Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/29 20:38:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472724.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_SRR3472724 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472724_1.fastq.gz SRR3472724_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 29 20:38:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472724.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	18,571,332
Mapped reads	18,411,607 / 99.14%
Unmapped reads	159,725 / 0.86%
Mapped paired reads	18,411,607 / 99.14%
Mapped reads, first in pair	9,233,873 / 49.72%
Mapped reads, second in pair	9,177,734 / 49.42%
Mapped reads, both in pair	18,319,678 / 98.64%
Mapped reads, singletons	91,929 / 0.5%
Secondary alignments	0
Supplementary alignments	64,556 / 0.35%
Read min/max/mean length	30 / 100 / 100.14
Duplicated reads (estimated)	11,769,401 / 63.37%
Duplication rate	46.69%
Clipped reads	1,559,161 / 8.4%

2.2. ACGT Content

Number/percentage of A's	490,775,011 / 27.1%
Number/percentage of C's	417,501,394 / 23.05%
Number/percentage of T's	487,724,240 / 26.93%
Number/percentage of G's	414,870,748 / 22.91%
Number/percentage of N's	351,354 / 0.02%

GC Percentage	45.96%

2.3. Coverage

Mean	0.5852
Standard Deviation	21.3969

2.4. Mapping Quality

Mean Mapping Quality	55.15

2.5. Insert size

Mean	23,667.92
Standard Deviation	1,480,267.42
P25/Median/P75	167 / 234 / 315

2.6. Mismatches and indels

General error rate	0.61%
Mismatches	10,834,621
Insertions	101,194
Mapped reads with at least one insertion	0.54%
Deletions	96,724
Mapped reads with at least one deletion	0.52%
Homopolymer indels	45.25%

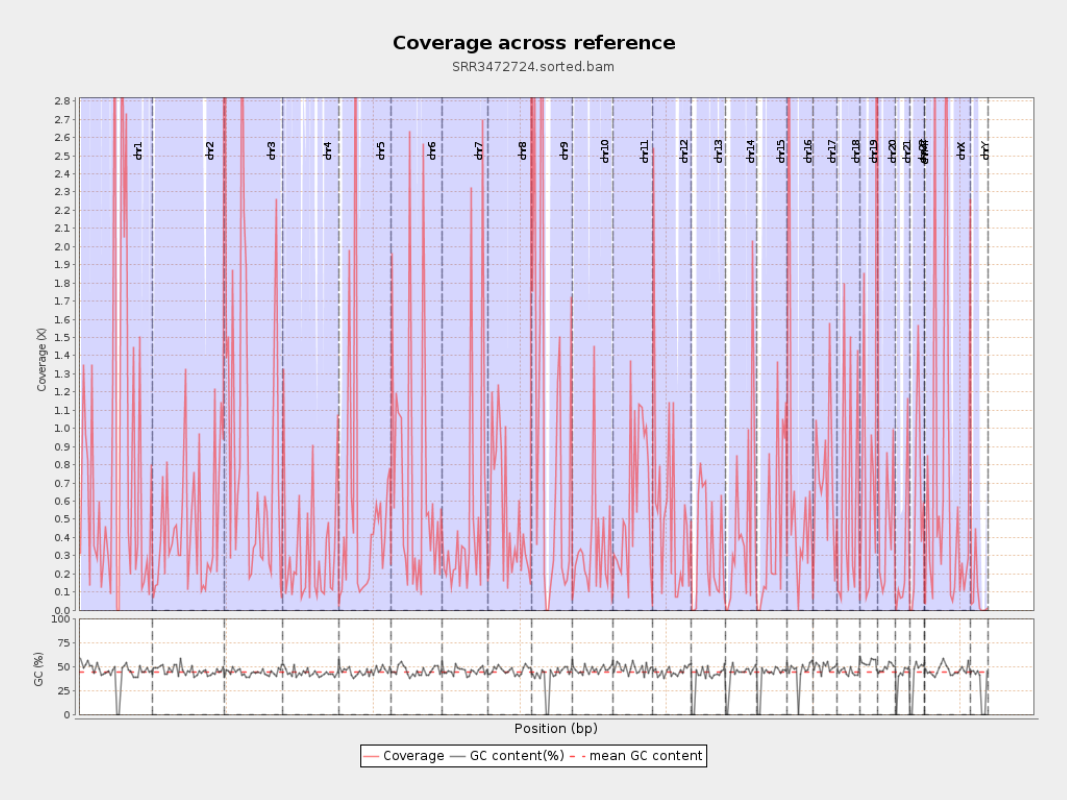
2.7. Chromosome stats

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

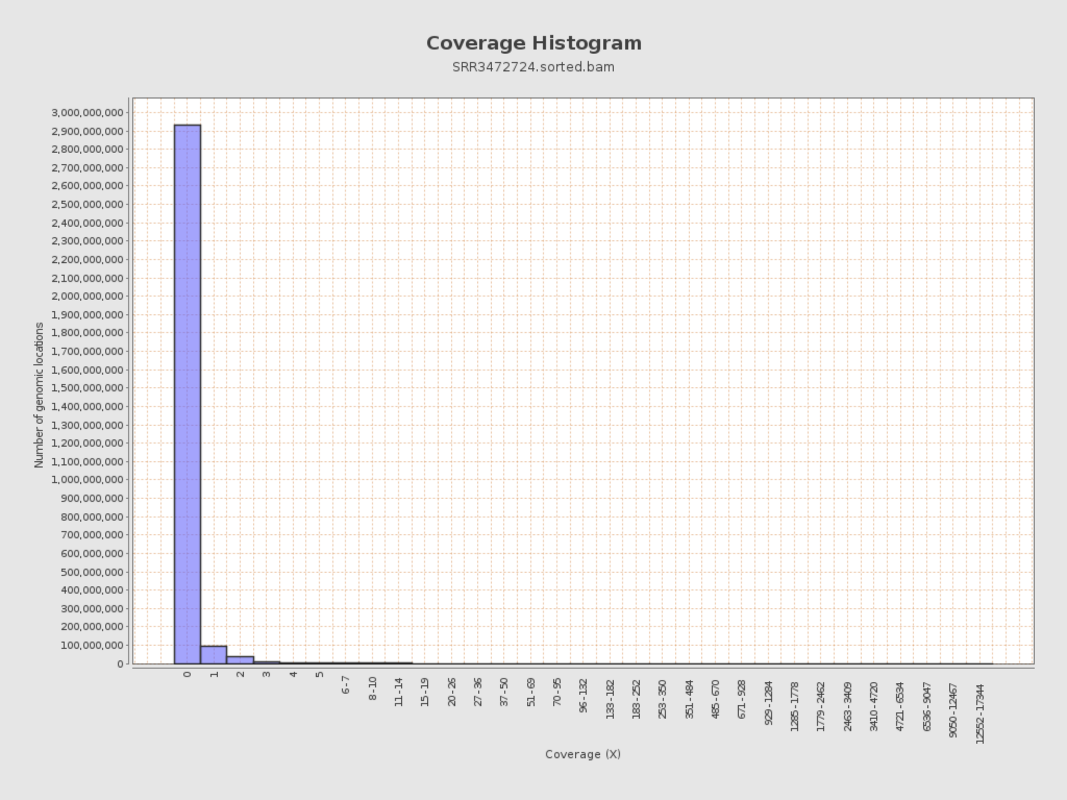
		bases	coverage	deviation
chr1	249250621	202663689	0.8131	32.8566
chr2	243199373	112852893	0.464	15.123
chr3	198022430	190985265	0.9645	25.1222
chr4	191154276	59297727	0.3102	9.9496
chr5	180915260	101173347	0.5592	17.7112
chr6	171115067	118037027	0.6898	22.718
chr7	159138663	83504731	0.5247	23.5514
chr8	146364022	74925404	0.5119	16.3497
chr9	141213431	142751849	1.0109	36.4888
chr10	135534747	46419667	0.3425	11.9739
chr11	135006516	82677060	0.6124	18.3223
chr12	133851895	75763835	0.566	16.8191
chr13	115169878	38700316	0.336	14.6221
chr14	107349540	47324286	0.4408	27.0316
chr15	102531392	44070398	0.4298	15.4198
chr16	90354753	58864013	0.6515	17.7941
chr17	81195210	56848668	0.7001	14.9507
chr18	78077248	46671076	0.5978	31.1049
chr19	59128983	46181513	0.781	20.8313
chr20	63025520	29939708	0.475	13.9445
chr21	48129895	13996592	0.2908	12.6694
chr22	51304566	28476734	0.5551	15.8973
chrMT	16571	2454	0.1481	0.5182
chrX	155270560	104238209	0.6713	22.1353

chrY	59373566	5122226	0.0863	4.1784

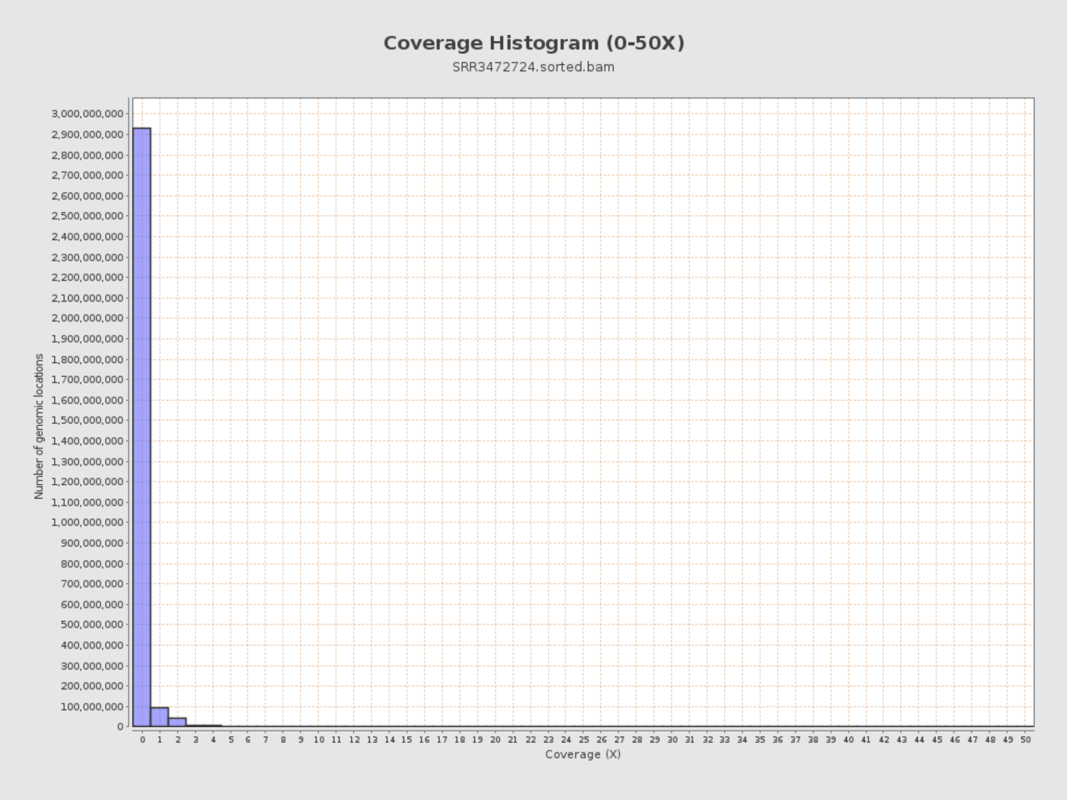
3. Results : Coverage across reference



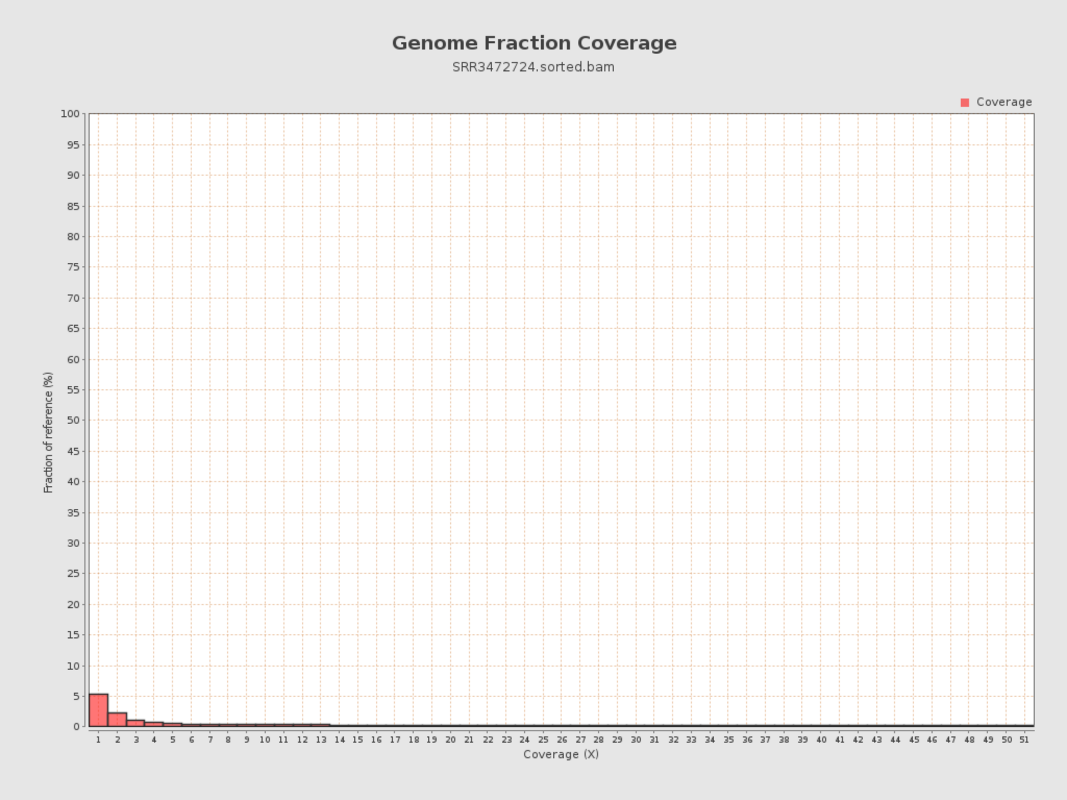
4. Results : Coverage Histogram



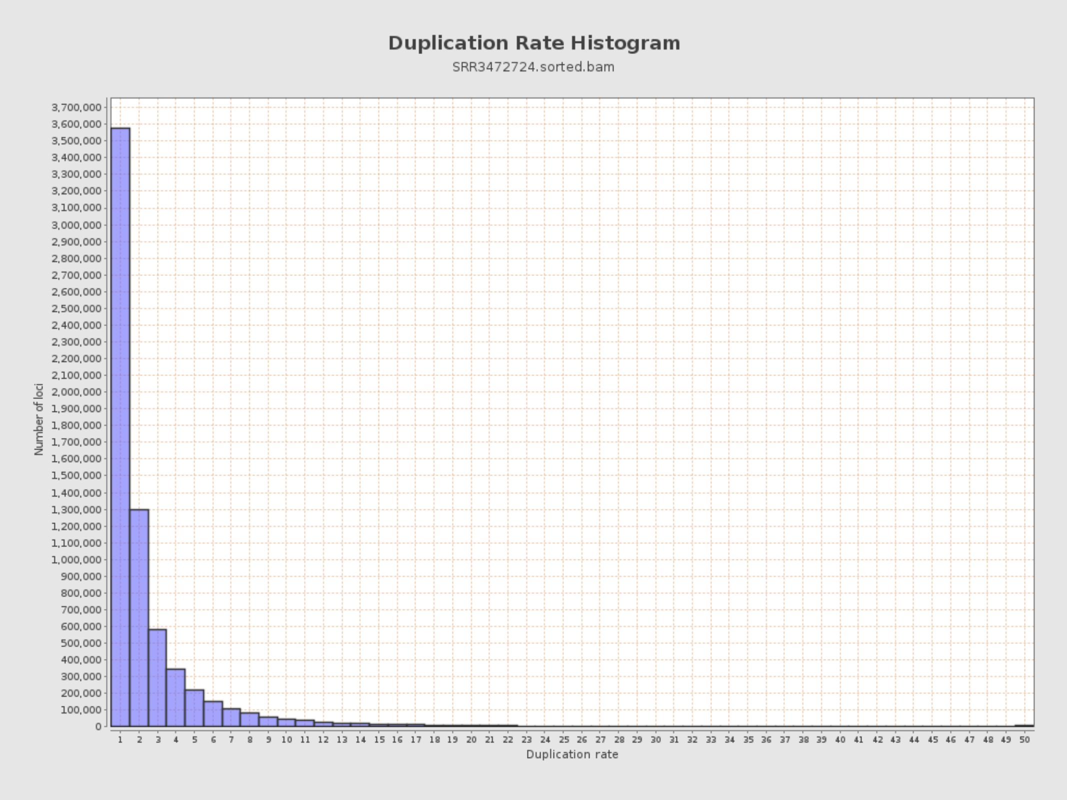
5. Results : Coverage Histogram (0-50X)



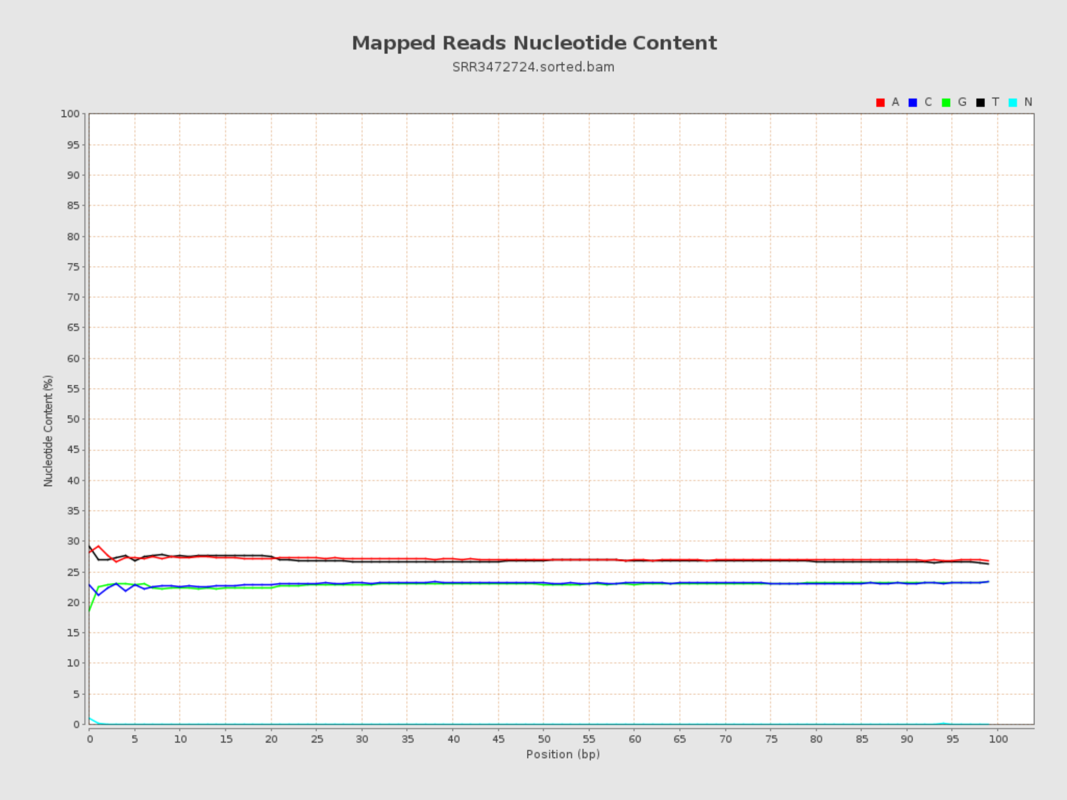
6. Results : Genome Fraction Coverage



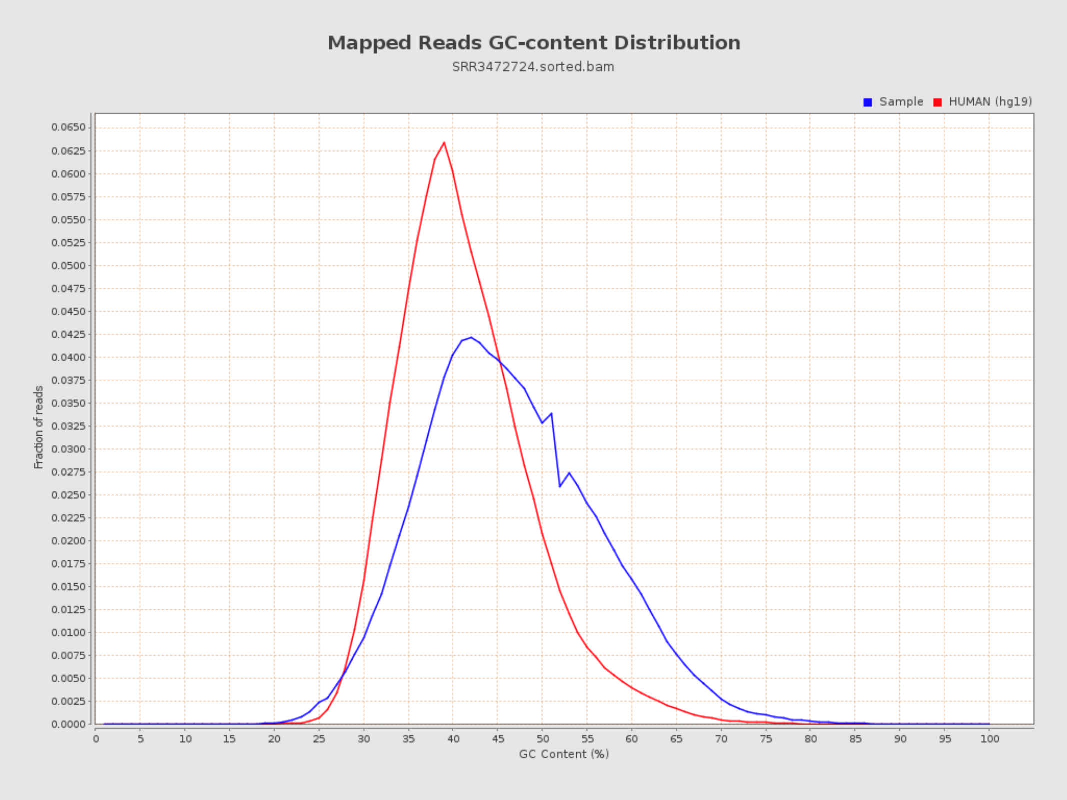
7. Results : Duplication Rate Histogram



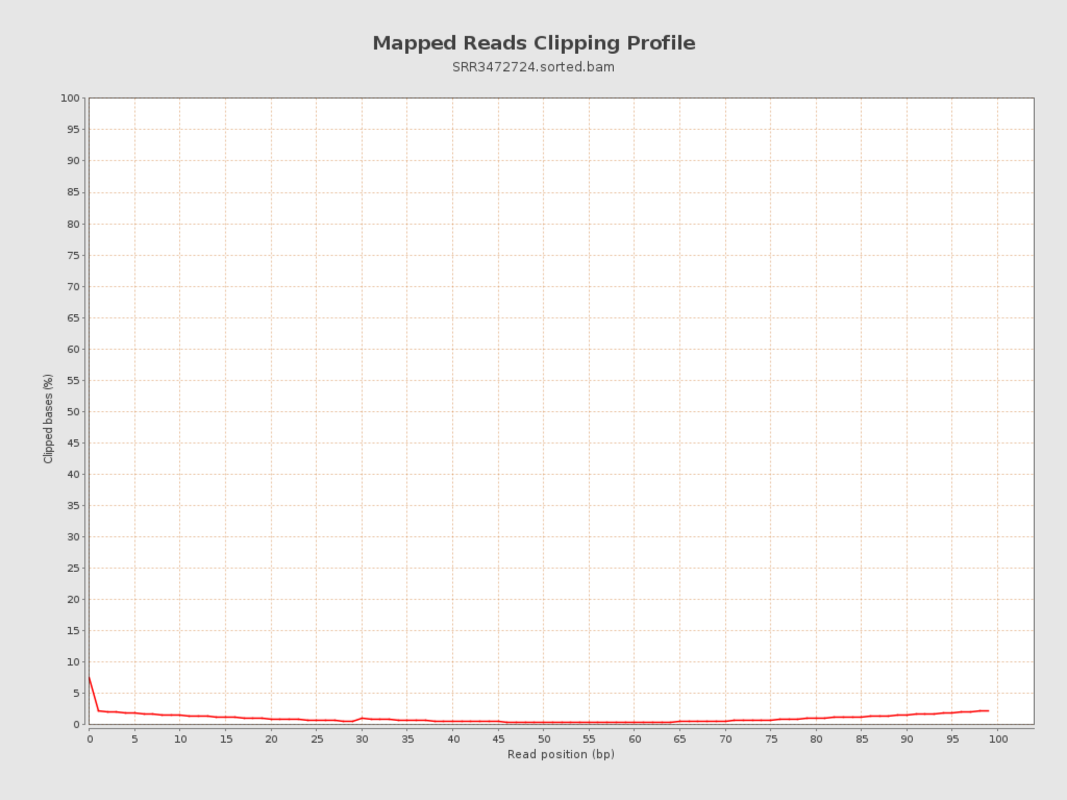
8. Results : Mapped Reads Nucleotide Content



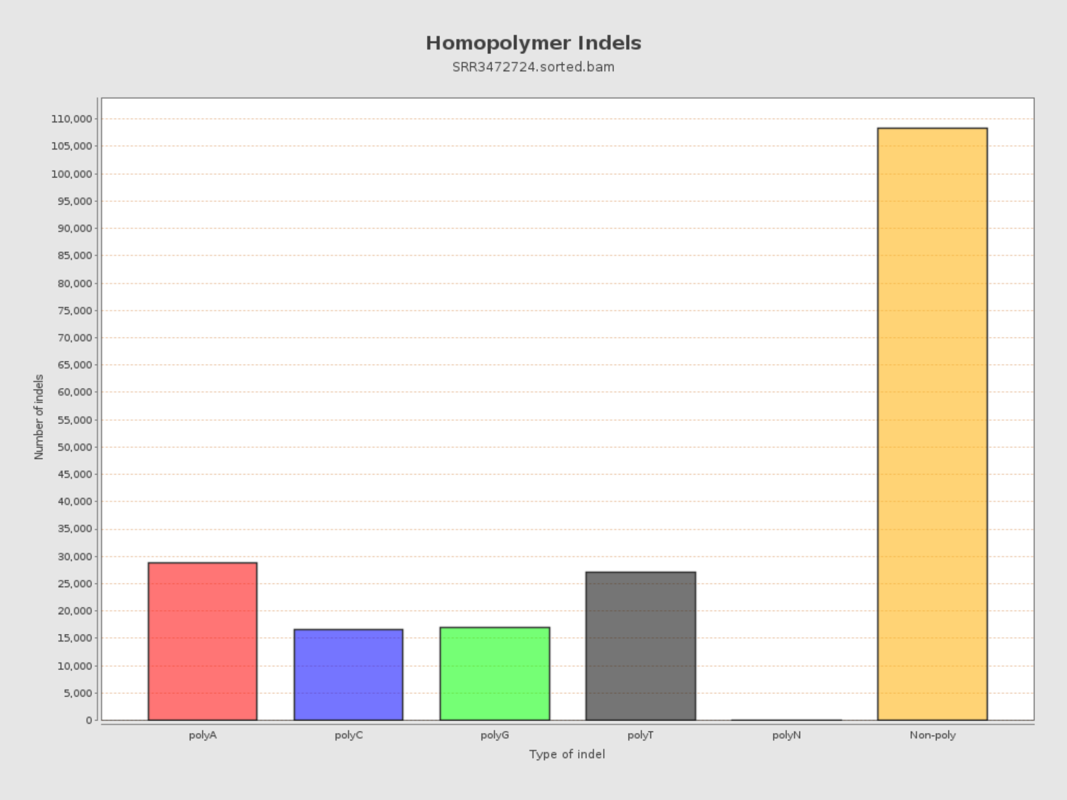
9. Results : Mapped Reads GC-content Distribution



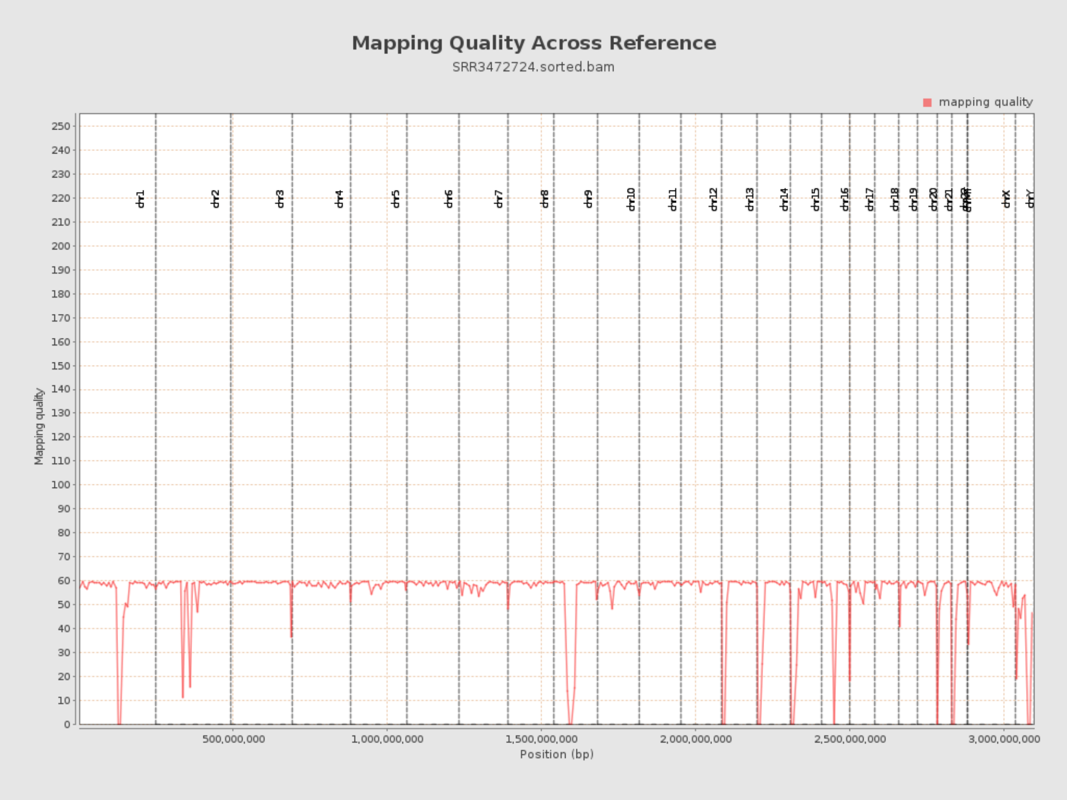
10. Results : Mapped Reads Clipping Profile



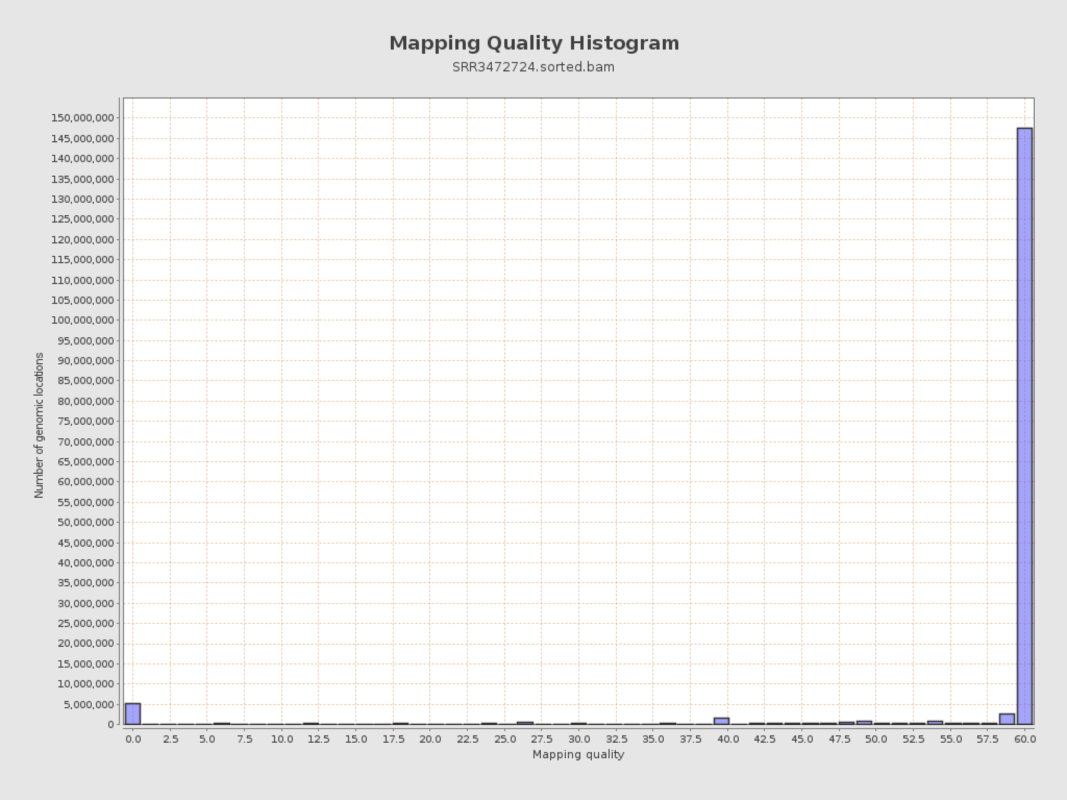
11. Results : Homopolymer Indels



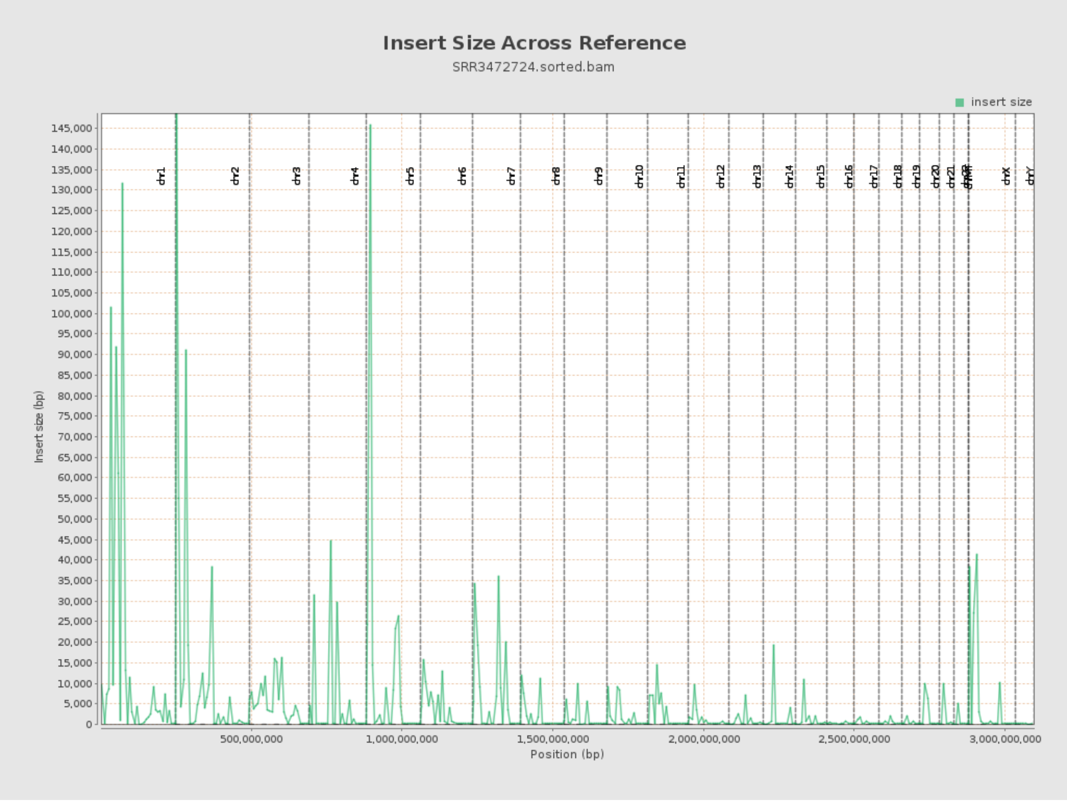
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram