Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 21:56:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472527.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_SRR3472527 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472527_1.fastq.gz SRR3472527_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 21:56:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472527.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	16,221,100
Mapped reads	16,076,893 / 99.11%
Unmapped reads	144,207 / 0.89%
Mapped paired reads	16,076,893 / 99.11%
Mapped reads, first in pair	8,059,295 / 49.68%
Mapped reads, second in pair	8,017,598 / 49.43%
Mapped reads, both in pair	15,997,776 / 98.62%
Mapped reads, singletons	79,117 / 0.49%
Secondary alignments	0
Supplementary alignments	68,316 / 0.42%
Read min/max/mean length	30 / 100 / 100.17
Duplicated reads (estimated)	10,494,566 / 64.7%
Duplication rate	46.09%
Clipped reads	1,424,298 / 8.78%

2.2. ACGT Content

Number/percentage of A's	434,108,461 / 27.45%
Number/percentage of C's	358,415,052 / 22.66%
Number/percentage of T's	432,153,368 / 27.33%
Number/percentage of G's	356,583,109 / 22.55%
Number/percentage of N's	247,092 / 0.02%

GC Percentage	45.21%

2.3. Coverage

Mean	0.5109
Standard Deviation	20.5364

2.4. Mapping Quality

Mean Mapping Quality	54.98

2.5. Insert size

Mean	30,408.65
Standard Deviation	1,744,929.67
P25/Median/P75	158 / 217 / 292

2.6. Mismatches and indels

General error rate	0.56%
Mismatches	8,740,521
Insertions	80,937
Mapped reads with at least one insertion	0.5%
Deletions	81,159
Mapped reads with at least one deletion	0.5%
Homopolymer indels	45.48%

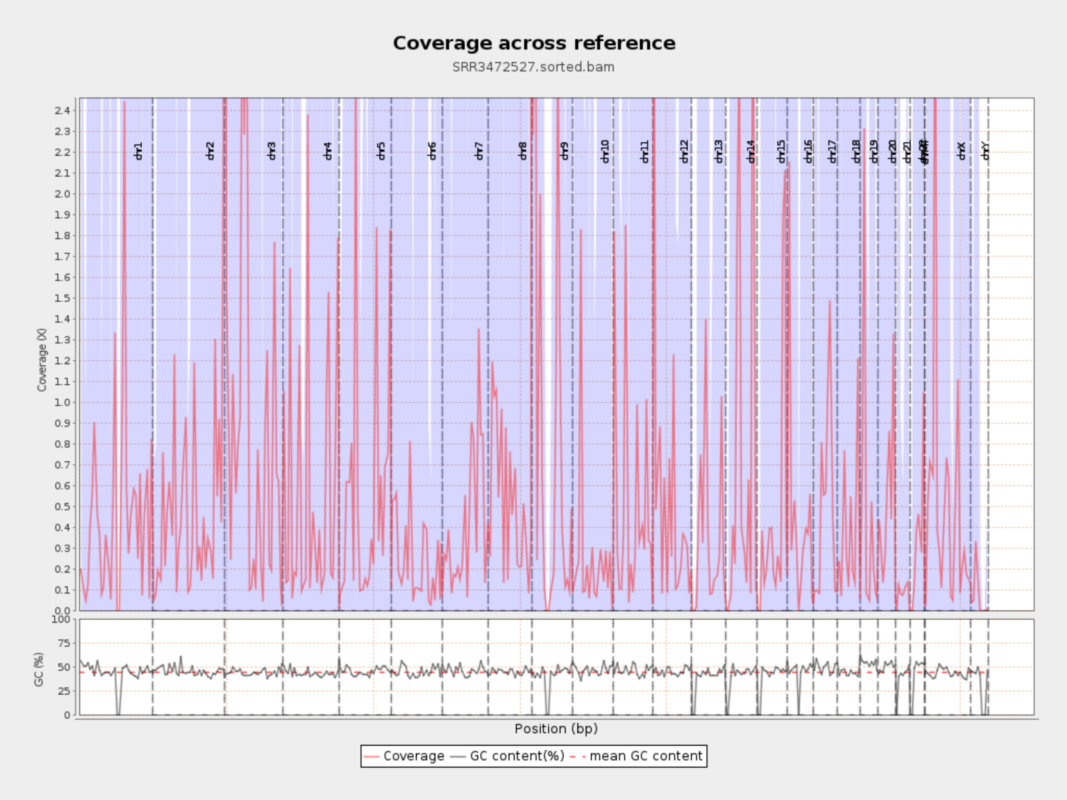
2.7. Chromosome stats

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

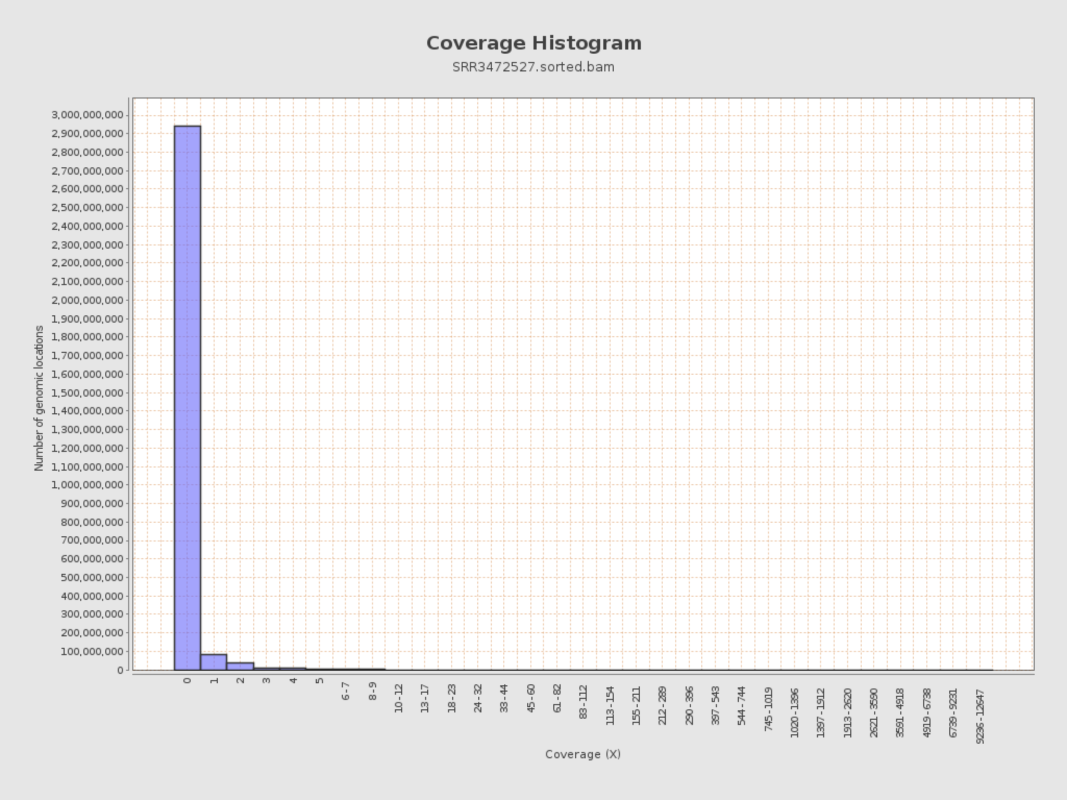
		bases	**coverage**	**deviation**
chr1	249250621	114900742	0.461	17.2366
chr2	243199373	114898243	0.4724	17.0483
chr3	198022430	190325002	0.9611	26.593
chr4	191154276	109192974	0.5712	27.587
chr5	180915260	101954321	0.5635	24.1789
chr6	171115067	41961019	0.2452	11.7756
chr7	159138663	66041795	0.415	13.813
chr8	146364022	77665007	0.5306	17.9595
chr9	141213431	131968354	0.9345	32.1675
chr10	135534747	35205076	0.2597	23.356
chr11	135006516	68498518	0.5074	24.1921
chr12	133851895	75753716	0.566	17.3547
chr13	115169878	41256320	0.3582	13.2154
chr14	107349540	79601199	0.7415	35.2648
chr15	102531392	48991153	0.4778	17.8114
chr16	90354753	40130906	0.4441	12.9528
chr17	81195210	41132322	0.5066	16.2956
chr18	78077248	30349390	0.3887	13.7957
chr19	59128983	30632382	0.5181	19.0235
chr20	63025520	33917181	0.5381	14.8384
chr21	48129895	4269400	0.0887	3.25
chr22	51304566	17757818	0.3461	15.5249
chrMT	16571	1514	0.0914	0.4369
chrX	155270560	80807147	0.5204	16.4901

chrY	59373566	4498529	0.0758	3.3527

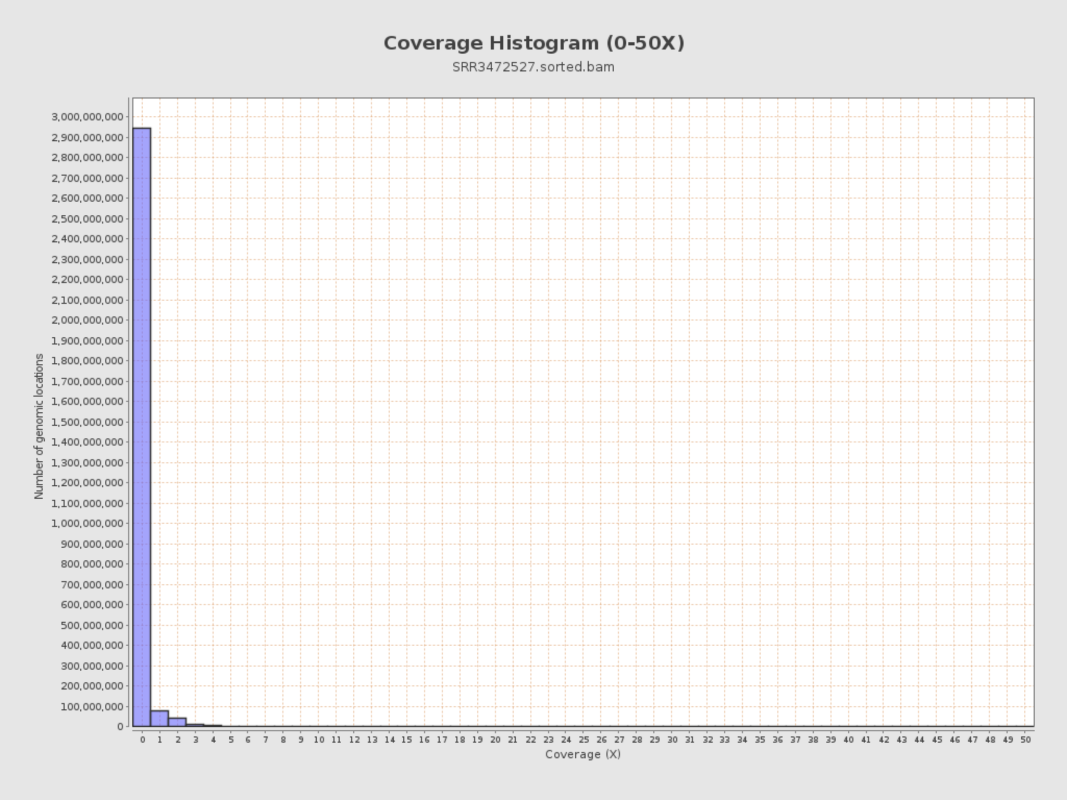
3. Results : Coverage across reference



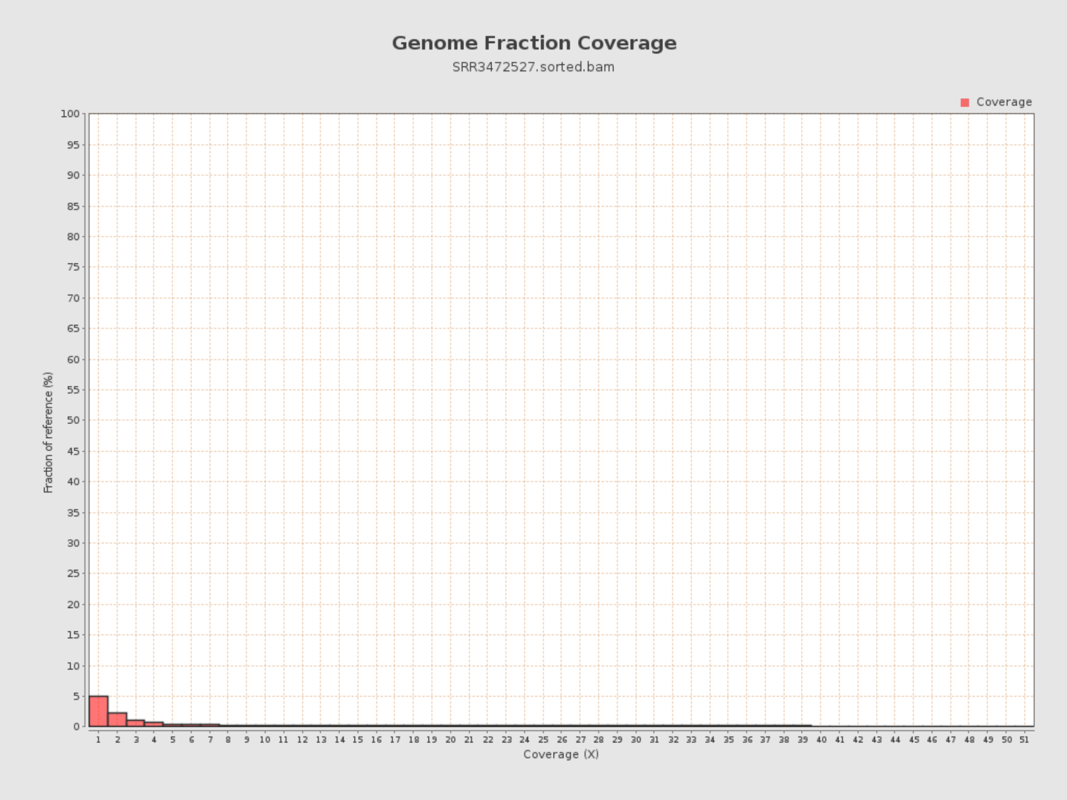
4. Results : Coverage Histogram



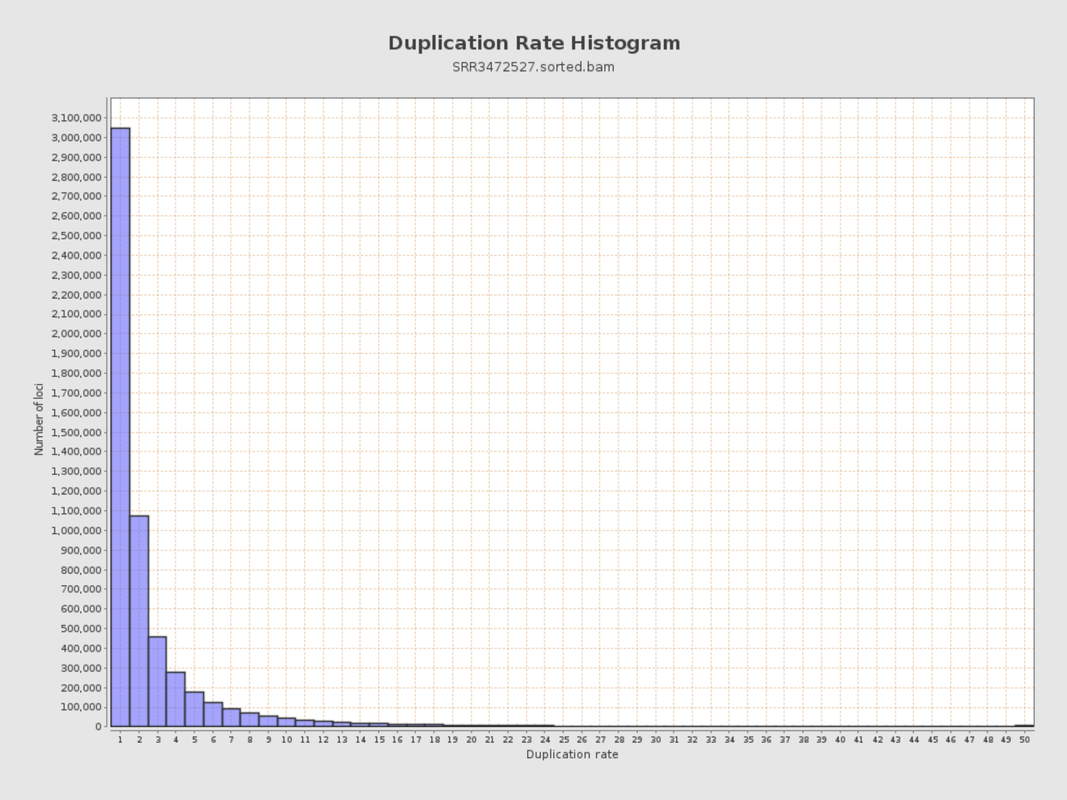
5. Results : Coverage Histogram (0-50X)



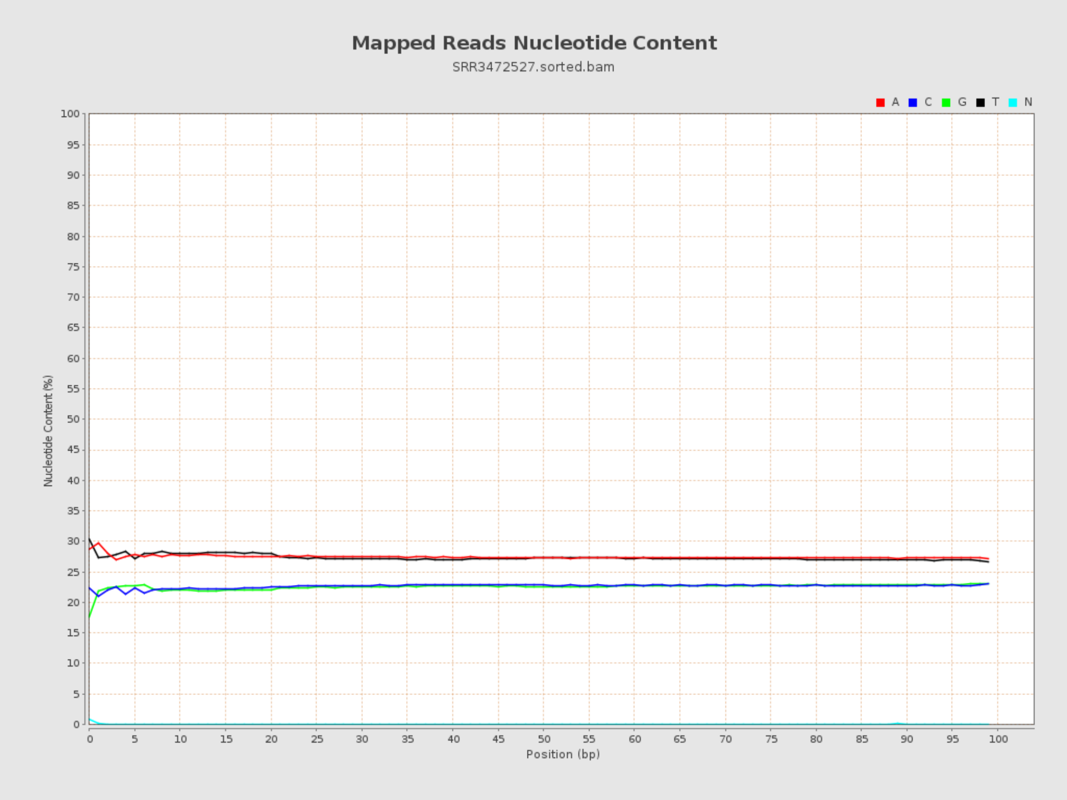
6. Results : Genome Fraction Coverage



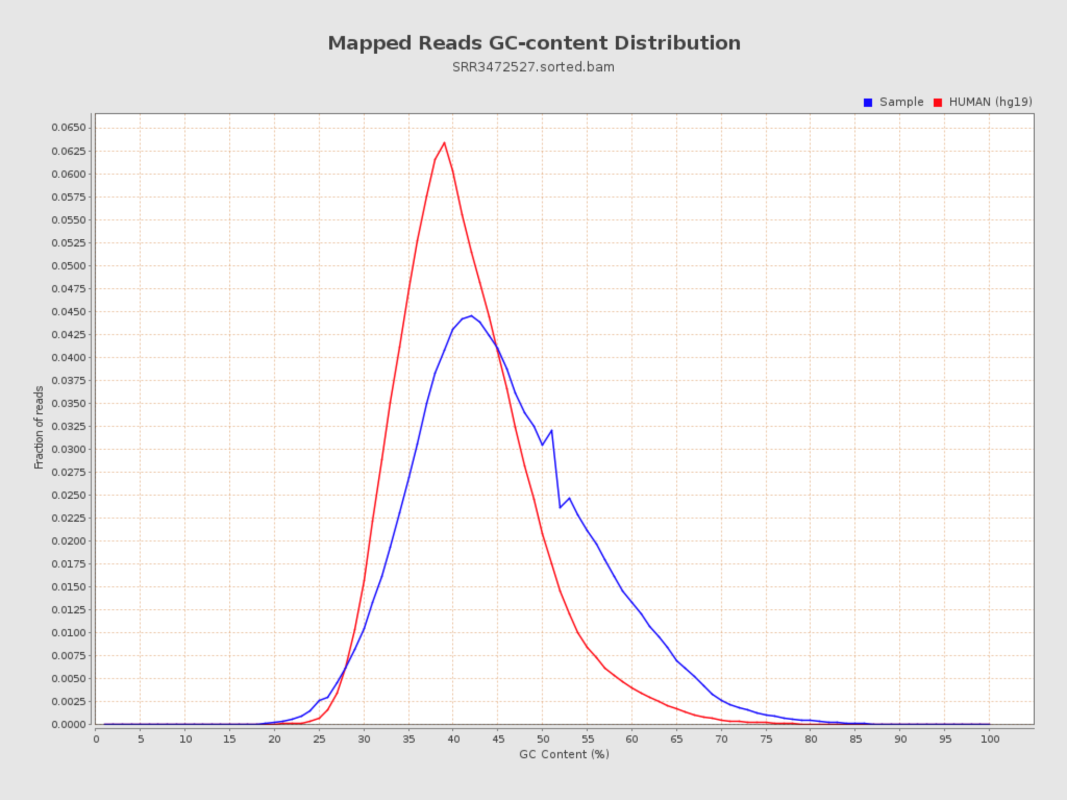
7. Results : Duplication Rate Histogram



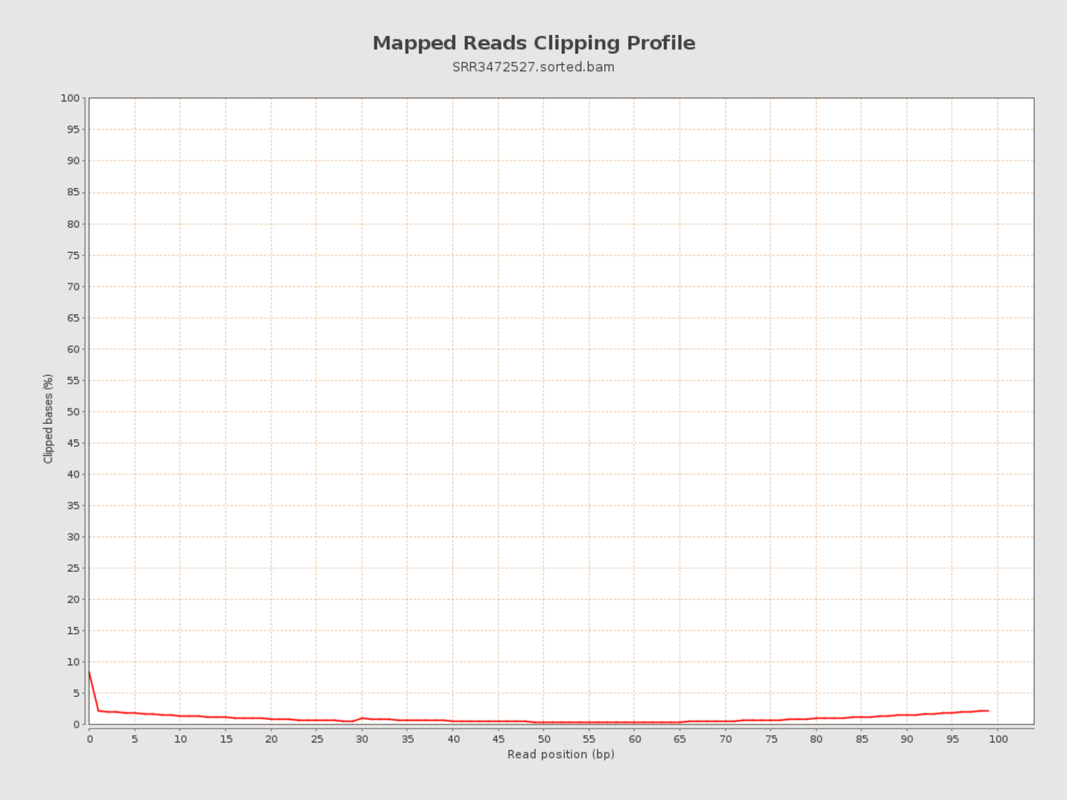
8. Results : Mapped Reads Nucleotide Content



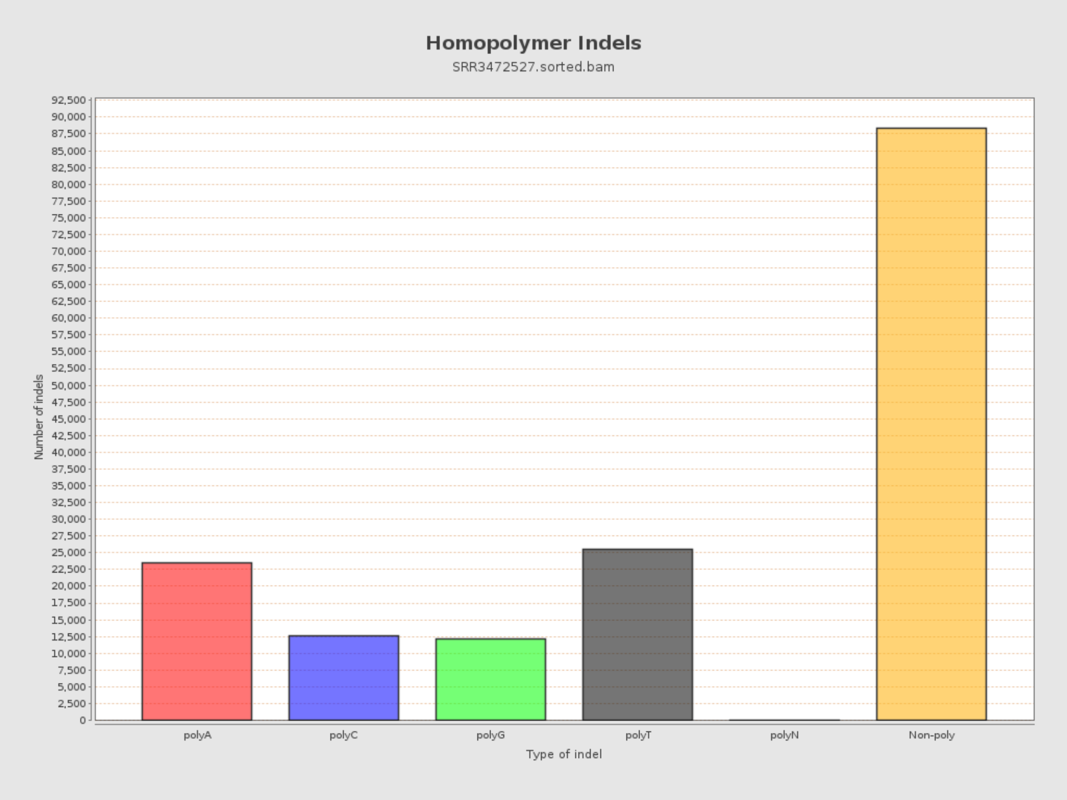
9. Results : Mapped Reads GC-content Distribution



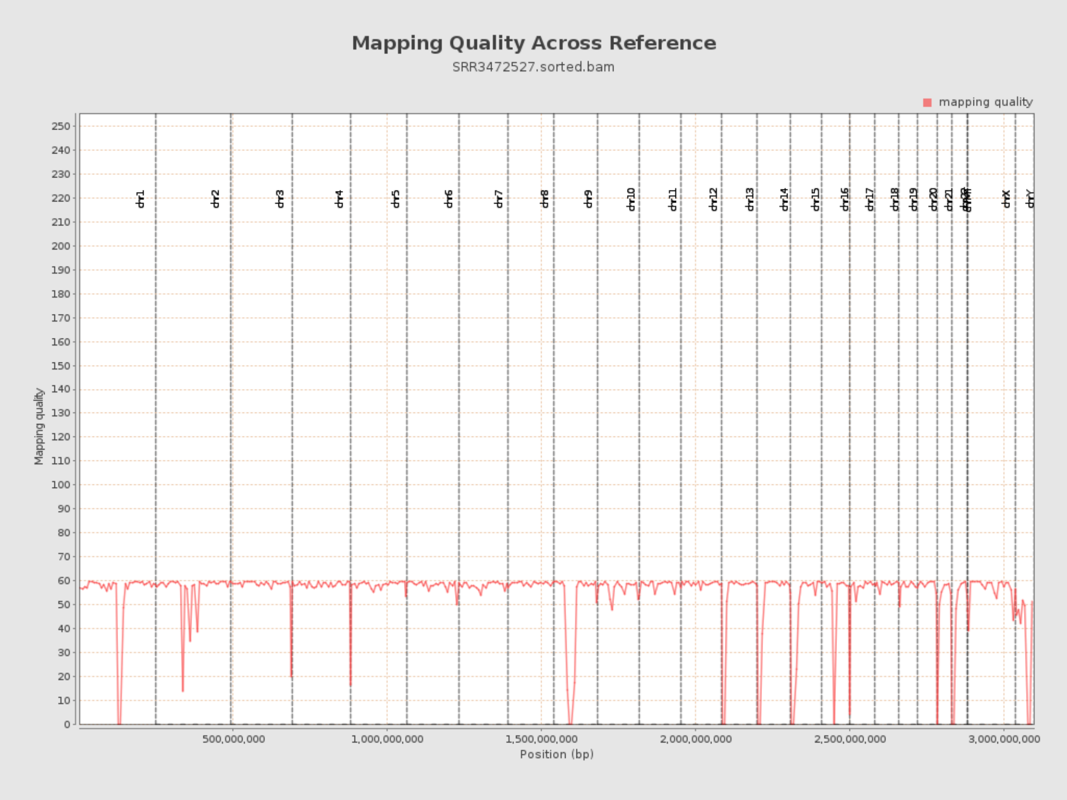
10. Results : Mapped Reads Clipping Profile



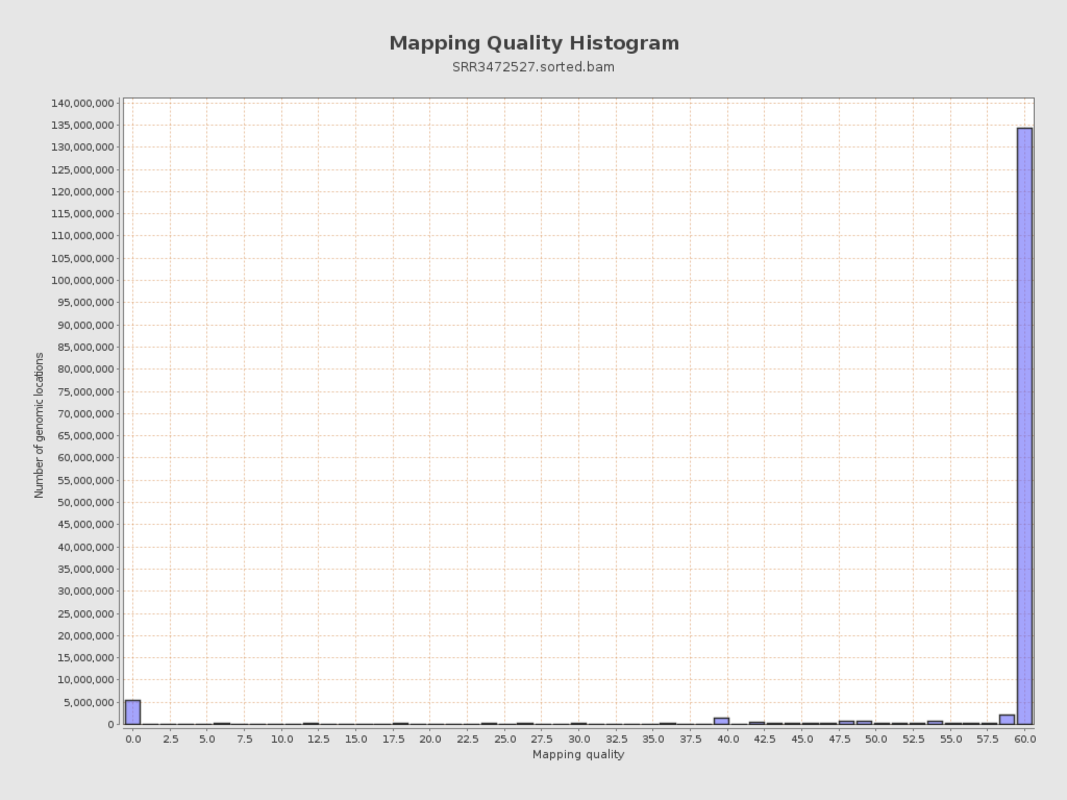
11. Results : Homopolymer Indels



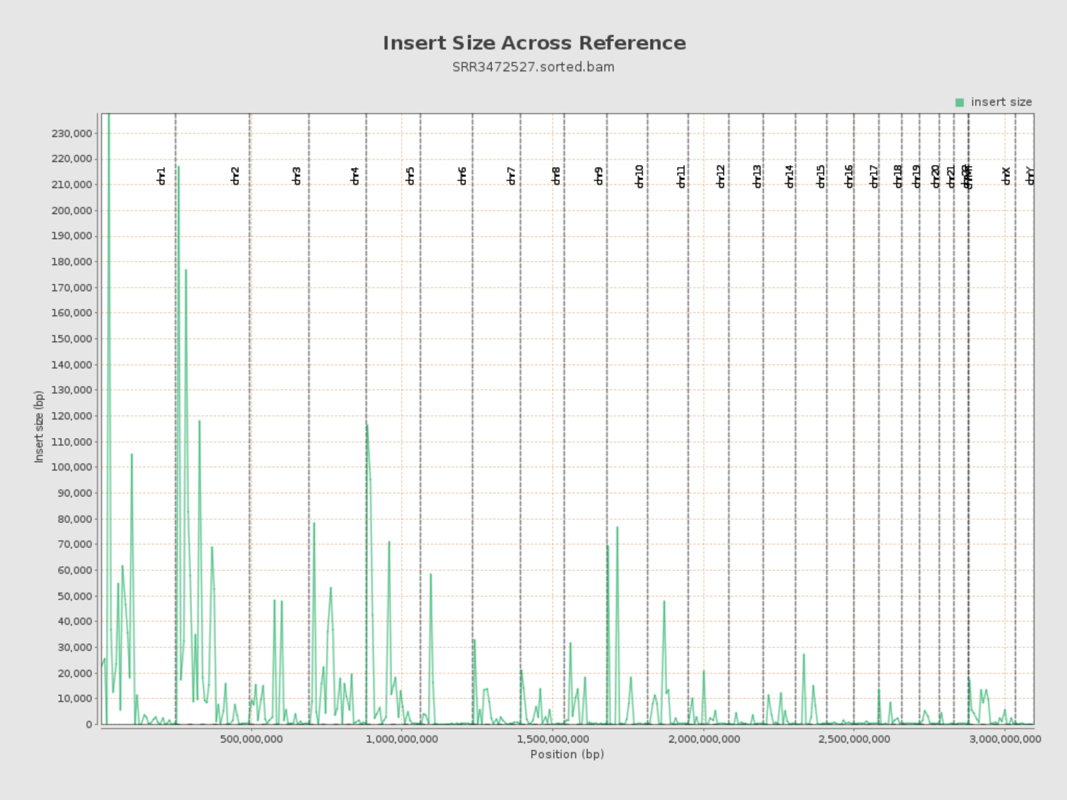
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram