Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 11:24:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124968.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_SRR3124968 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124968_1.fastq.gz SRR3124968_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 11:24:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124968.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,944,054
Mapped reads	5,866,103 / 98.69%
Unmapped reads	77,951 / 1.31%
Mapped paired reads	5,866,103 / 98.69%
Mapped reads, first in pair	2,939,143 / 49.45%
Mapped reads, second in pair	2,926,960 / 49.24%
Mapped reads, both in pair	5,839,354 / 98.24%
Mapped reads, singletons	26,749 / 0.45%
Secondary alignments	0
Supplementary alignments	54,206 / 0.91%
Read min/max/mean length	30 / 101 / 101.36
Duplicated reads (estimated)	681,946 / 11.47%
Duplication rate	8.39%
Clipped reads	3,350,680 / 56.37%

2.2. ACGT Content

Number/percentage of A's	143,601,689 / 28.91%
Number/percentage of C's	90,202,452 / 18.16%
Number/percentage of T's	150,898,544 / 30.38%
Number/percentage of G's	112,039,621 / 22.55%
Number/percentage of N's	5,064 / 0%

GC Percentage	40.71%

2.3. Coverage

Mean	0.1606
Standard Deviation	1.9675

2.4. Mapping Quality

Mean Mapping Quality	52.45

2.5. Insert size

Mean	74,907.27
Standard Deviation	2,568,674.53
P25/Median/P75	121 / 166 / 231

2.6. Mismatches and indels

General error rate	0.77%
Mismatches	3,655,704
Insertions	76,713
Mapped reads with at least one insertion	1.27%
Deletions	158,663
Mapped reads with at least one deletion	2.65%
Homopolymer indels	46.03%

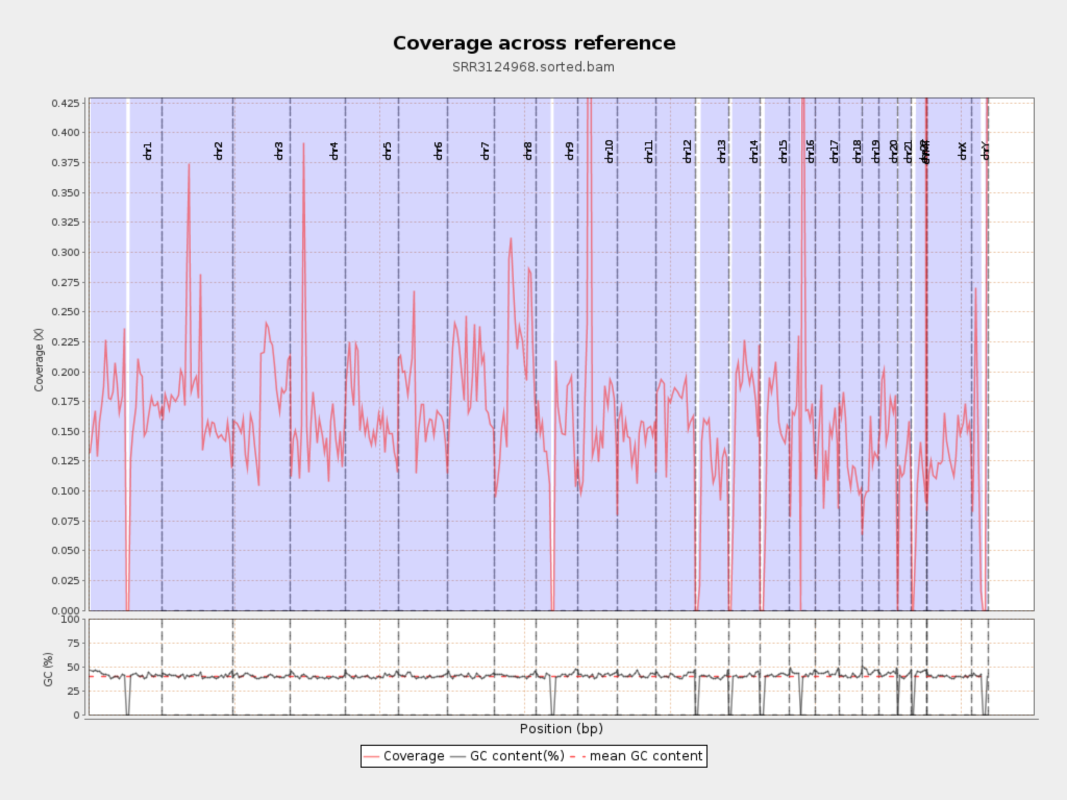
2.7. Chromosome stats

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

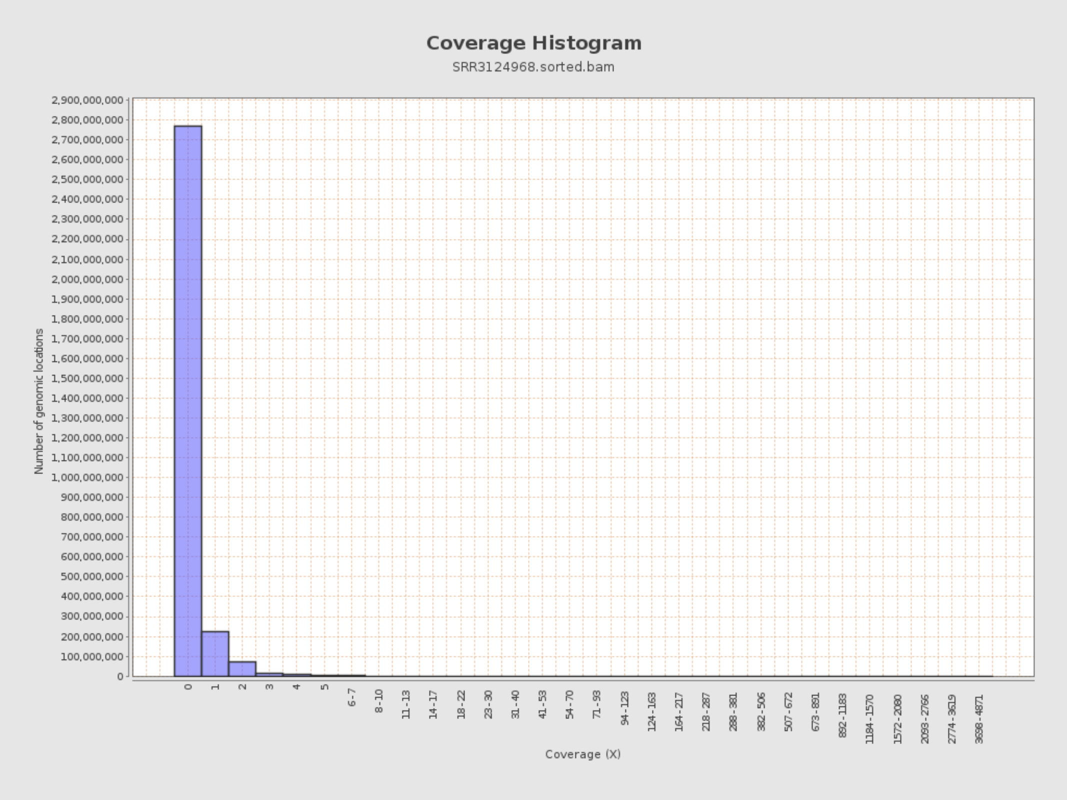
		bases	coverage	deviation
chr1	249250621	40636756	0.163	1.4269
chr2	243199373	43610947	0.1793	2.1639
chr3	198022430	34684502	0.1752	0.6268
chr4	191154276	29389848	0.1537	1.5387
chr5	180915260	29375660	0.1624	0.5734
chr6	171115067	29641152	0.1732	0.8793
chr7	159138663	31375430	0.1972	1.4823
chr8	146364022	30388997	0.2076	0.7923
chr9	141213431	19723469	0.1397	1.6672
chr10	135534747	27000281	0.1992	6.8771
chr11	135006516	19668082	0.1457	0.8451
chr12	133851895	23310816	0.1742	0.5682
chr13	115169878	12670114	0.11	0.4366
chr14	107349540	17123574	0.1595	0.6301
chr15	102531392	14005204	0.1366	0.5235
chr16	90354753	17074573	0.189	3.2245
chr17	81195210	10980350	0.1352	1.2891
chr18	78077248	10210234	0.1308	1.8152
chr19	59128983	6962437	0.1177	0.9463
chr20	63025520	10461227	0.166	0.705
chr21	48129895	5515903	0.1146	0.8879
chr22	51304566	4173713	0.0814	0.4476
chrMT	16571	120391	7.2652	5.116
chrX	155270560	20794341	0.1339	0.677

chrY	59373566	8143451	0.1372	3.1791

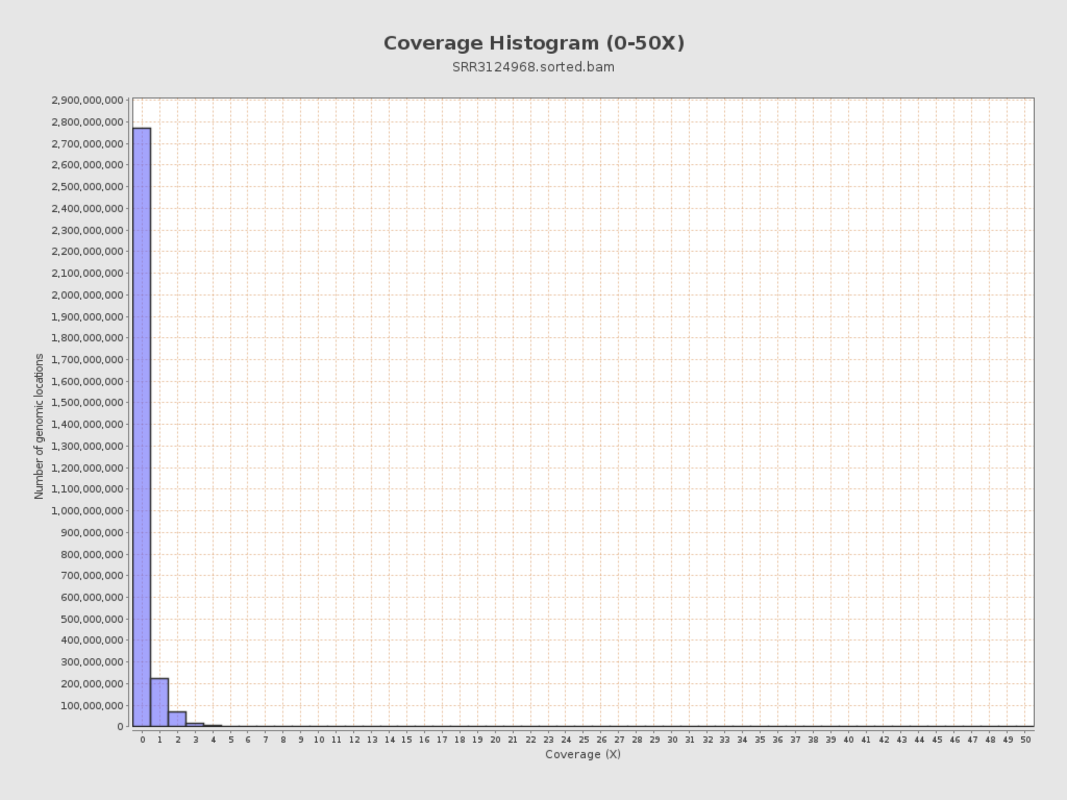
3. Results : Coverage across reference



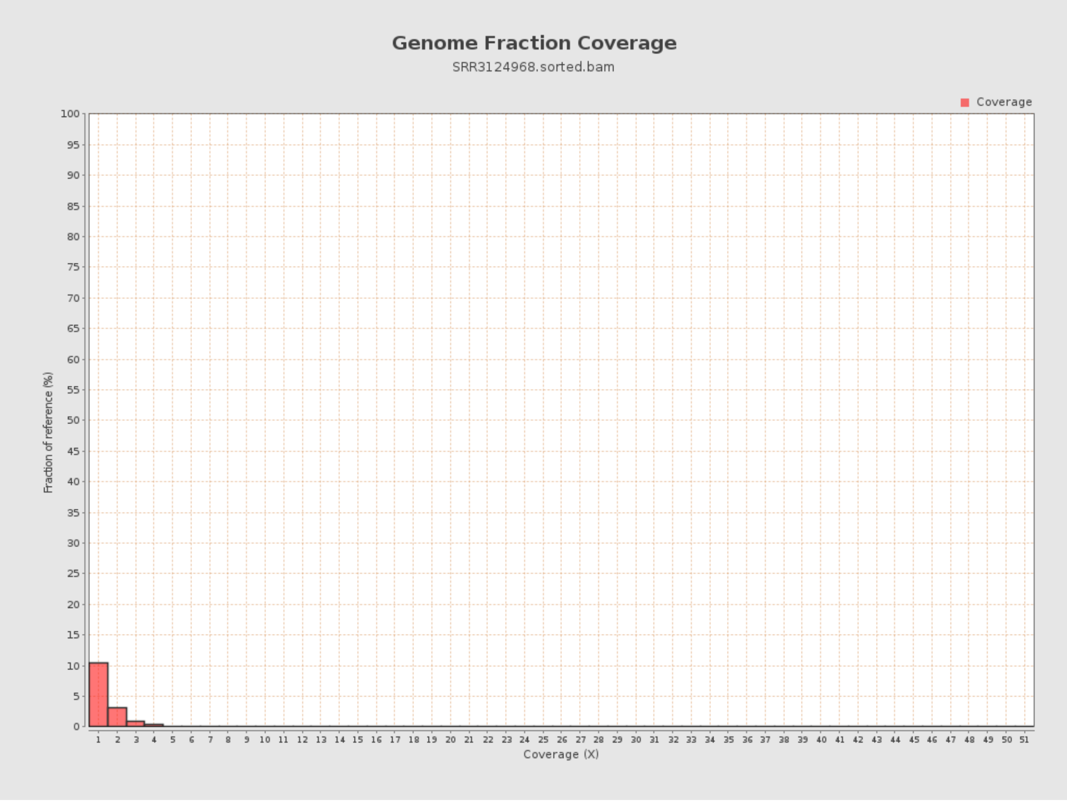
4. Results : Coverage Histogram



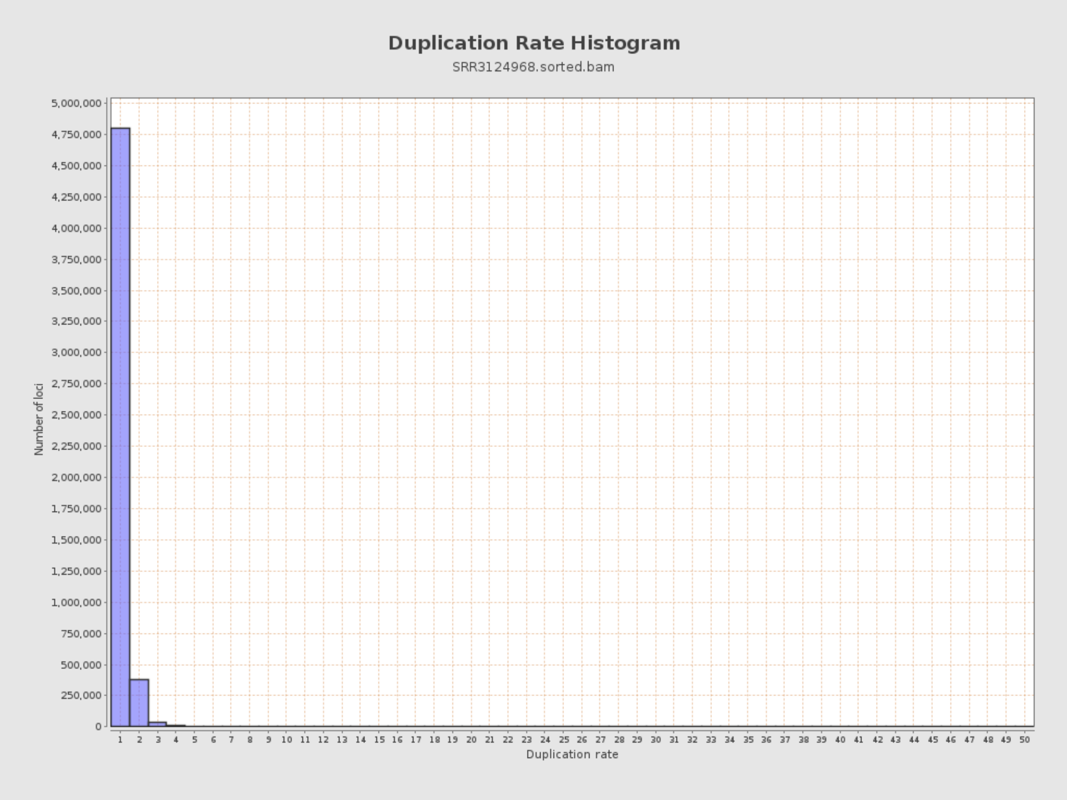
5. Results : Coverage Histogram (0-50X)



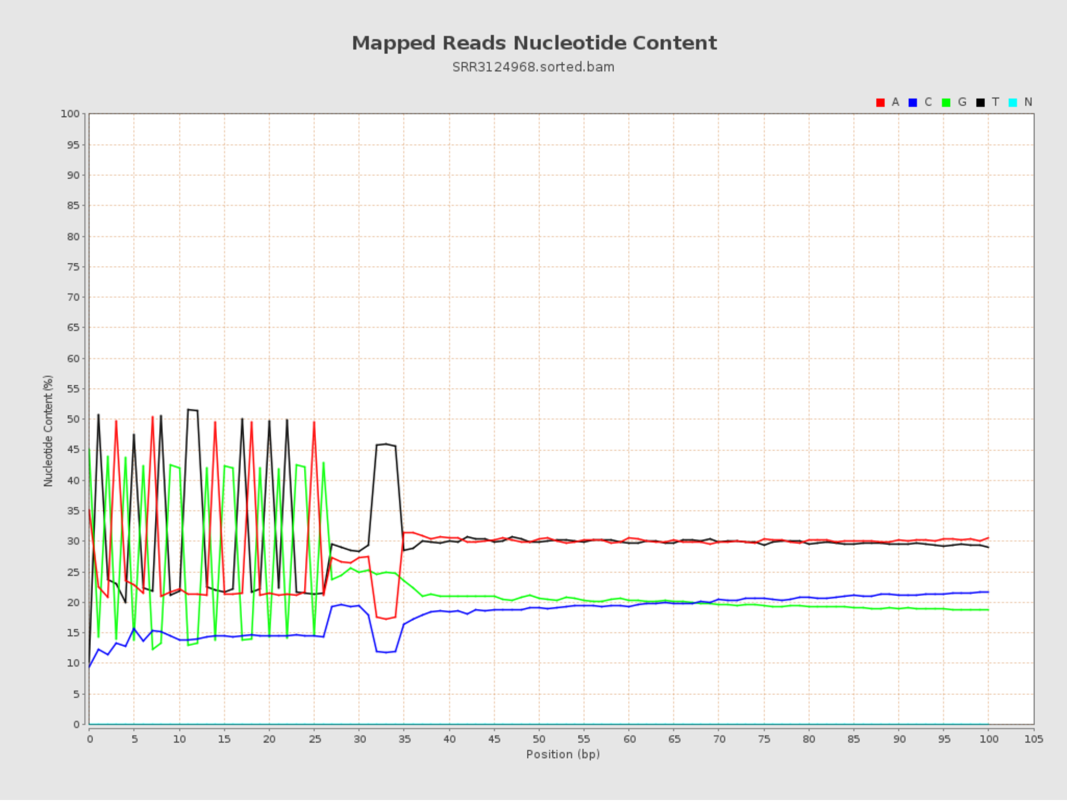
6. Results : Genome Fraction Coverage



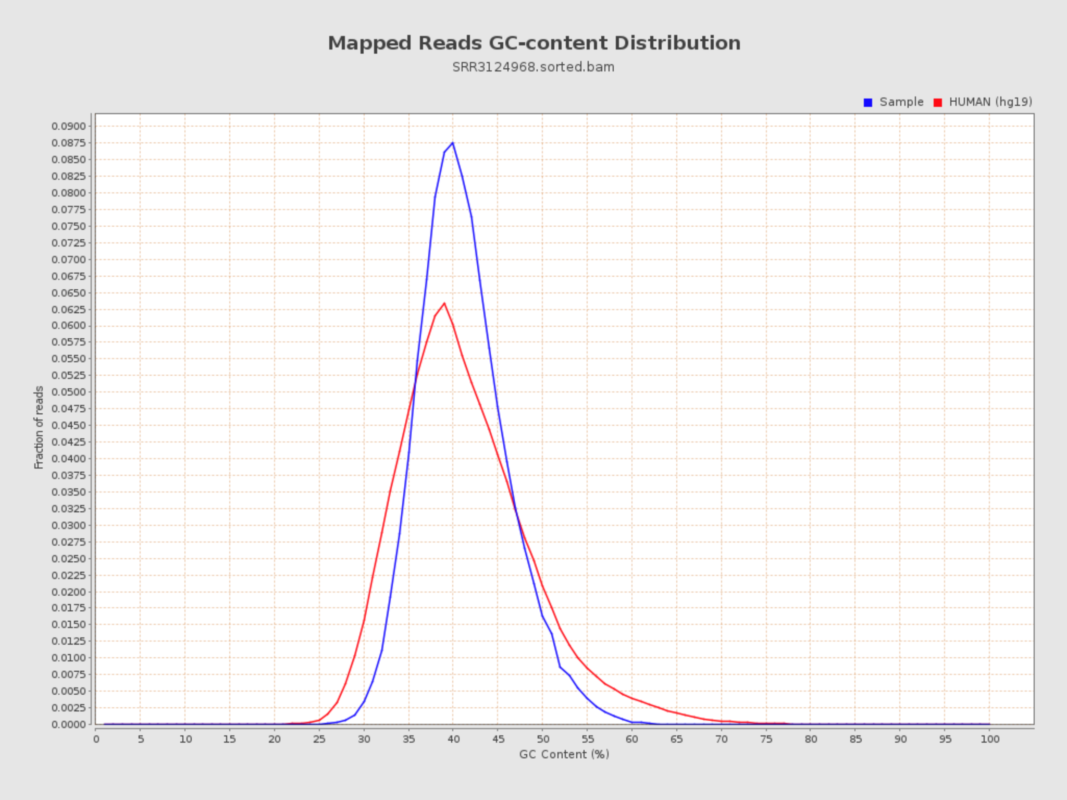
7. Results : Duplication Rate Histogram



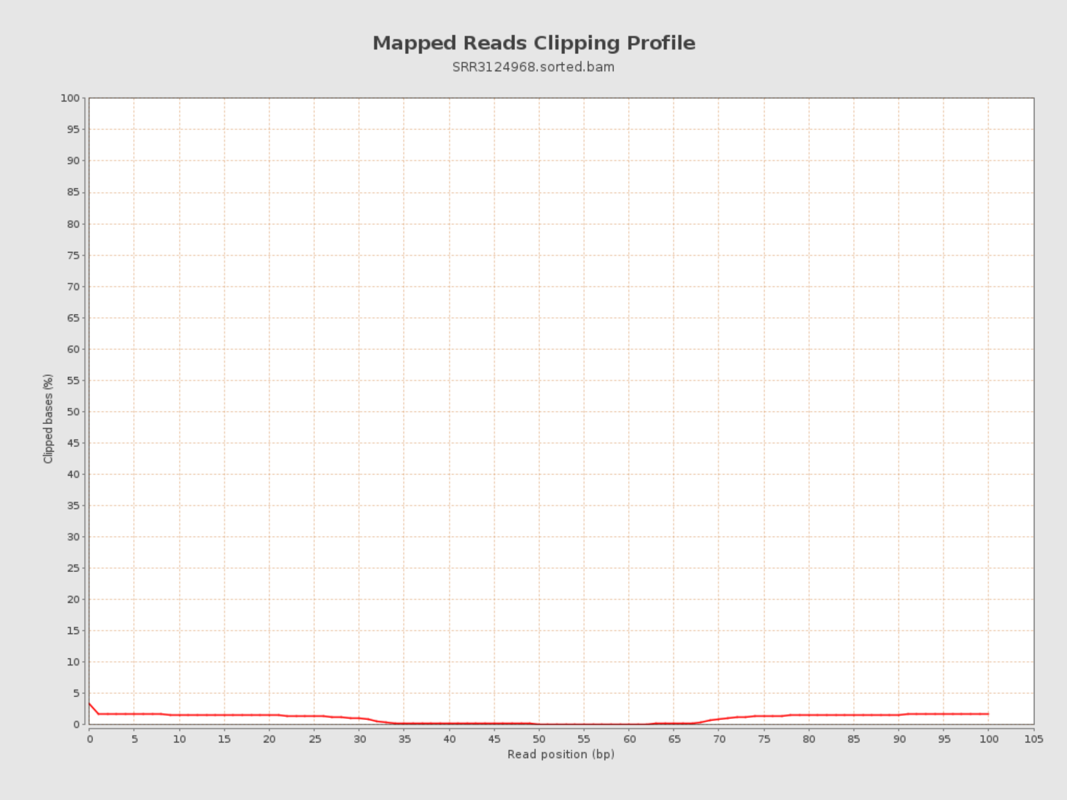
8. Results : Mapped Reads Nucleotide Content



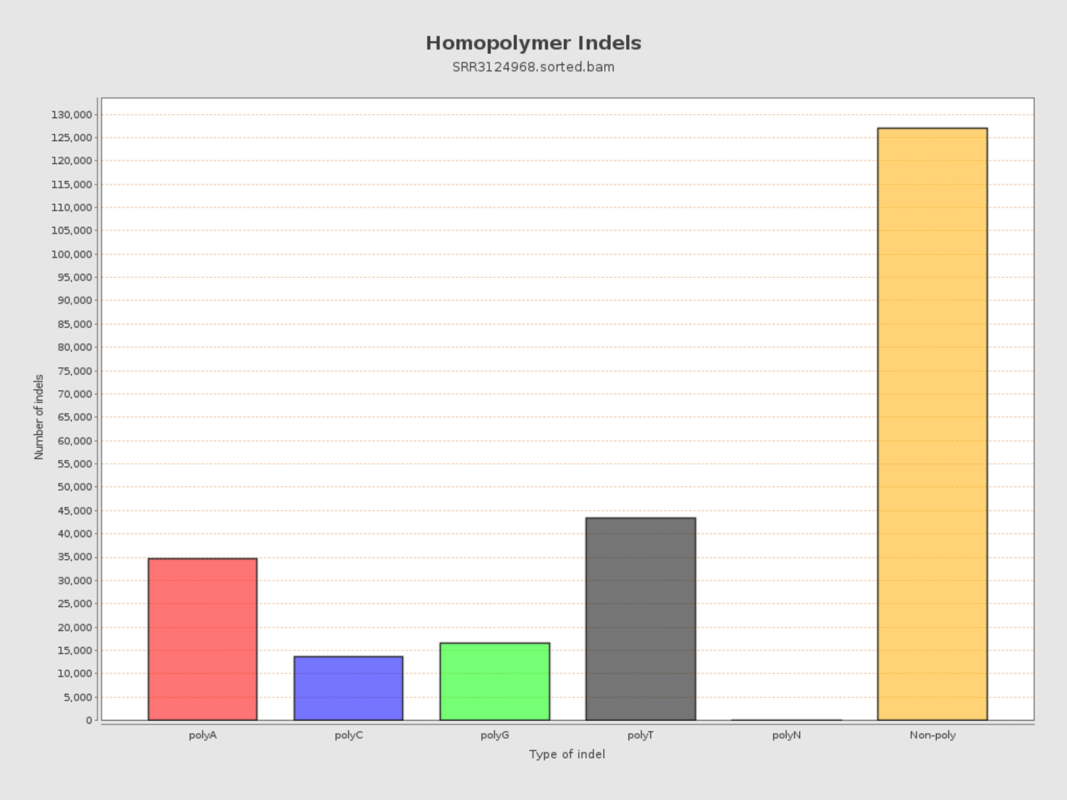
9. Results : Mapped Reads GC-content Distribution



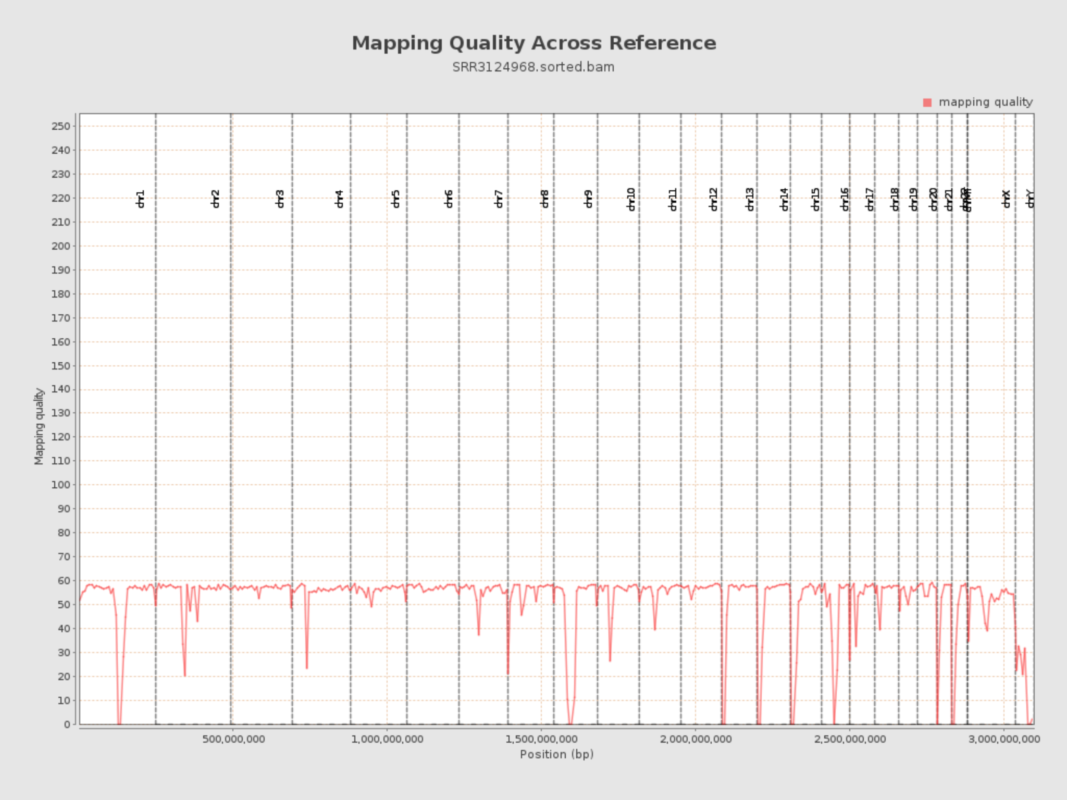
10. Results : Mapped Reads Clipping Profile



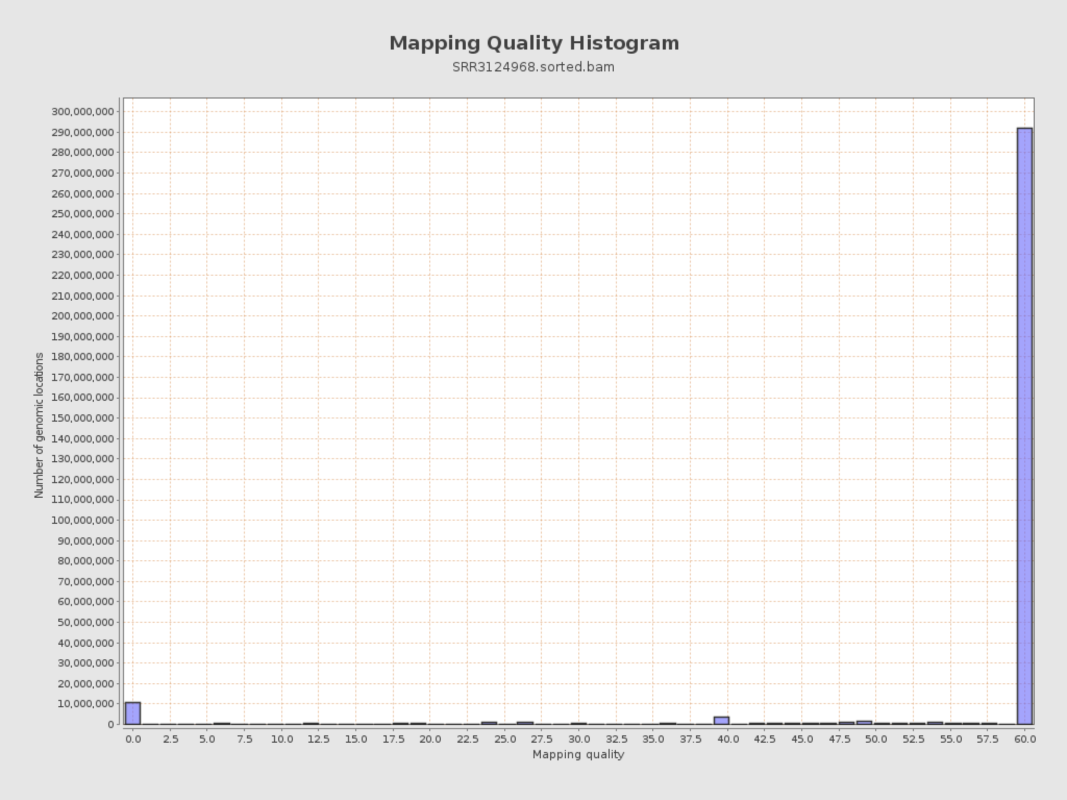
11. Results : Homopolymer Indels



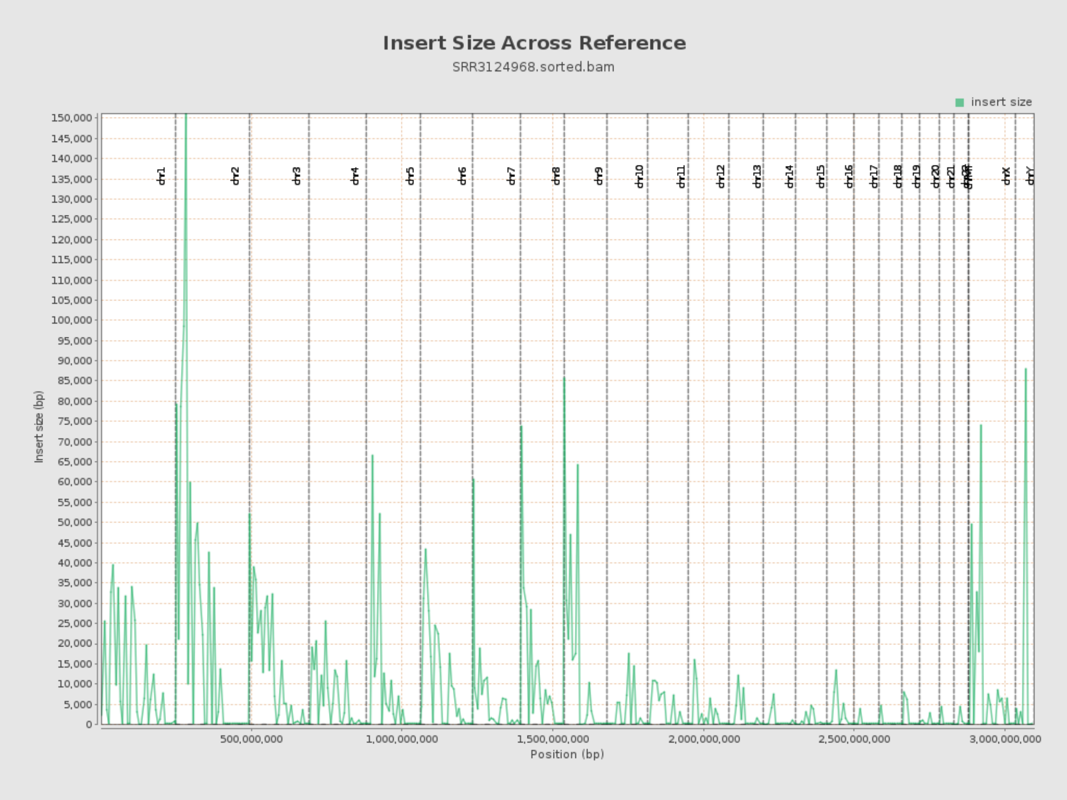
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram