Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 15:23:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472505.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_SRR3472505 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472505_1.fastq.gz SRR3472505_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 15:23:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472505.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	13,625,580
Mapped reads	12,934,124 / 94.93%
Unmapped reads	691,456 / 5.07%
Mapped paired reads	12,934,124 / 94.93%
Mapped reads, first in pair	6,305,685 / 46.28%
Mapped reads, second in pair	6,628,439 / 48.65%
Mapped reads, both in pair	12,432,790 / 91.25%
Mapped reads, singletons	501,334 / 3.68%
Secondary alignments	0
Supplementary alignments	80,399 / 0.59%
Read min/max/mean length	30 / 100 / 100.22
Duplicated reads (estimated)	7,340,234 / 53.87%
Duplication rate	41.82%
Clipped reads	1,676,953 / 12.31%

2.2. ACGT Content

Number/percentage of A's	366,243,740 / 29.48%
Number/percentage of C's	276,627,154 / 22.27%
Number/percentage of T's	328,132,937 / 26.41%
Number/percentage of G's	271,251,787 / 21.83%
Number/percentage of N's	167,972 / 0.01%

GC Percentage	44.1%

2.3. Coverage

Mean	0.4014
Standard Deviation	12.9272

2.4. Mapping Quality

Mean Mapping Quality	54.04

2.5. Insert size

Mean	53,755.22
Standard Deviation	2,231,954.61
P25/Median/P75	168 / 238 / 324

2.6. Mismatches and indels

General error rate	1.86%
Mismatches	22,933,690
Insertions	67,851
Mapped reads with at least one insertion	0.52%
Deletions	66,098
Mapped reads with at least one deletion	0.5%
Homopolymer indels	45.2%

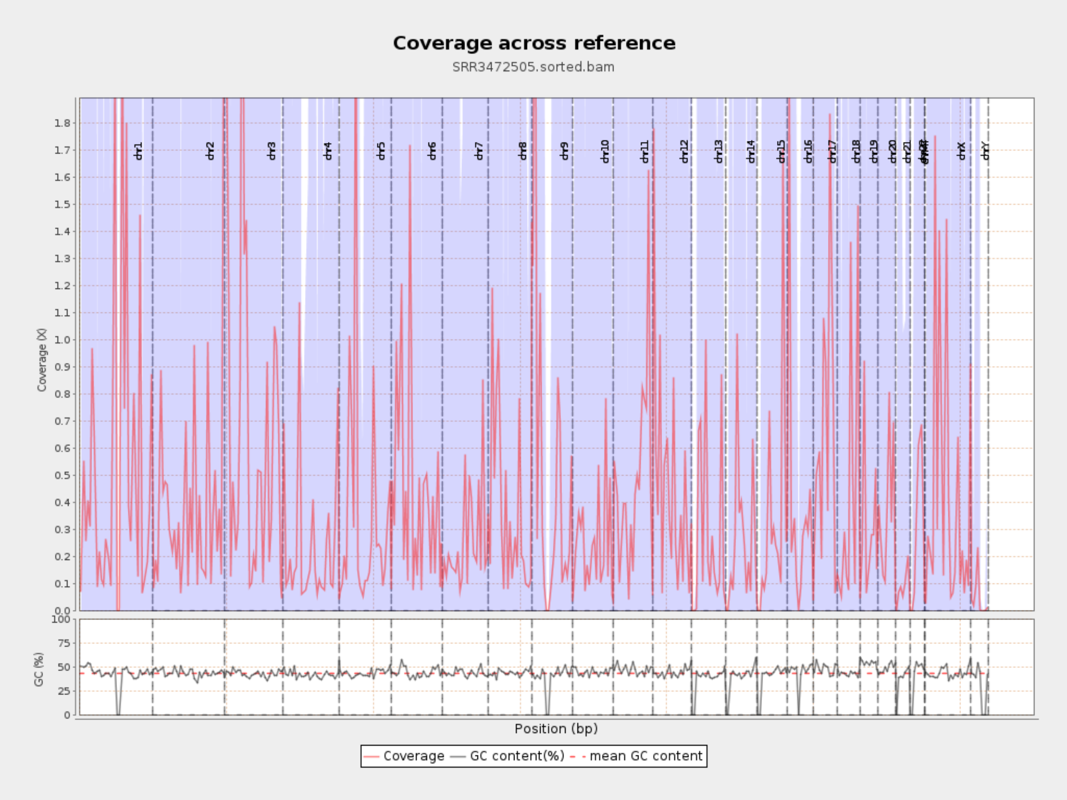
2.7. Chromosome stats

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

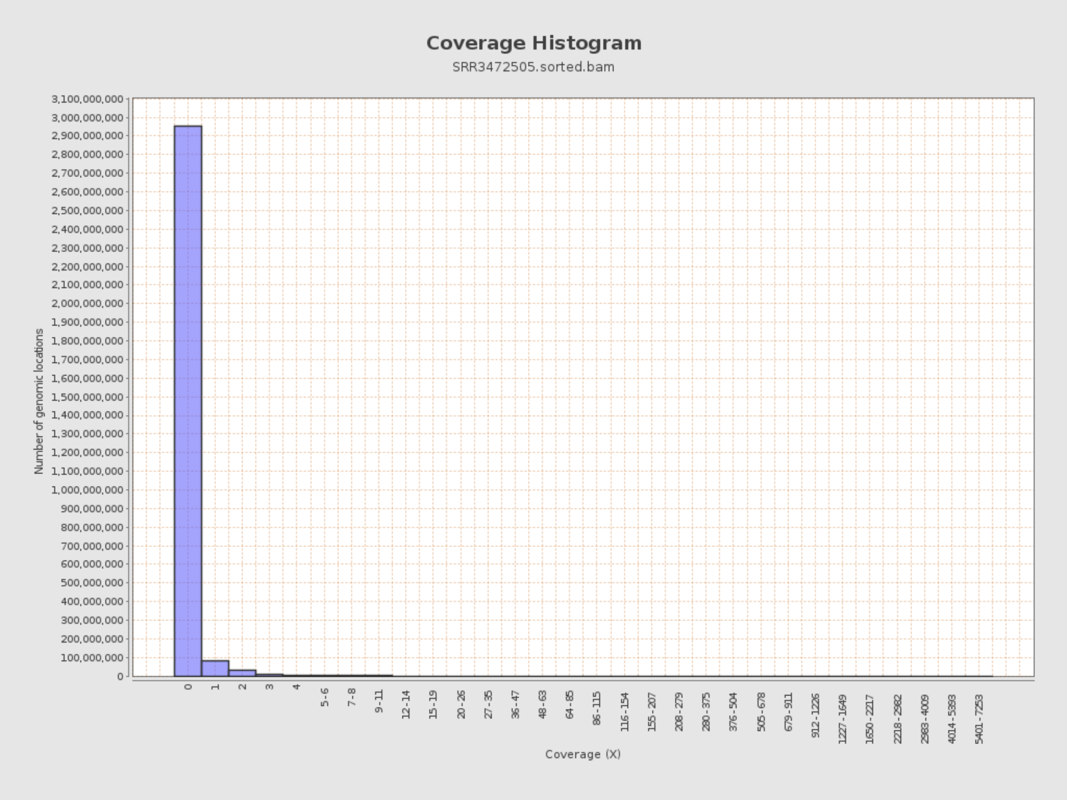
		bases	coverage	deviation
chr1	249250621	133099303	0.534	17.3937
chr2	243199373	88999612	0.366	11.8481
chr3	198022430	148622897	0.7505	17.5757
chr4	191154276	44124975	0.2308	7.3013
chr5	180915260	67151014	0.3712	13.9984
chr6	171115067	75625694	0.442	11.2937
chr7	159138663	40616728	0.2552	8.5431
chr8	146364022	54156872	0.37	12.2361
chr9	141213431	75420691	0.5341	13.3612
chr10	135534747	35218649	0.2598	9.5048
chr11	135006516	65453437	0.4848	15.3418
chr12	133851895	62152261	0.4643	13.1531
chr13	115169878	33361300	0.2897	10.5509
chr14	107349540	27898830	0.2599	7.8465
chr15	102531392	35647221	0.3477	13.7683
chr16	90354753	34822388	0.3854	10.103
chr17	81195210	52067378	0.6413	14.6482
chr18	78077248	34598161	0.4431	17.7052
chr19	59128983	19692177	0.333	7.4771
chr20	63025520	23810253	0.3778	10.5071
chr21	48129895	4486697	0.0932	2.9608
chr22	51304566	15433882	0.3008	10.3729
chrMT	16571	1535	0.0926	0.3408
chrX	155270560	67182995	0.4327	17.223

chrY	59373566	2940659	0.0495	3.9155

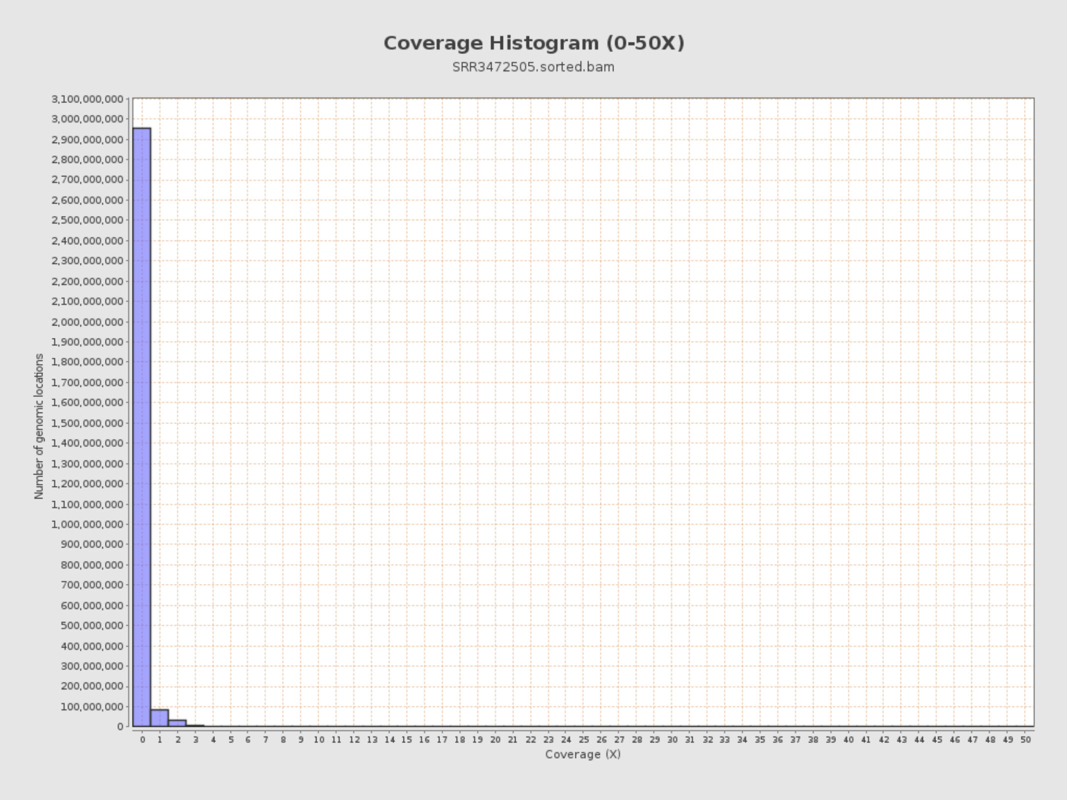
3. Results : Coverage across reference



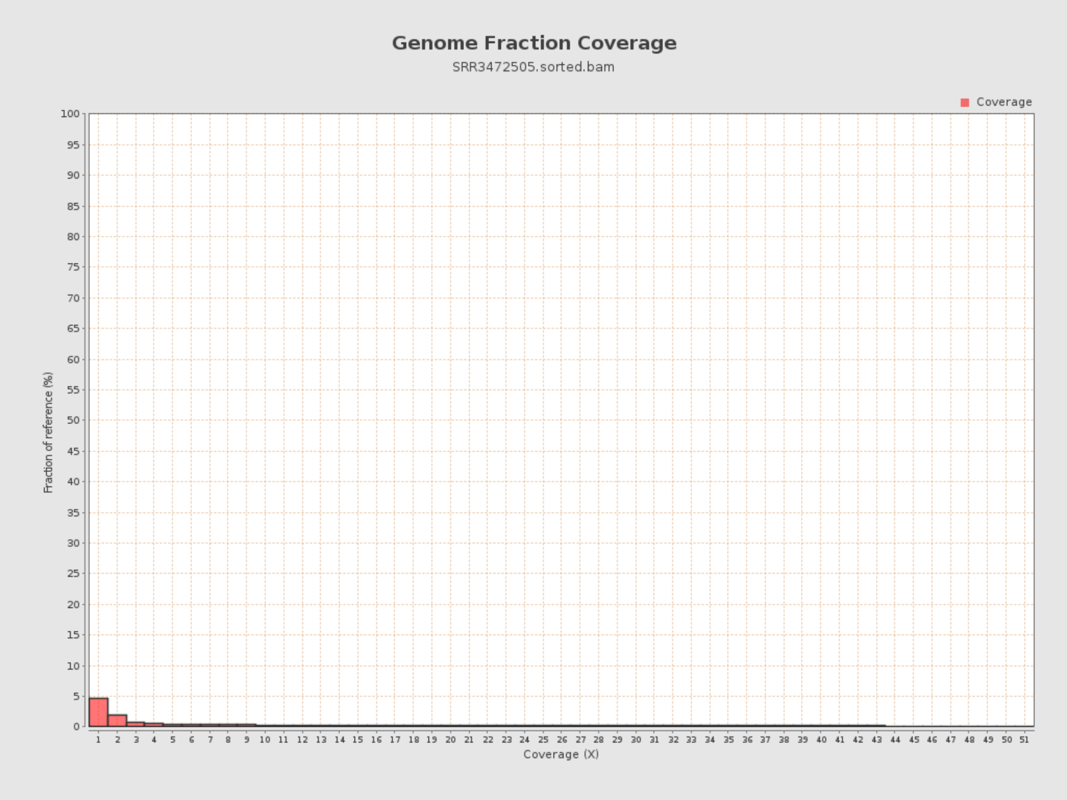
4. Results : Coverage Histogram



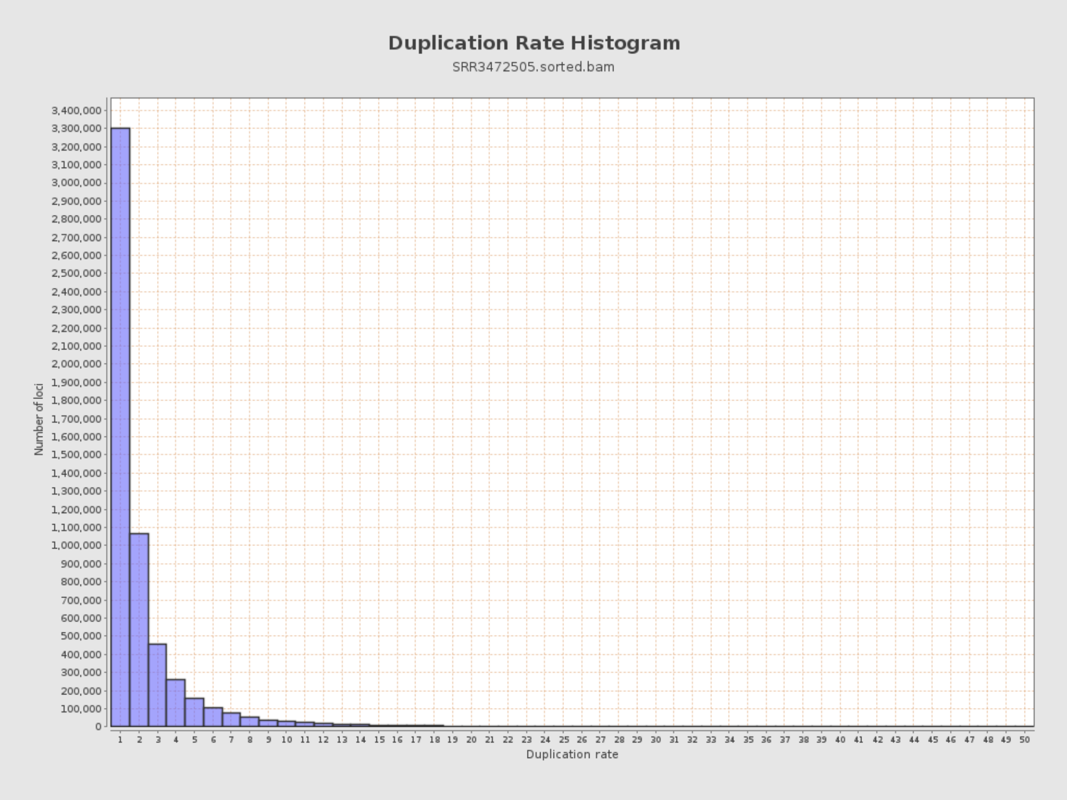
5. Results : Coverage Histogram (0-50X)



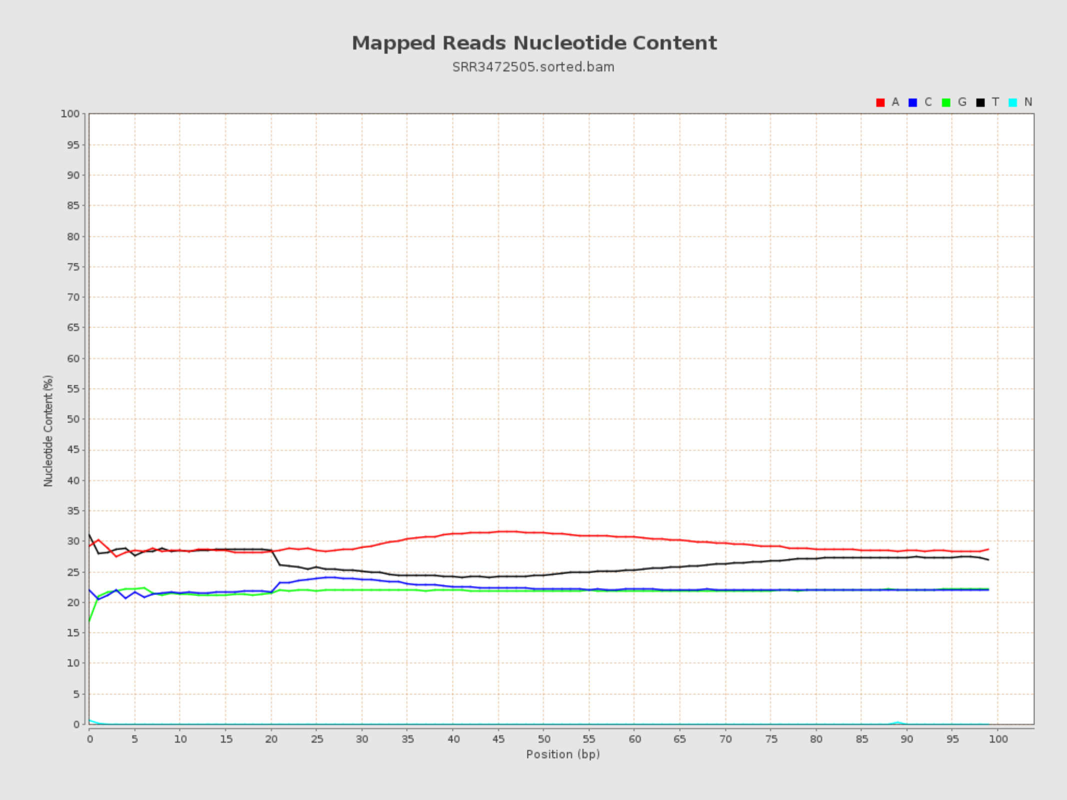
6. Results : Genome Fraction Coverage



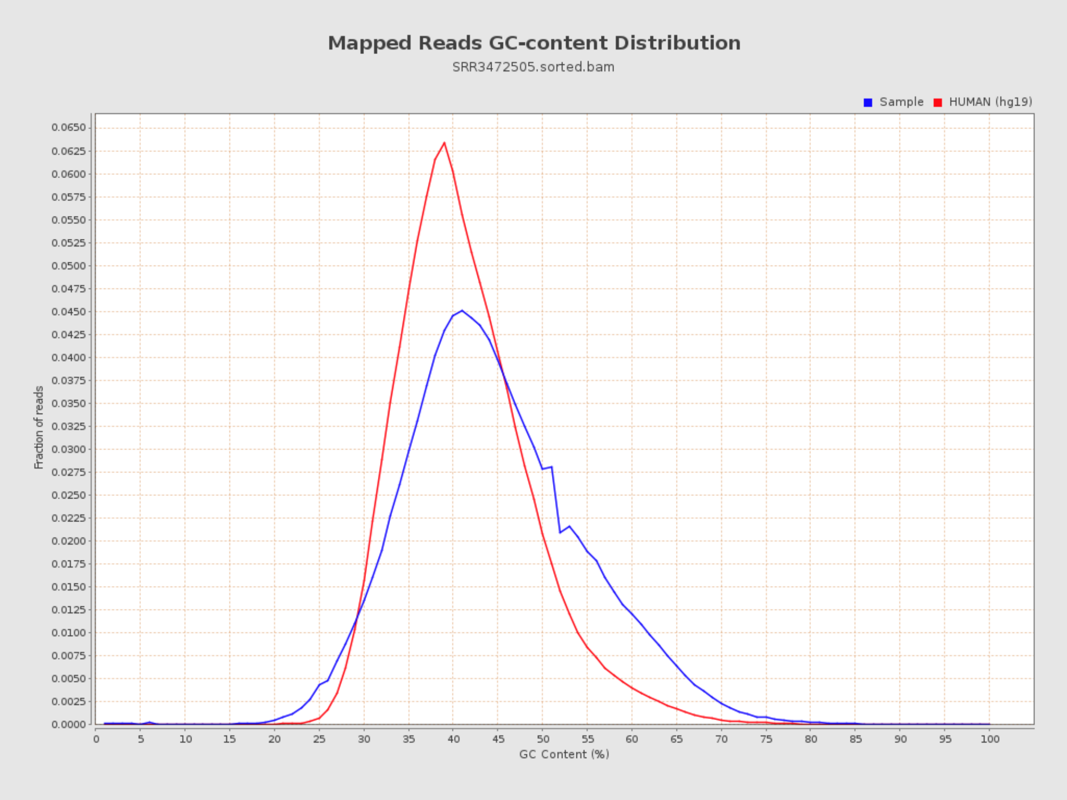
7. Results : Duplication Rate Histogram



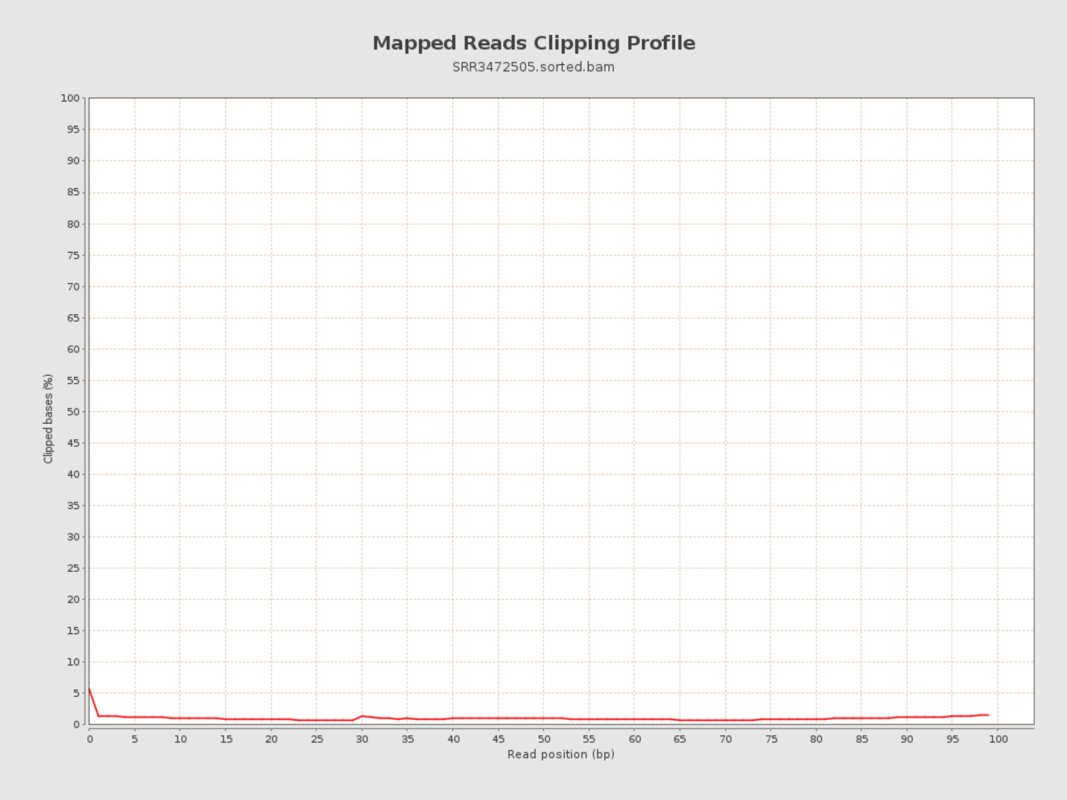
8. Results : Mapped Reads Nucleotide Content



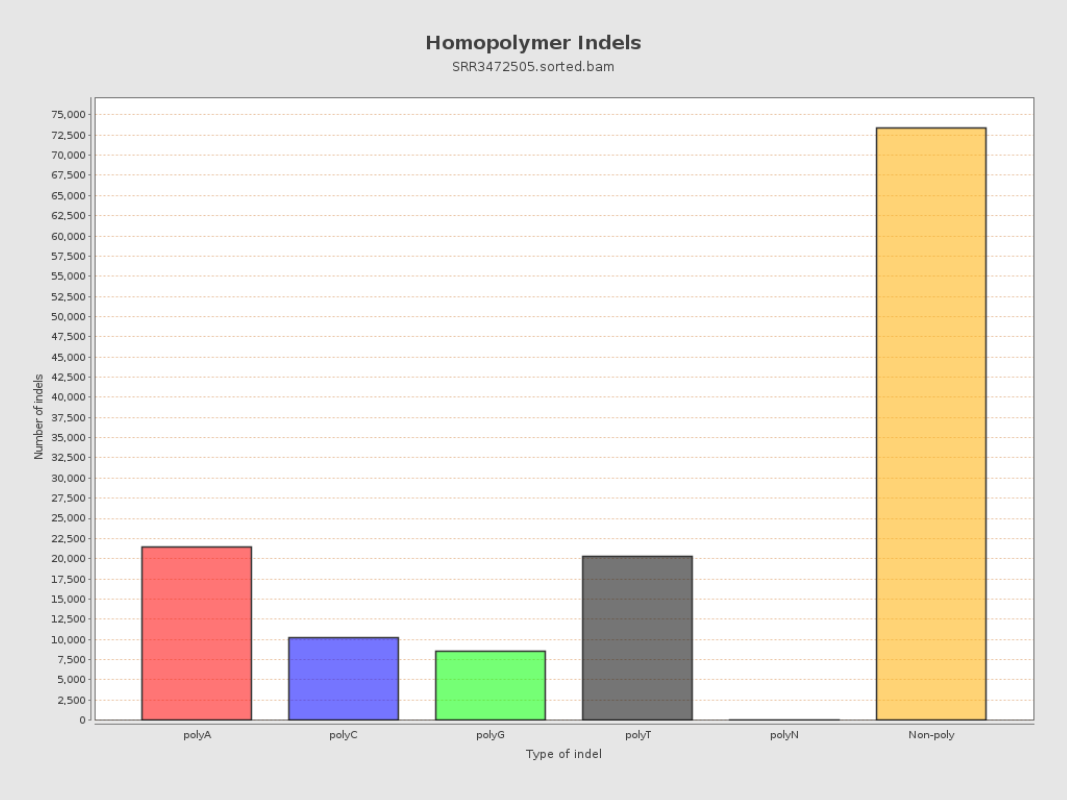
9. Results : Mapped Reads GC-content Distribution



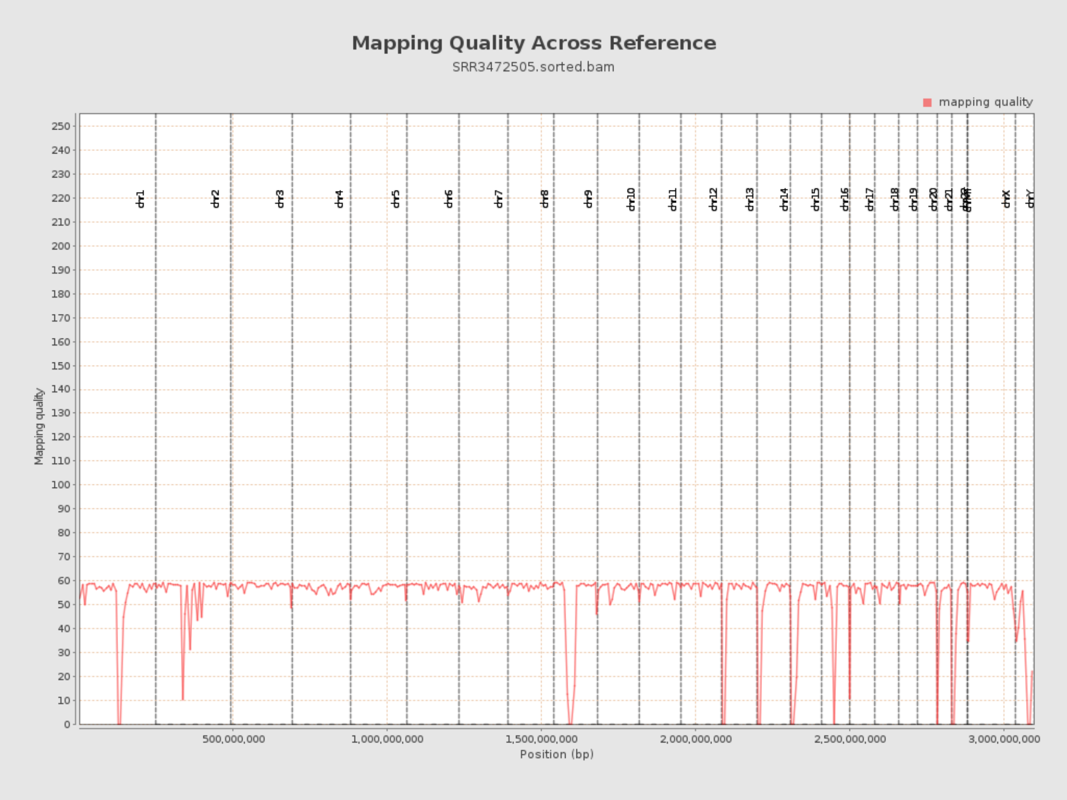
10. Results : Mapped Reads Clipping Profile



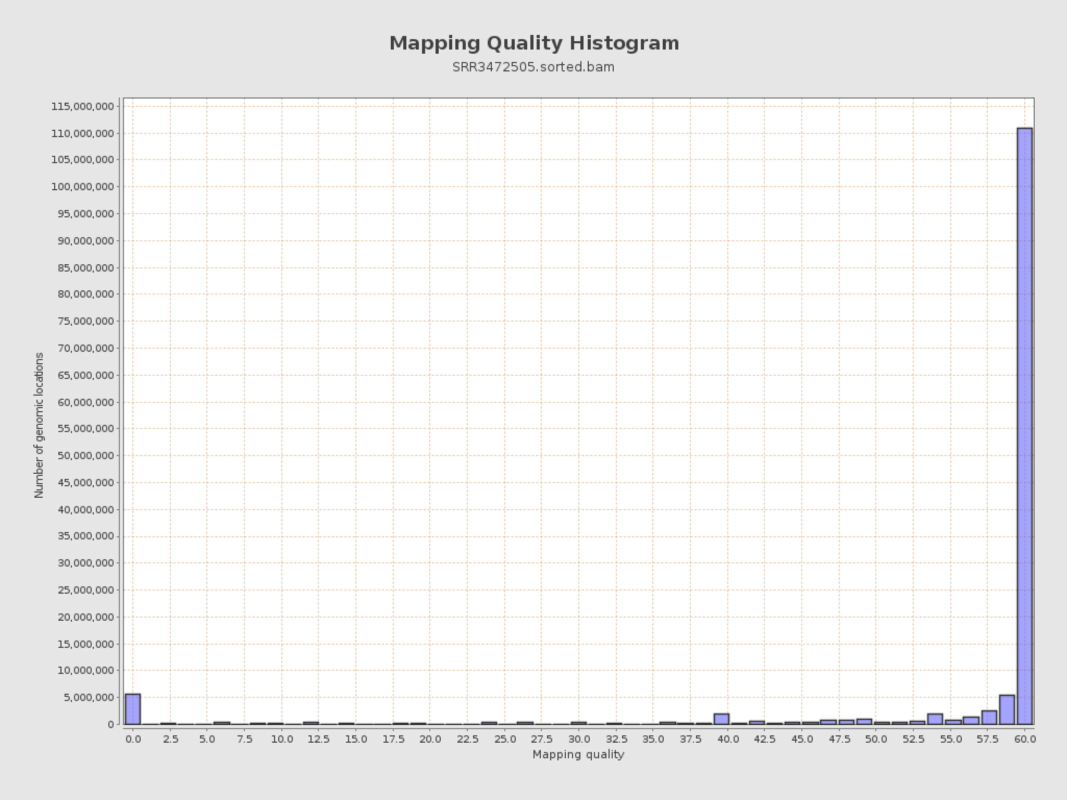
11. Results : Homopolymer Indels



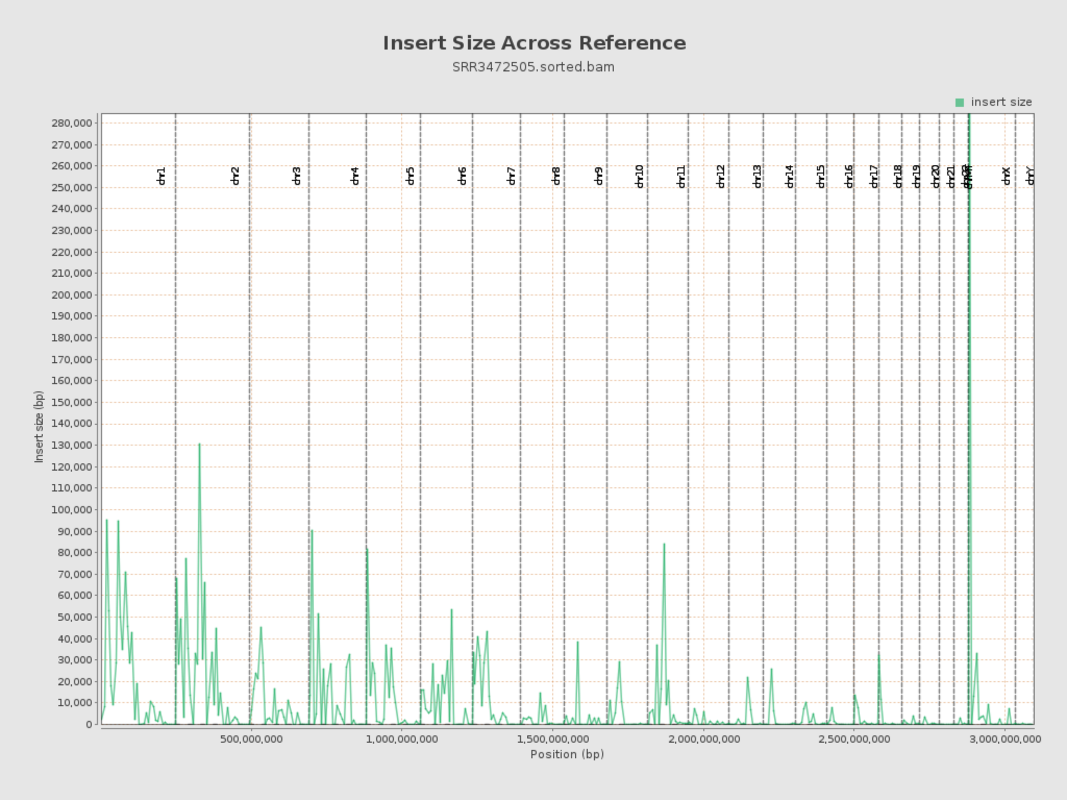
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram