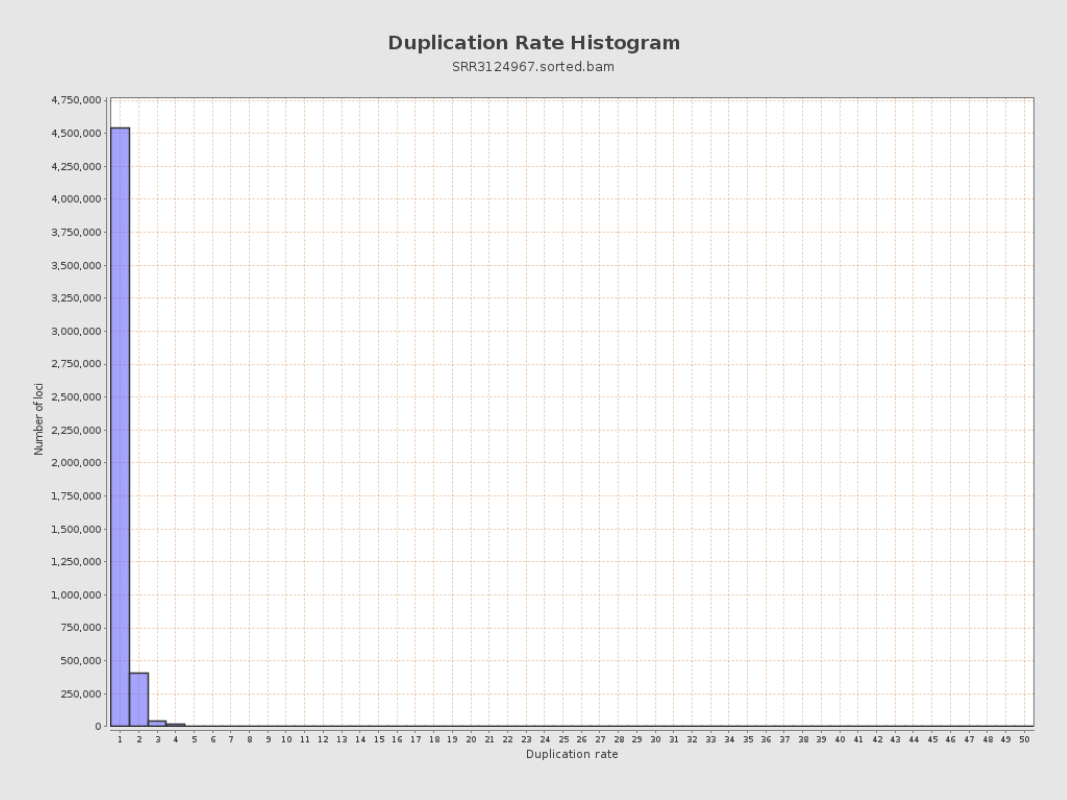
5. Results : Coverage Histogram (0-50X)



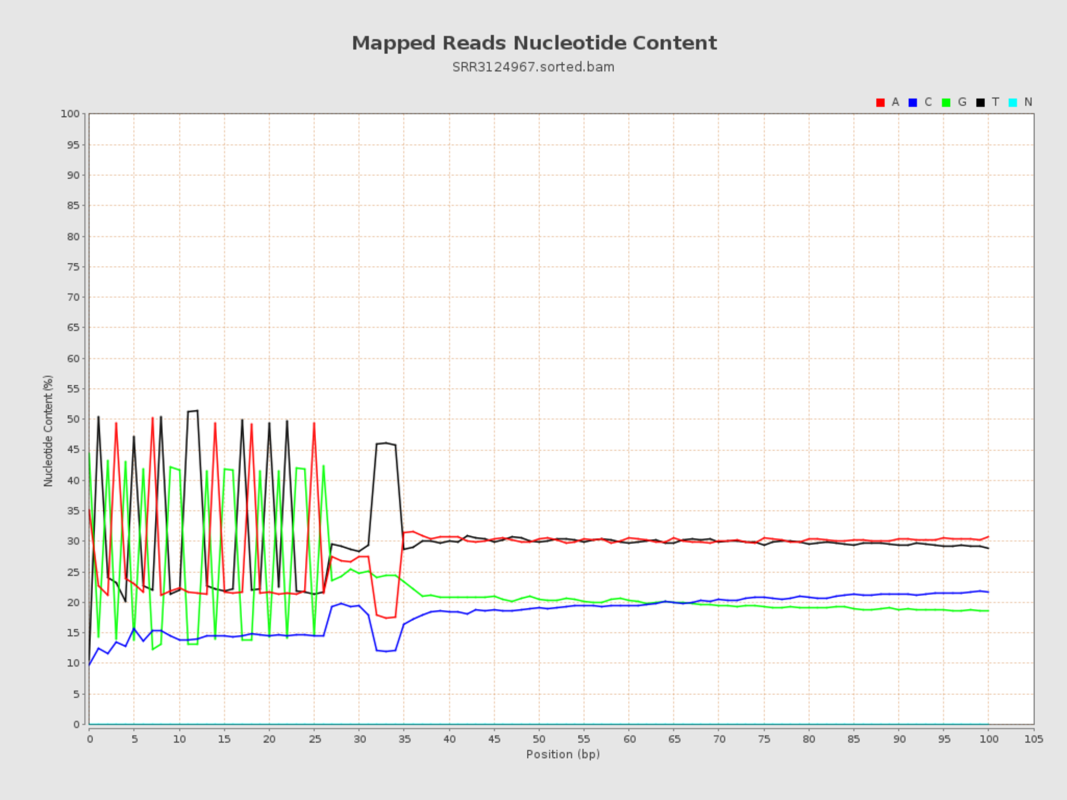
6. Results : Genome Fraction Coverage



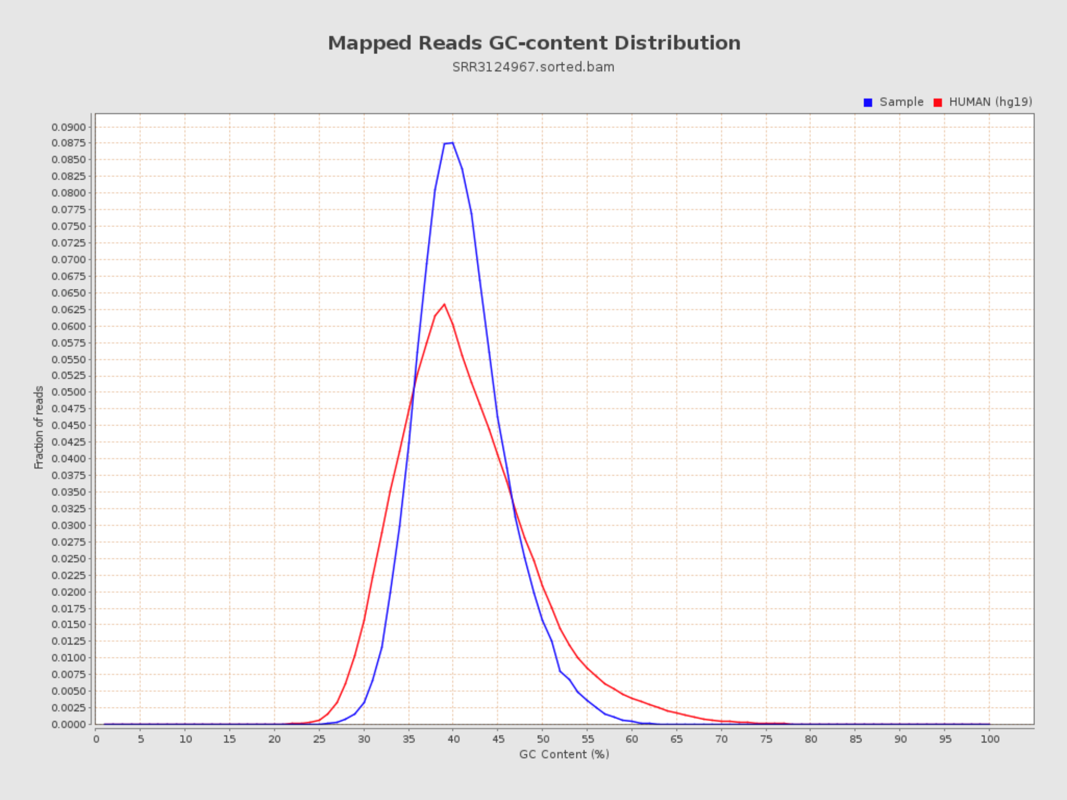
7. Results : Duplication Rate Histogram



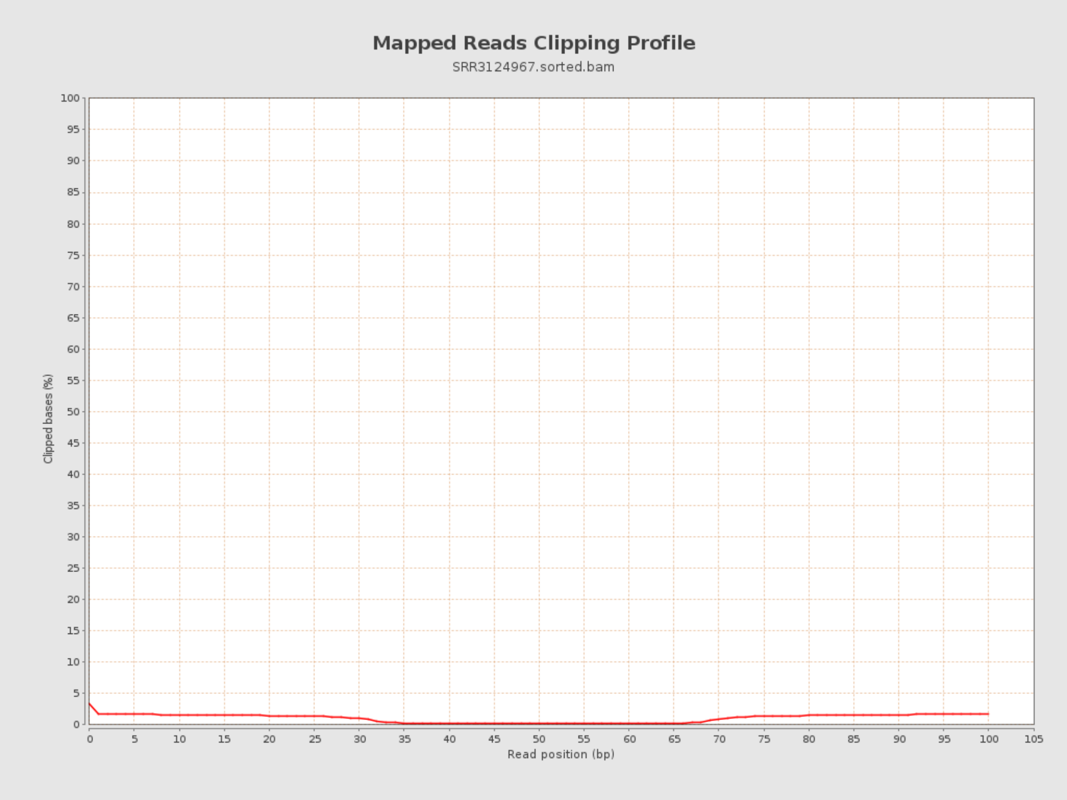
8. Results : Mapped Reads Nucleotide Content



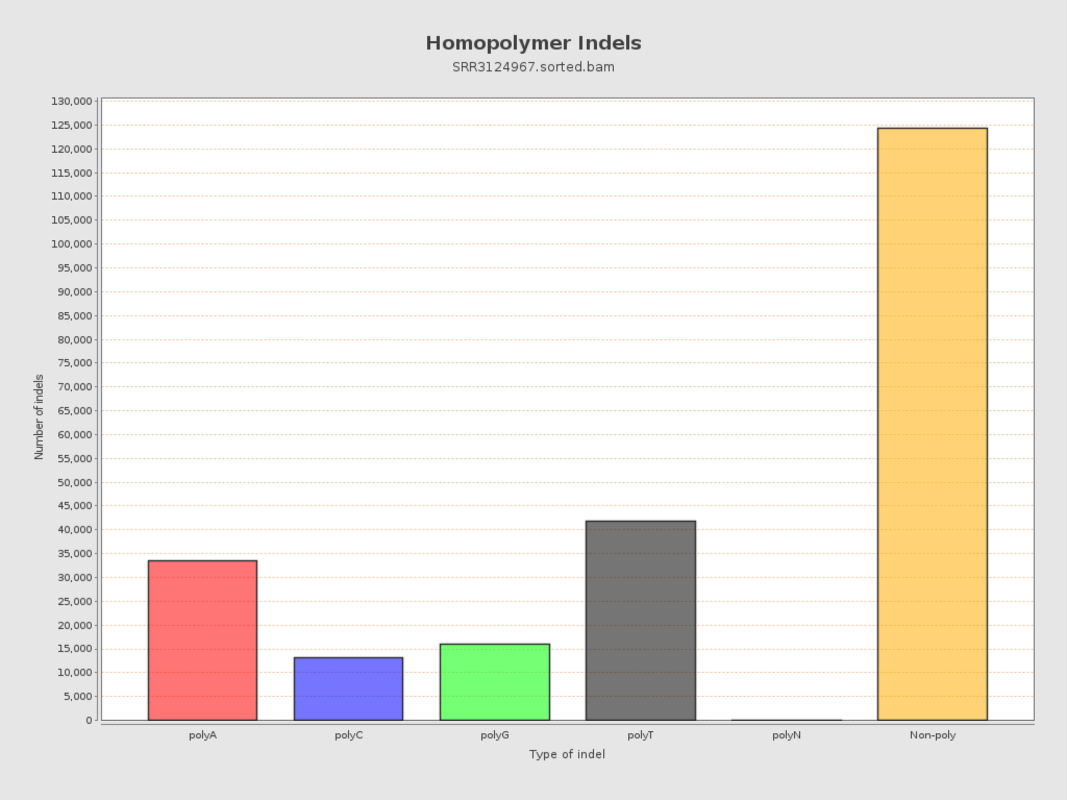
9. Results : Mapped Reads GC-content Distribution



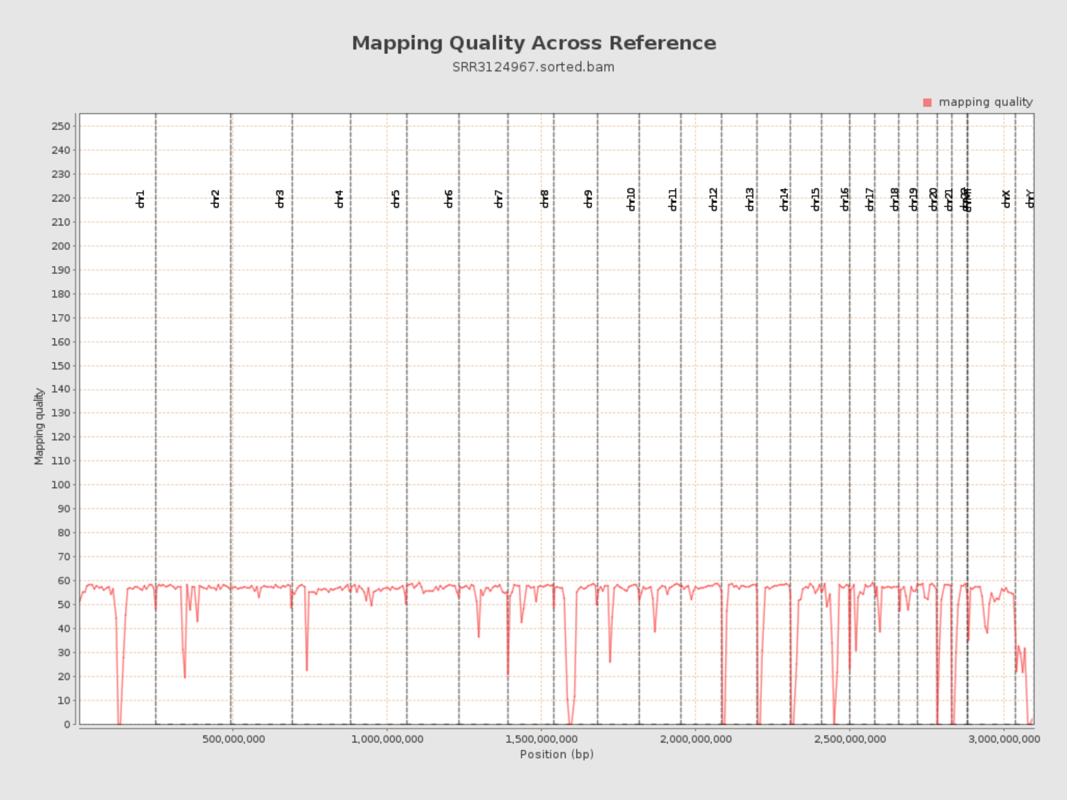
10. Results : Mapped Reads Clipping Profile



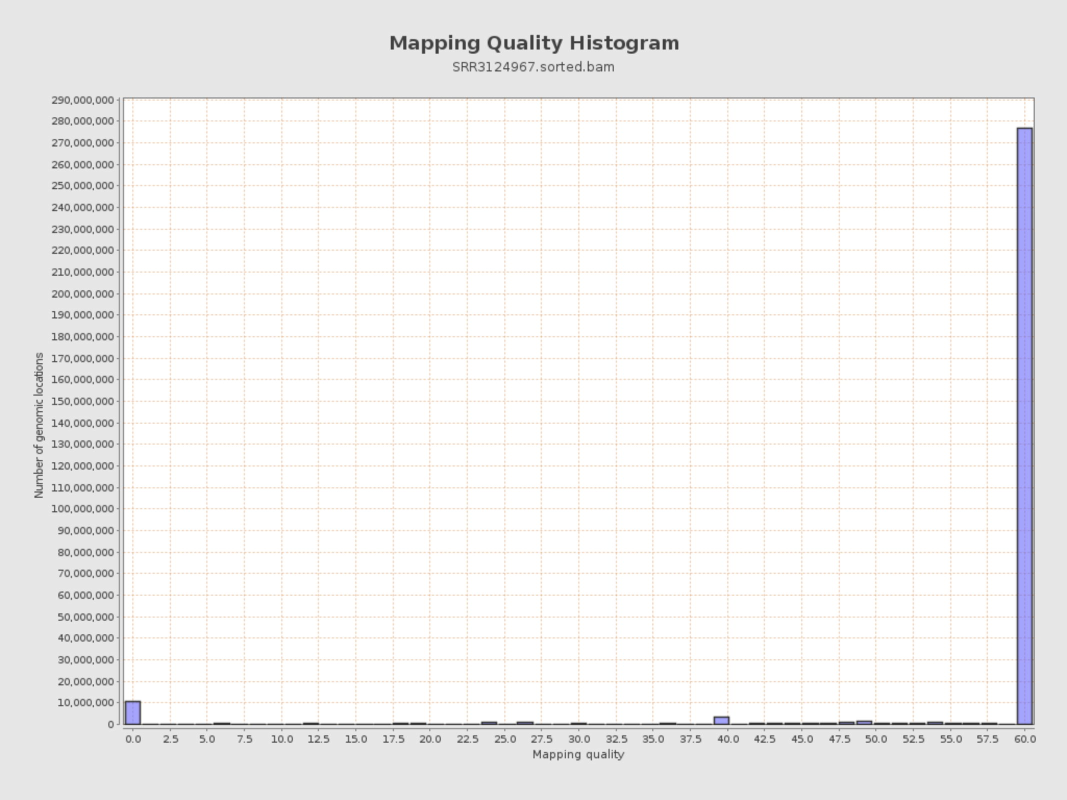
11. Results : Homopolymer Indels



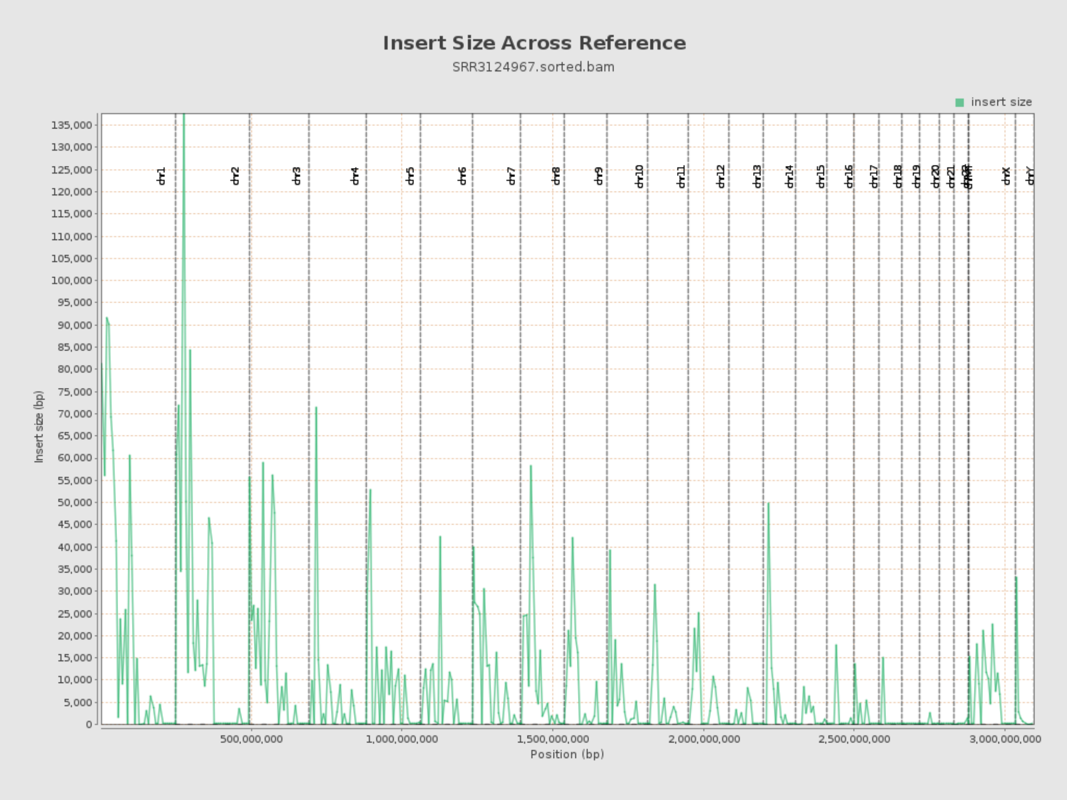
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram