Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/29 08:25:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472686.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_SRR3472686 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472686_1.fastq.gz SRR3472686_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 29 08:25:00 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472686.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	20,846,184
Mapped reads	20,682,000 / 99.21%
Unmapped reads	164,184 / 0.79%
Mapped paired reads	20,682,000 / 99.21%
Mapped reads, first in pair	10,364,743 / 49.72%
Mapped reads, second in pair	10,317,257 / 49.49%
Mapped reads, both in pair	20,569,498 / 98.67%
Mapped reads, singletons	112,502 / 0.54%
Secondary alignments	0
Supplementary alignments	125,787 / 0.6%
Read min/max/mean length	30 / 101 / 99.88
Duplicated reads (estimated)	14,895,393 / 71.45%
Duplication rate	49.82%
Clipped reads	1,469,572 / 7.05%

2.2. ACGT Content

Number/percentage of A's	552,041,004 / 27.09%
Number/percentage of C's	469,700,643 / 23.05%
Number/percentage of T's	550,937,131 / 27.04%
Number/percentage of G's	464,437,069 / 22.79%
Number/percentage of N's	392,142 / 0.02%

GC Percentage	45.85%

2.3. Coverage

Mean	0.6583
Standard Deviation	30.0702

2.4. Mapping Quality

Mean Mapping Quality	54.81

2.5. Insert size

Mean	21,388.63
Standard Deviation	1,462,264.31
P25/Median/P75	161 / 218 / 289

2.6. Mismatches and indels

General error rate	0.63%
Mismatches	12,688,132
Insertions	127,628
Mapped reads with at least one insertion	0.61%
Deletions	108,896
Mapped reads with at least one deletion	0.52%
Homopolymer indels	48.28%

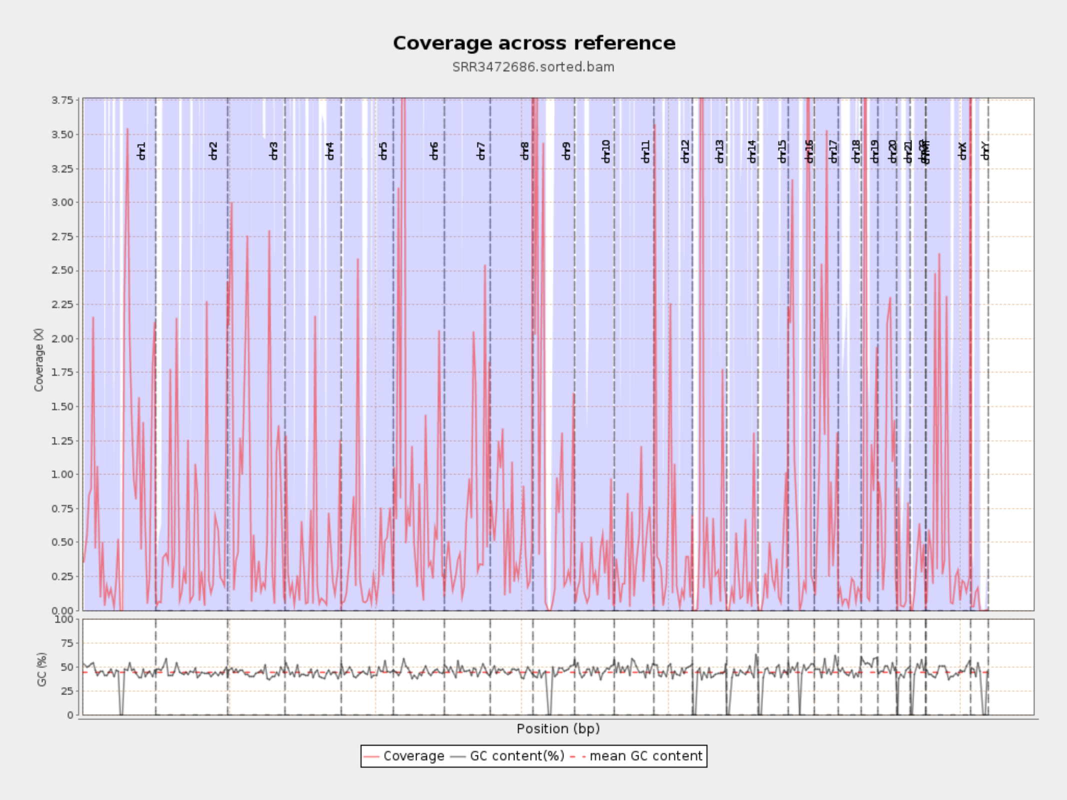
2.7. Chromosome stats

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

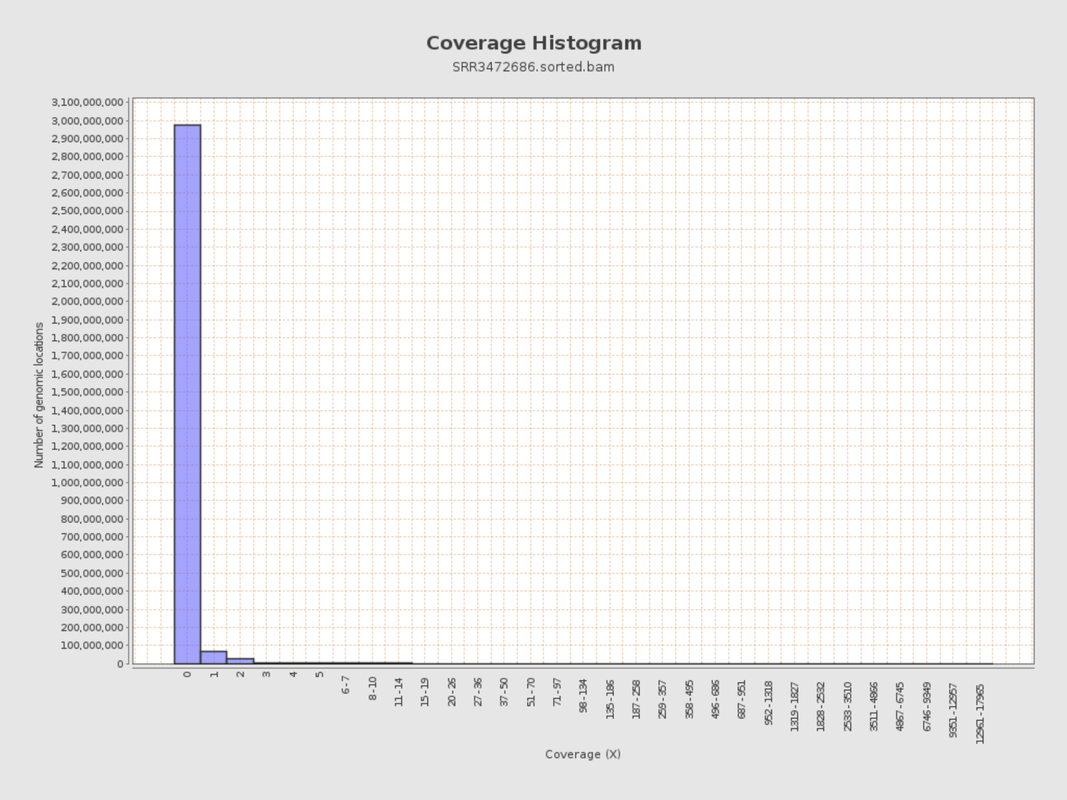
		bases	coverage	deviation
chr1	249250621	212892498	0.8541	27.4074
chr2	243199373	124144415	0.5105	24.5301
chr3	198022430	187201306	0.9454	32.1734
chr4	191154276	73175711	0.3828	21.1975
chr5	180915260	71074890	0.3929	15.4988
chr6	171115067	185586573	1.0846	41.215
chr7	159138663	111839021	0.7028	30.5198
chr8	146364022	86672345	0.5922	24.2887
chr9	141213431	143855829	1.0187	48.3021
chr10	135534747	40989539	0.3024	13.2463
chr11	135006516	54844630	0.4062	17.999
chr12	133851895	81111635	0.606	31.1188
chr13	115169878	99347321	0.8626	55.1161
chr14	107349540	29057080	0.2707	13.1981
chr15	102531392	28602193	0.279	14.8033
chr16	90354753	113192397	1.2528	46.3457
chr17	81195210	93401044	1.1503	36.2431
chr18	78077248	9311580	0.1193	4.8738
chr19	59128983	79355948	1.3421	52.8859
chr20	63025520	70136452	1.1128	36.0235
chr21	48129895	14718157	0.3058	20.0443
chr22	51304566	15293881	0.2981	9.0585
chrMT	16571	2533	0.1529	0.4735
chrX	155270560	109196750	0.7033	27.12

chrY	59373566	2751638	0.0463	3.1555

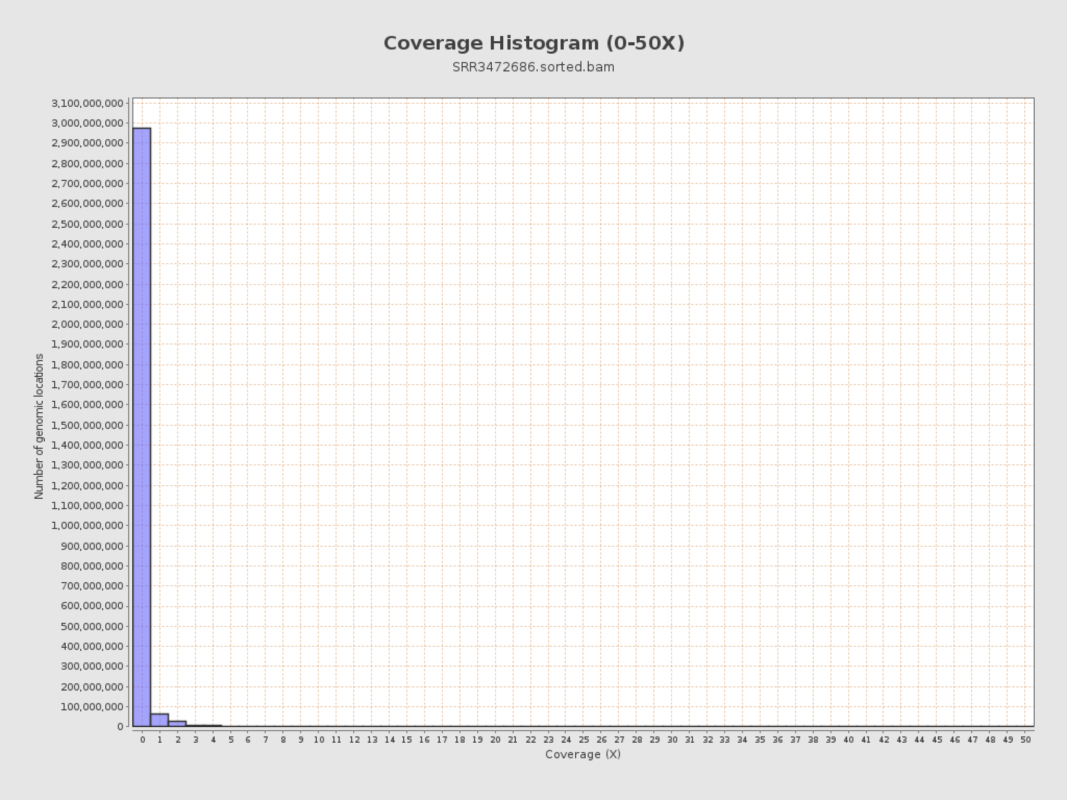
3. Results : Coverage across reference



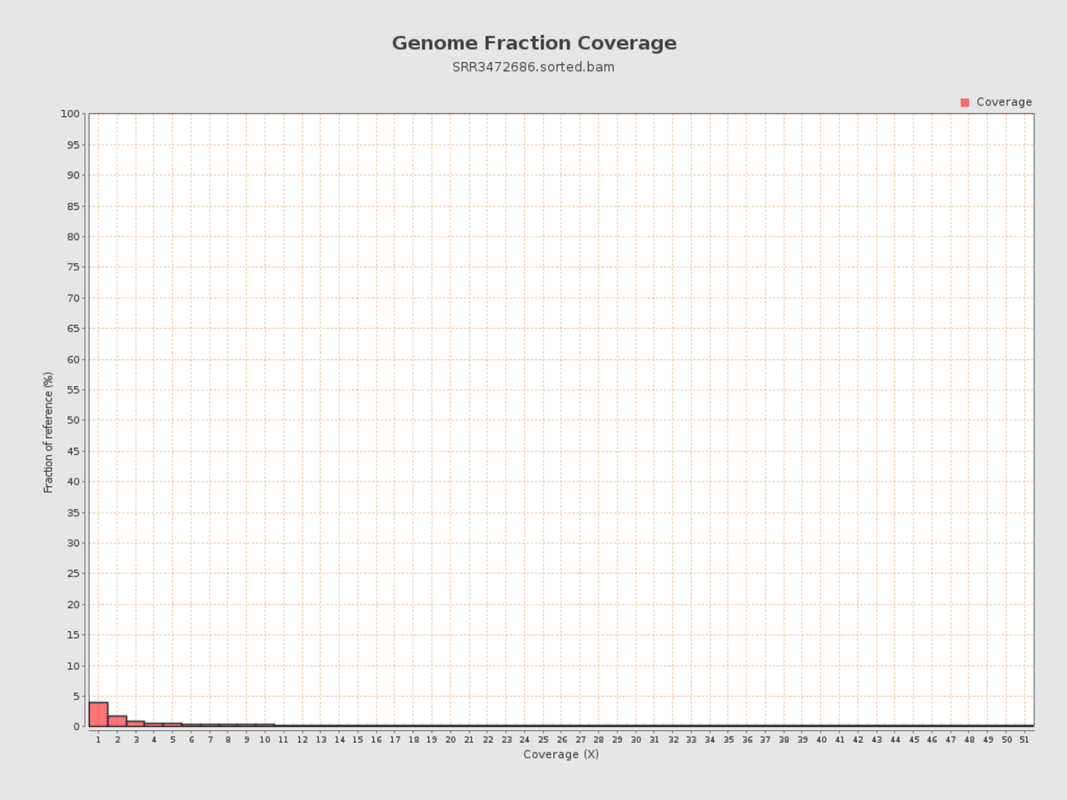
4. Results : Coverage Histogram



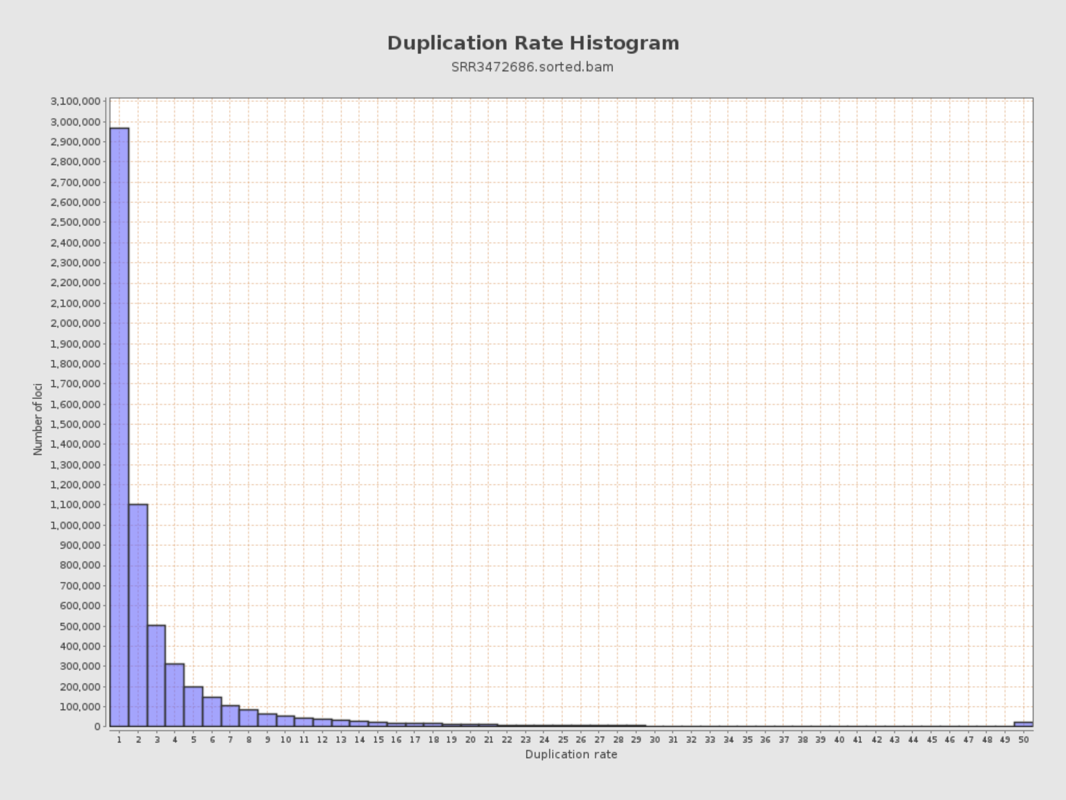
5. Results : Coverage Histogram (0-50X)



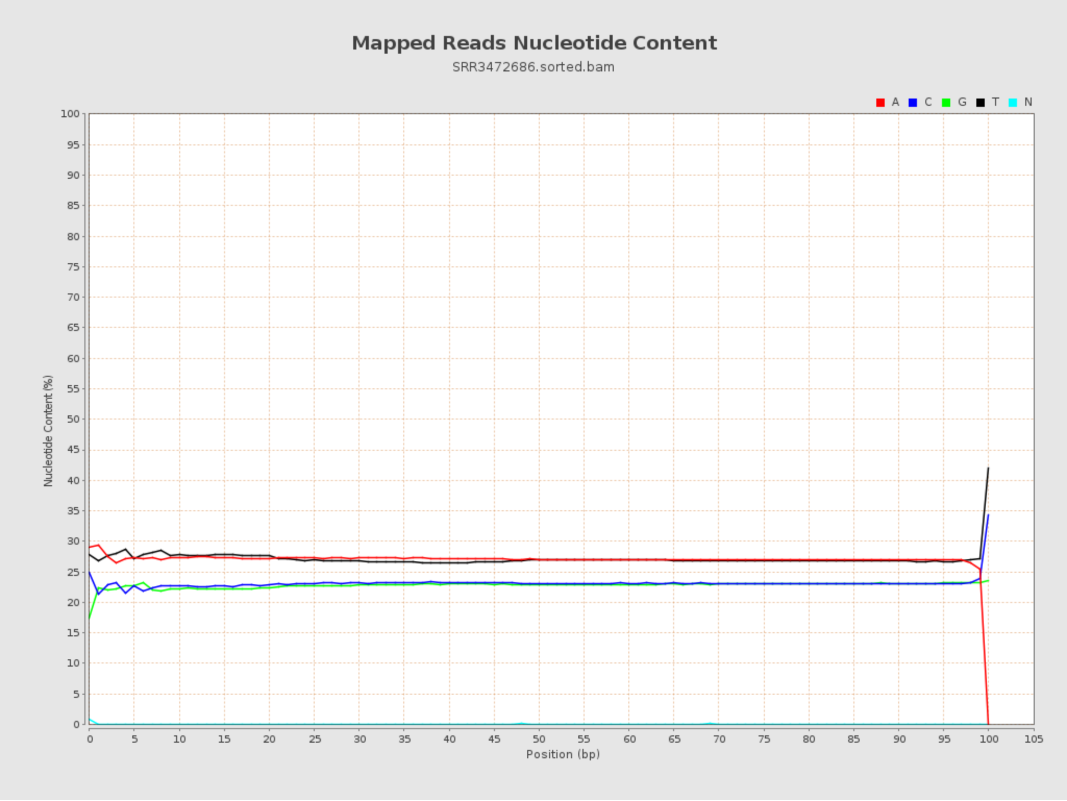
6. Results : Genome Fraction Coverage



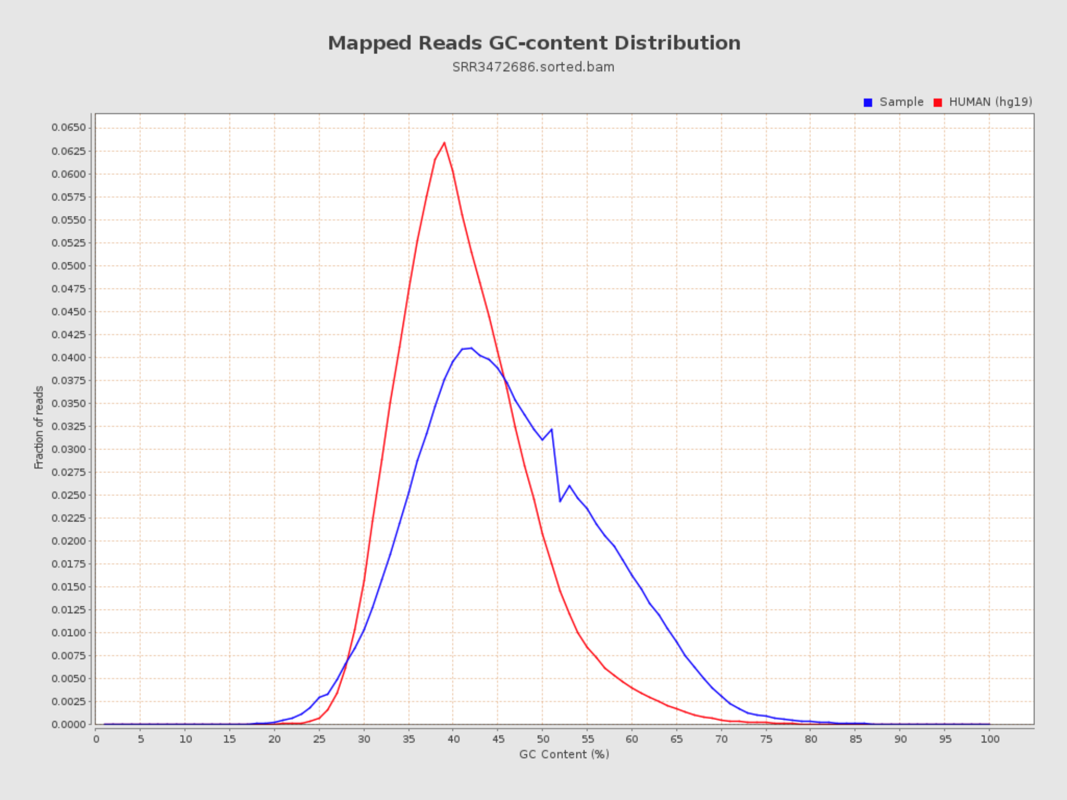
7. Results : Duplication Rate Histogram



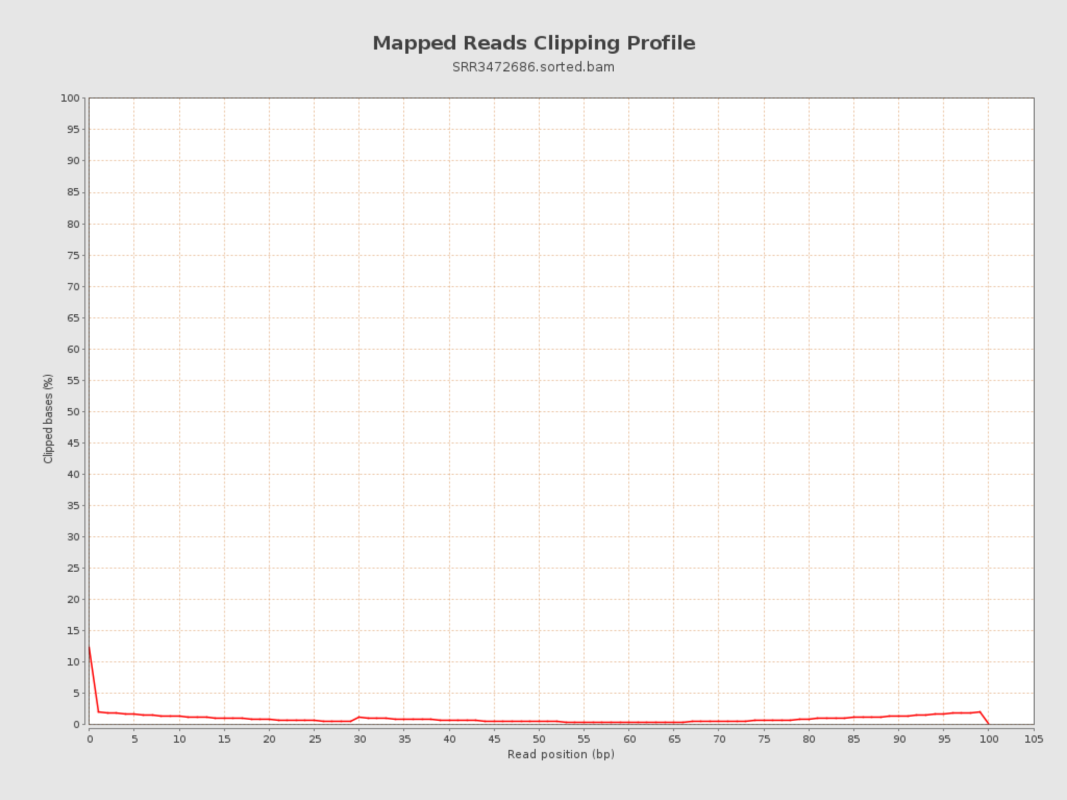
8. Results : Mapped Reads Nucleotide Content



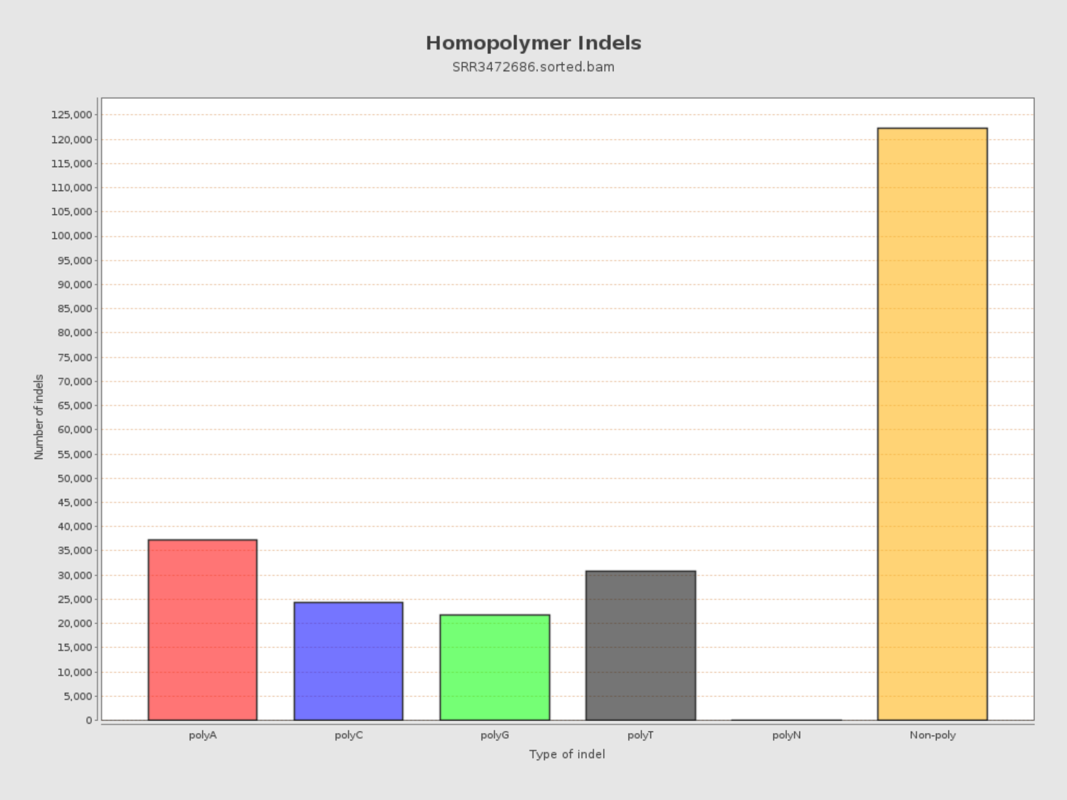
9. Results : Mapped Reads GC-content Distribution



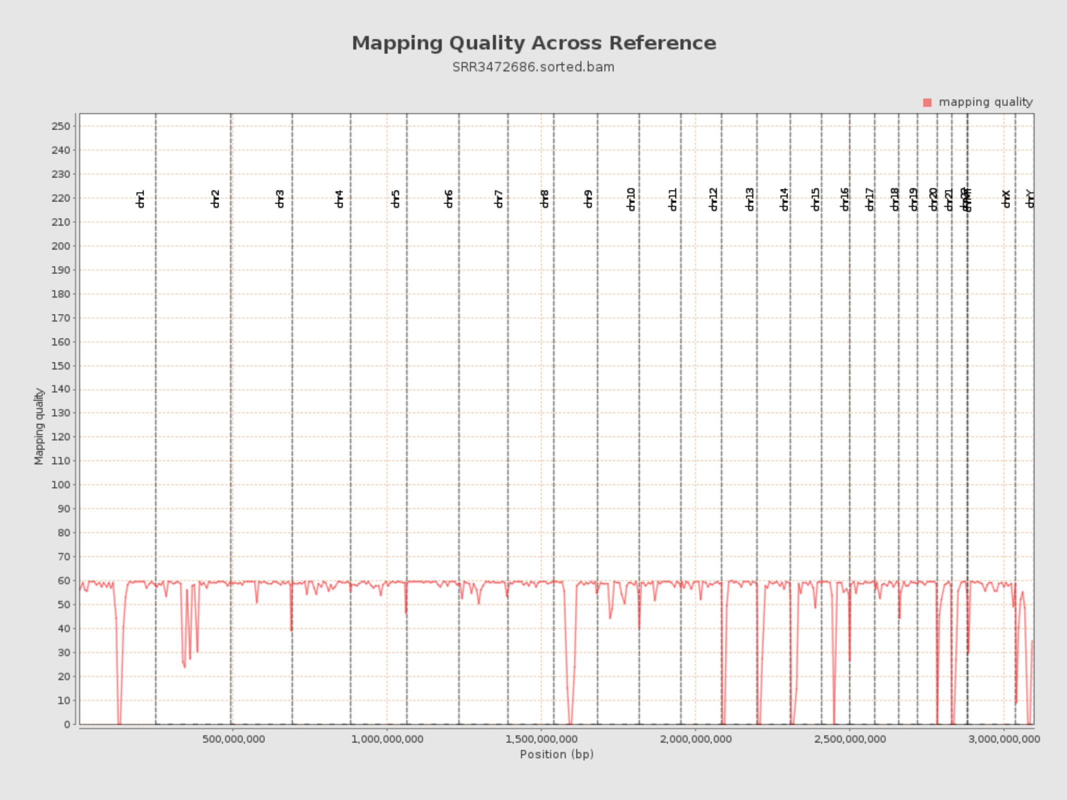
10. Results : Mapped Reads Clipping Profile



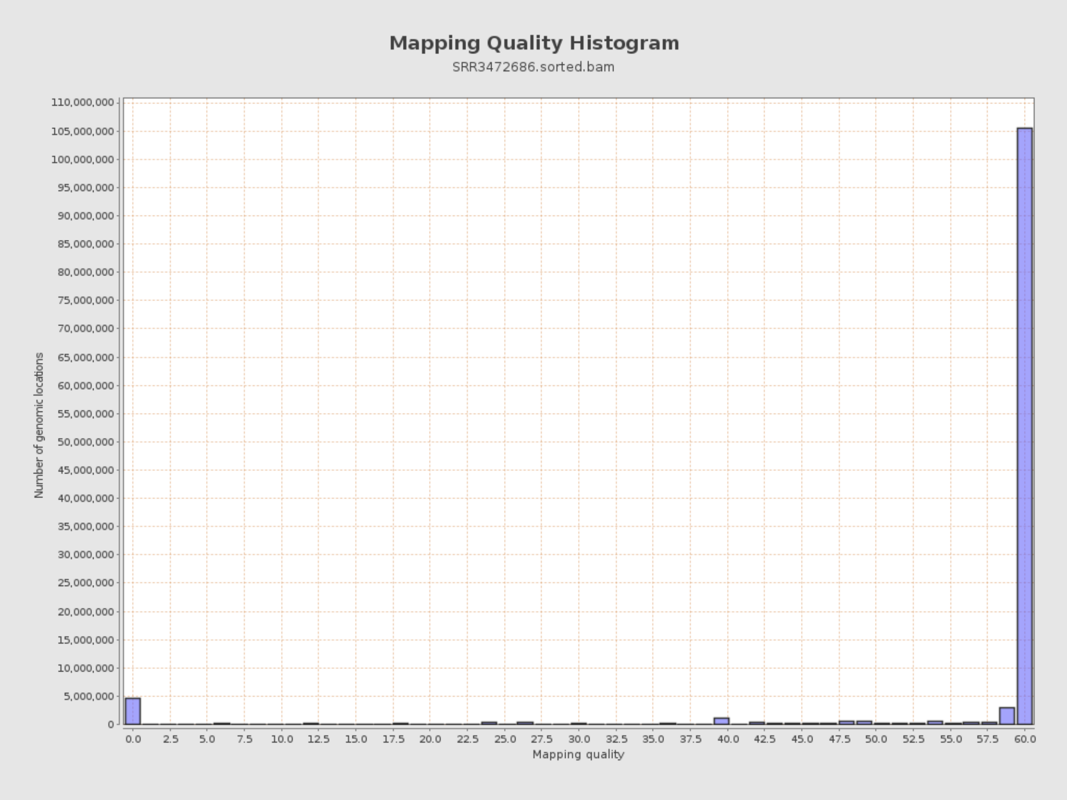
11. Results : Homopolymer Indels



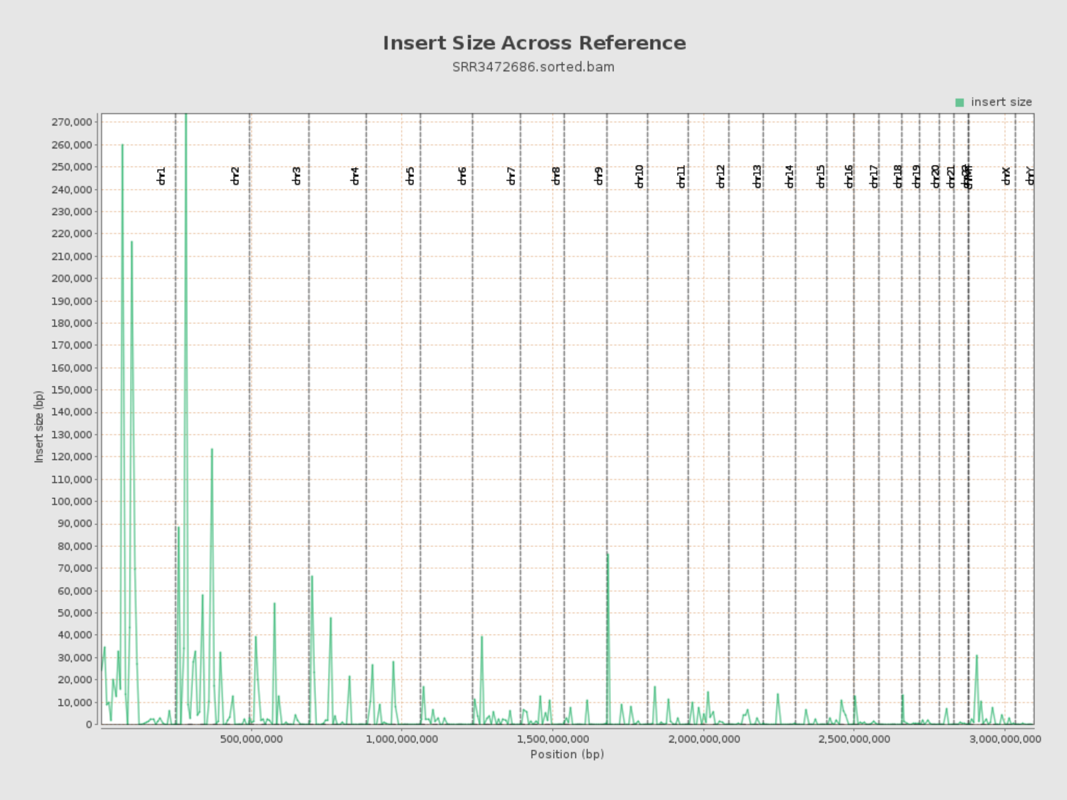
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram