Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 03:36:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472466.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_SRR3472466 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472466_1.fastq.gz SRR3472466_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 03:36:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472466.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	12,905,066
Mapped reads	12,608,380 / 97.7%
Unmapped reads	296,686 / 2.3%
Mapped paired reads	12,608,380 / 97.7%
Mapped reads, first in pair	6,338,650 / 49.12%
Mapped reads, second in pair	6,269,730 / 48.58%
Mapped reads, both in pair	12,508,616 / 96.93%
Mapped reads, singletons	99,764 / 0.77%
Secondary alignments	0
Supplementary alignments	48,346 / 0.37%
Read min/max/mean length	30 / 100 / 98.61
Duplicated reads (estimated)	7,399,119 / 57.33%
Duplication rate	44.85%
Clipped reads	904,428 / 7.01%

2.2. ACGT Content

Number/percentage of A's	331,694,184 / 26.9%
Number/percentage of C's	285,276,132 / 23.13%
Number/percentage of T's	332,999,704 / 27%
Number/percentage of G's	283,046,806 / 22.95%
Number/percentage of N's	152,734 / 0.01%

GC Percentage	46.09%

2.3. Coverage

Mean	0.3984
Standard Deviation	13.3576

2.4. Mapping Quality

Mean Mapping Quality	55.1

2.5. Insert size

Mean	20,918.74
Standard Deviation	1,431,819.42
P25/Median/P75	147 / 204 / 273

2.6. Mismatches and indels

General error rate	0.53%
Mismatches	6,415,390
Insertions	72,129
Mapped reads with at least one insertion	0.57%
Deletions	59,923
Mapped reads with at least one deletion	0.47%
Homopolymer indels	46%

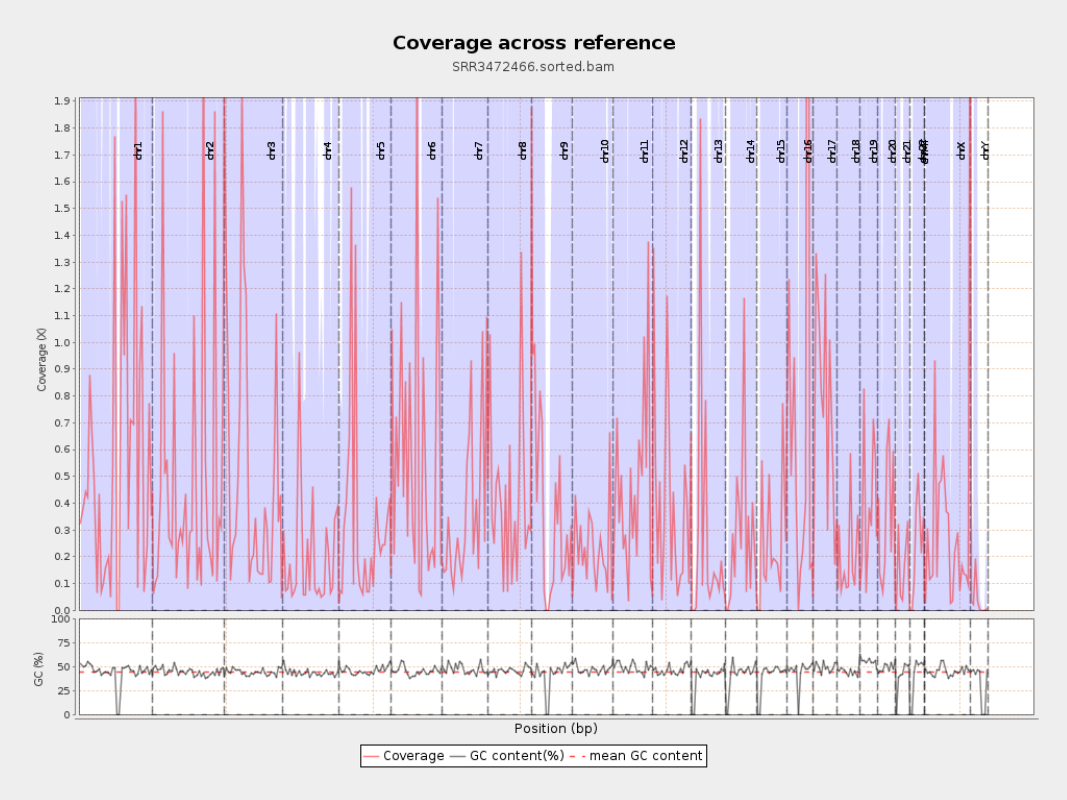
2.7. Chromosome stats

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

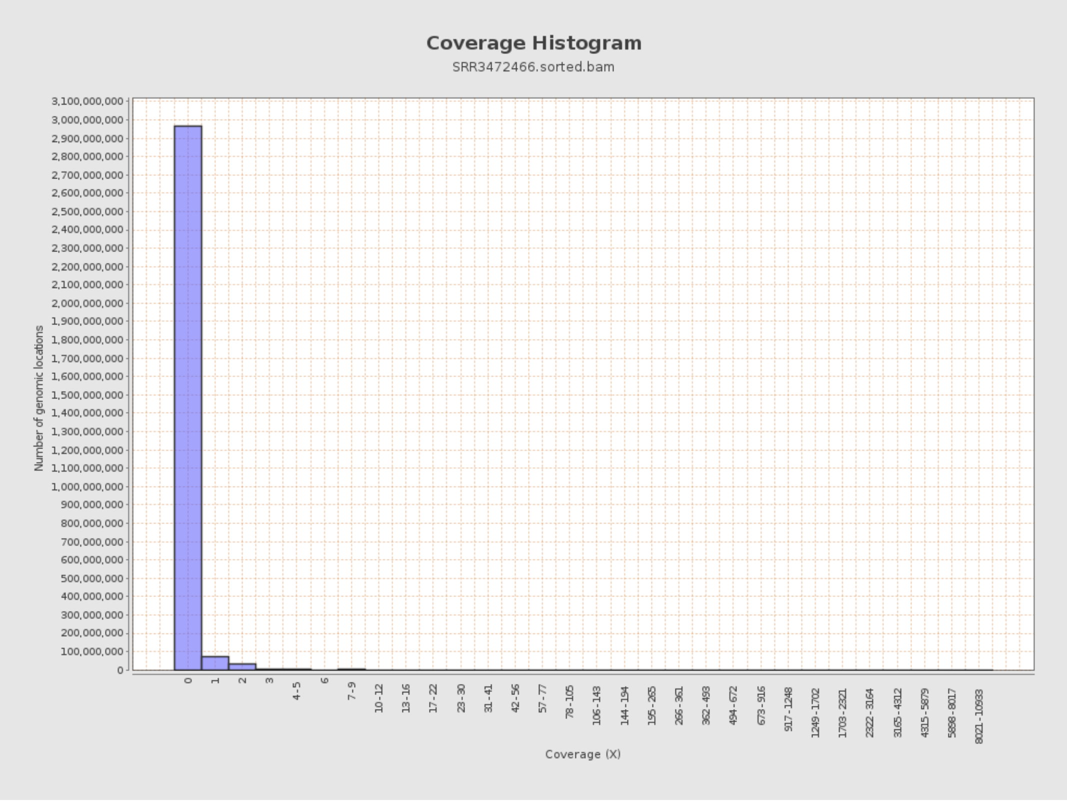
		bases	coverage	deviation
chr1	249250621	143452560	0.5755	16.0744
chr2	243199373	118308917	0.4865	21.1923
chr3	198022430	105933058	0.535	12.4636
chr4	191154276	37302426	0.1951	6.88
chr5	180915260	59527109	0.329	11.1376
chr6	171115067	99738783	0.5829	14.8586
chr7	159138663	60952826	0.383	13.2711
chr8	146364022	62983847	0.4303	12.5285
chr9	141213431	52172196	0.3695	11.3847
chr10	135534747	30878010	0.2278	9.2964
chr11	135006516	61821291	0.4579	16.9302
chr12	133851895	54086921	0.4041	11.7915
chr13	115169878	30111904	0.2615	12.8059
chr14	107349540	29483757	0.2747	9.6141
chr15	102531392	26117090	0.2547	7.59
chr16	90354753	69641270	0.7708	23.9132
chr17	81195210	59897375	0.7377	15.9757
chr18	78077248	16277500	0.2085	6.4132
chr19	59128983	24443912	0.4134	10.6695
chr20	63025520	21992694	0.3489	8.8329
chr21	48129895	7626494	0.1585	6.4927
chr22	51304566	12163049	0.2371	6.2343
chrMT	16571	914	0.0552	0.2409
chrX	155270560	46234614	0.2978	9.4655

chrY	59373566	2166965	0.0365	2.5621

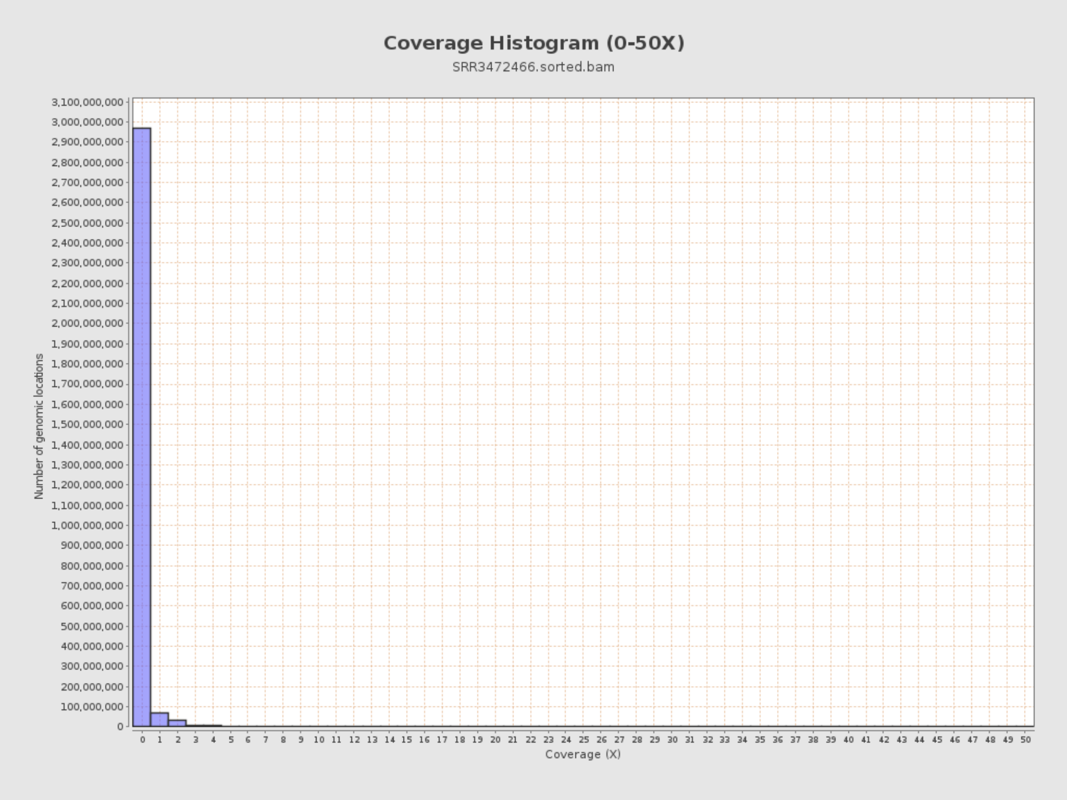
3. Results : Coverage across reference



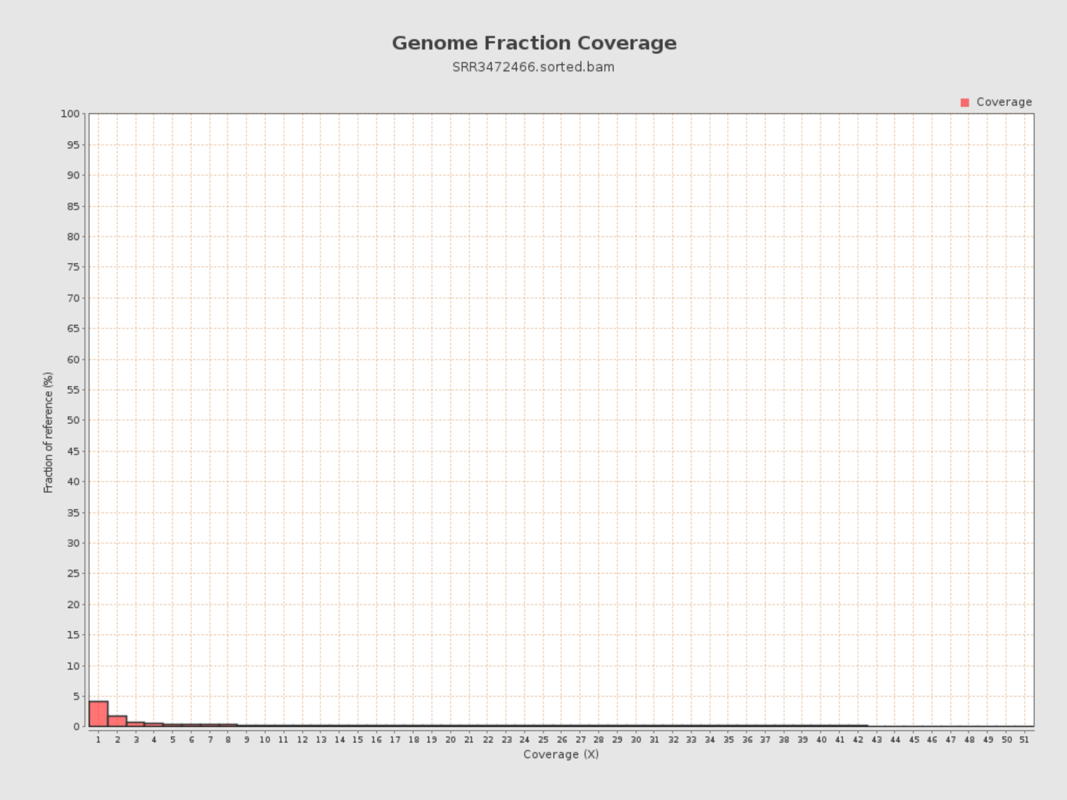
4. Results : Coverage Histogram



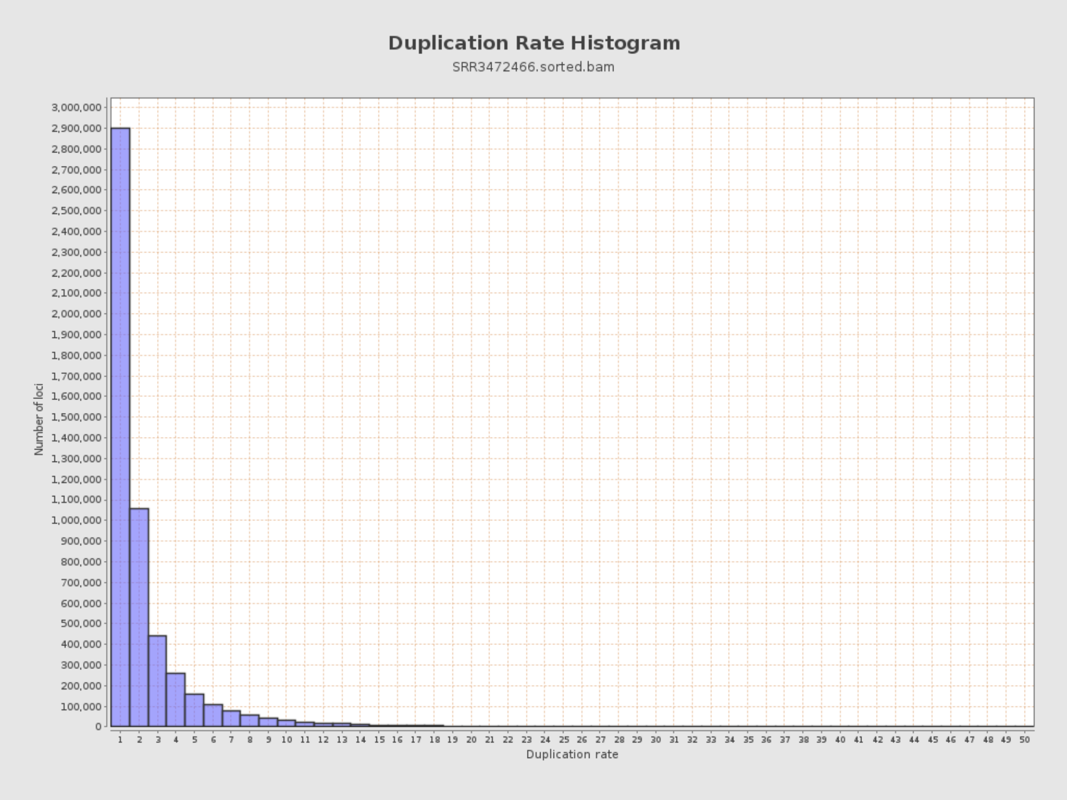
5. Results : Coverage Histogram (0-50X)



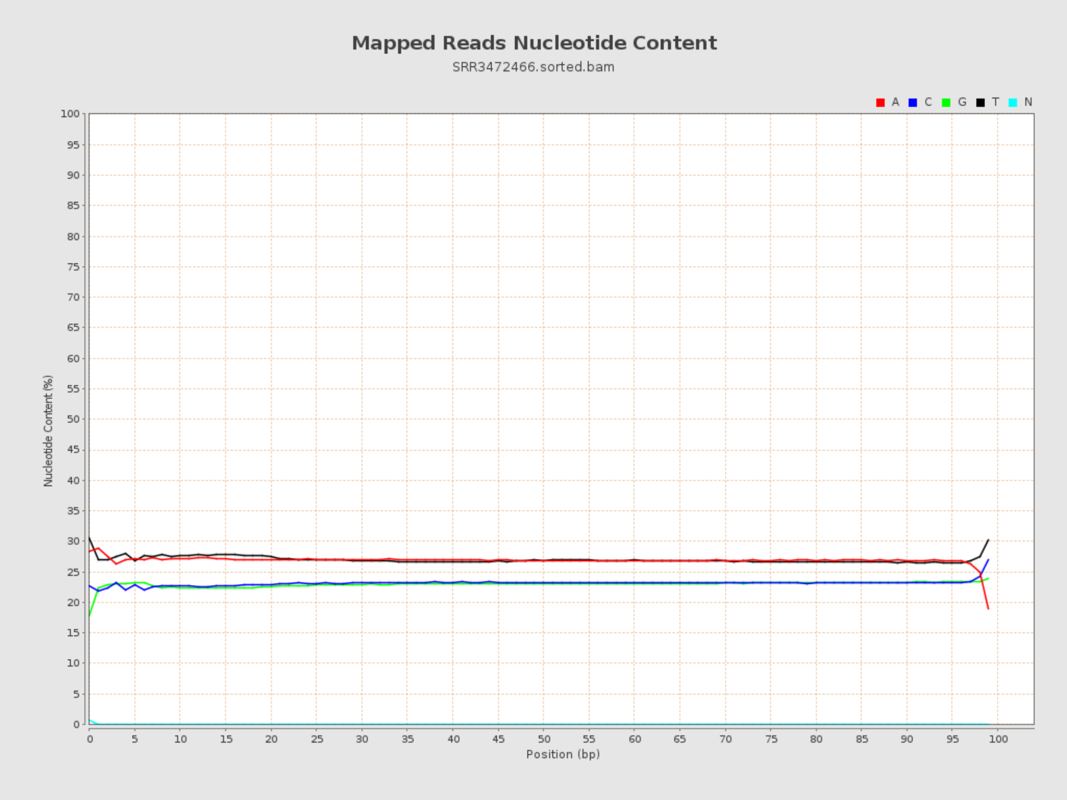
6. Results : Genome Fraction Coverage



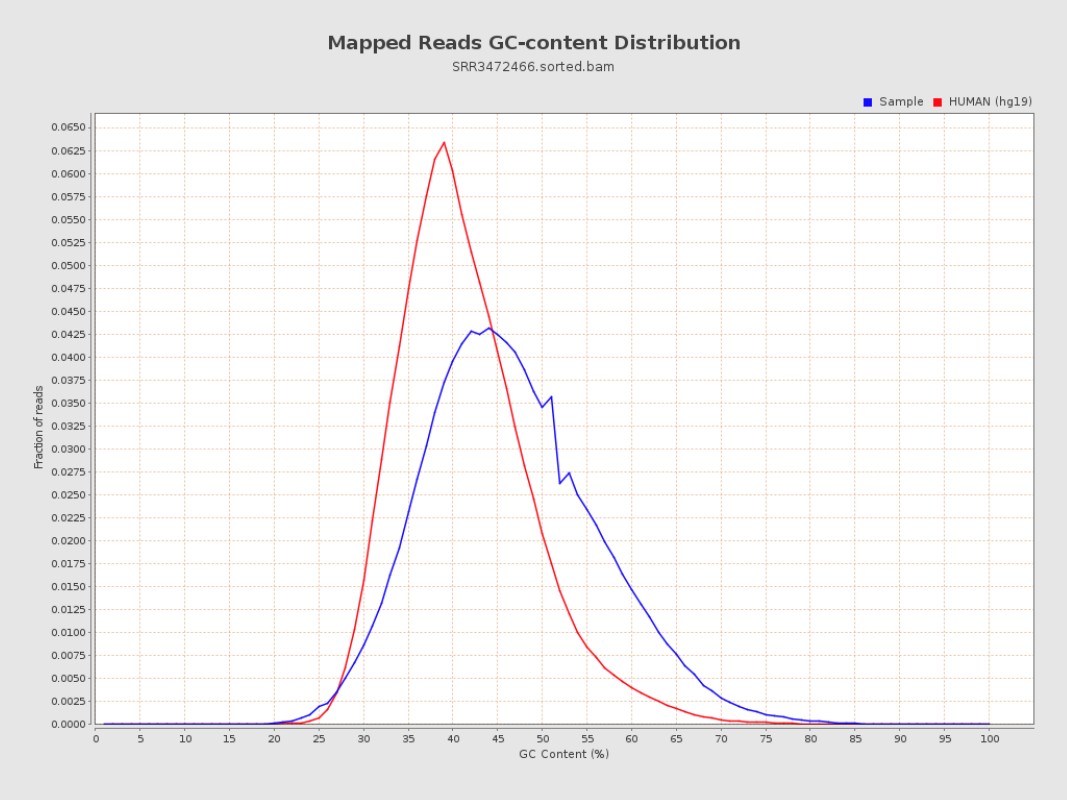
7. Results : Duplication Rate Histogram



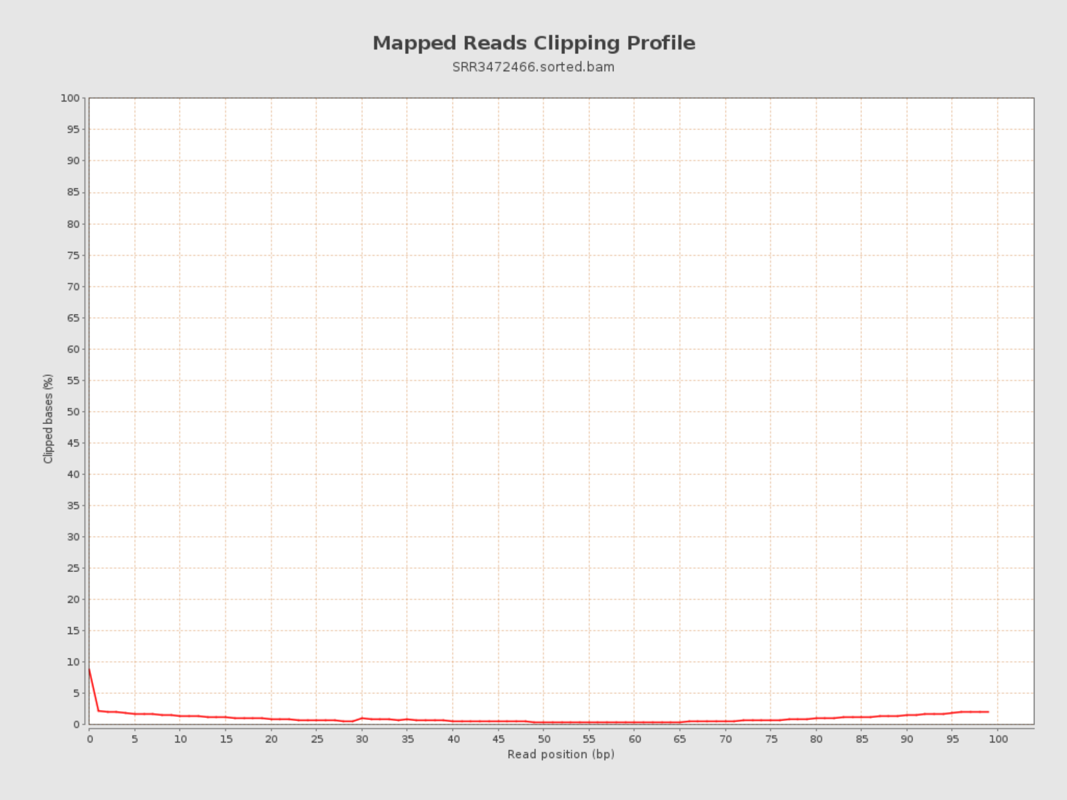
8. Results : Mapped Reads Nucleotide Content



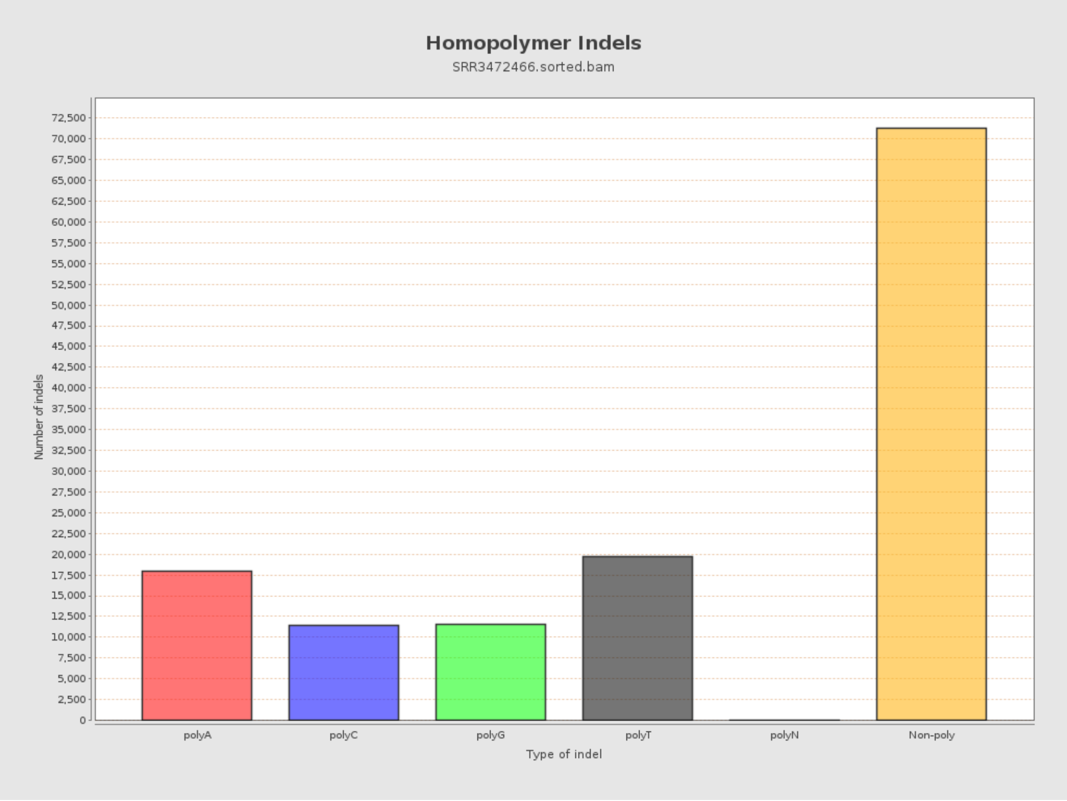
9. Results : Mapped Reads GC-content Distribution



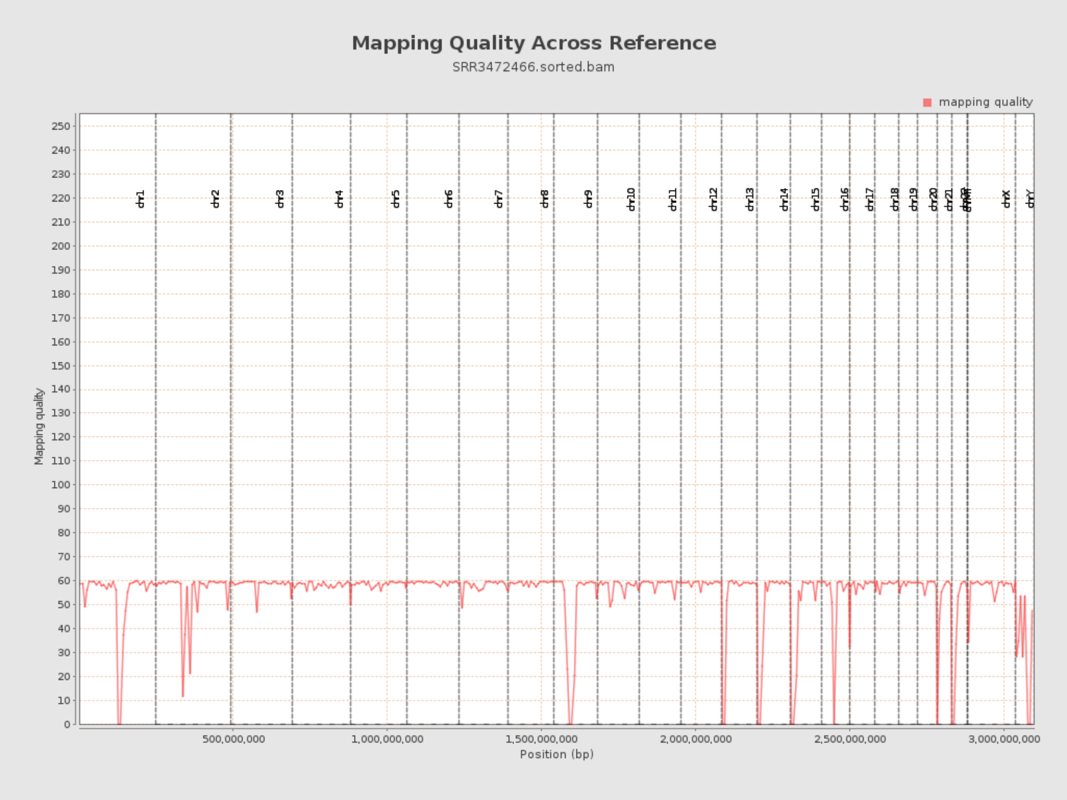
10. Results : Mapped Reads Clipping Profile



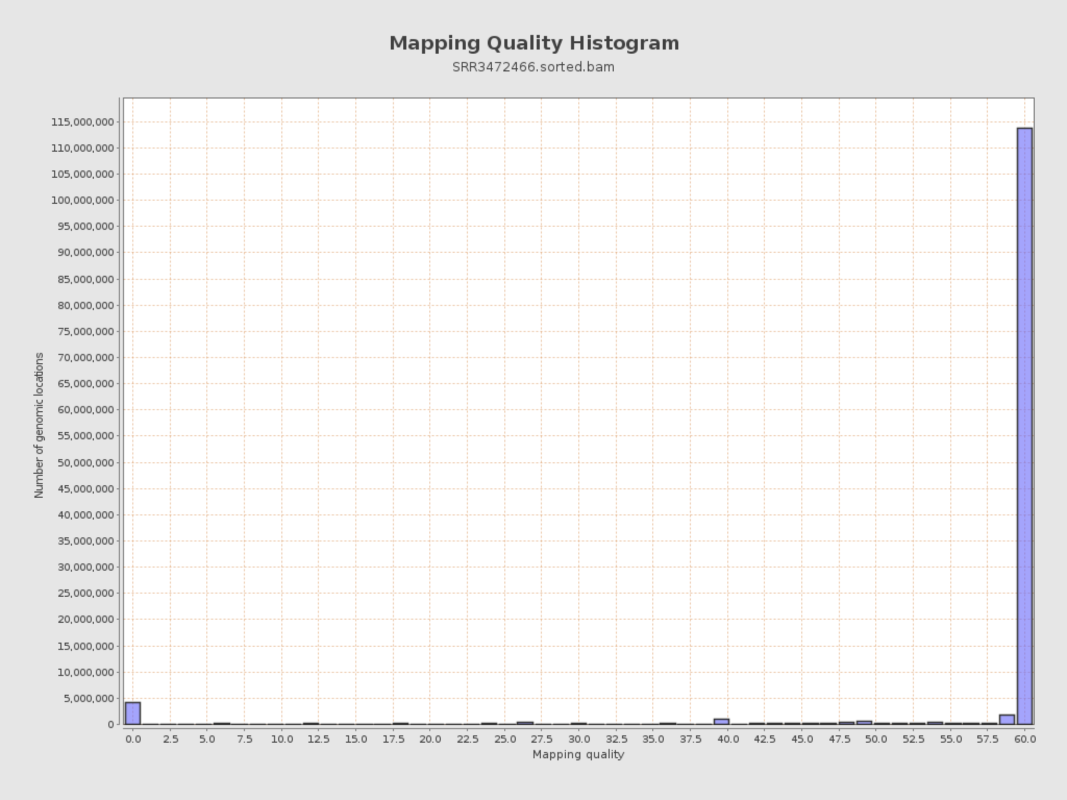
11. Results : Homopolymer Indels



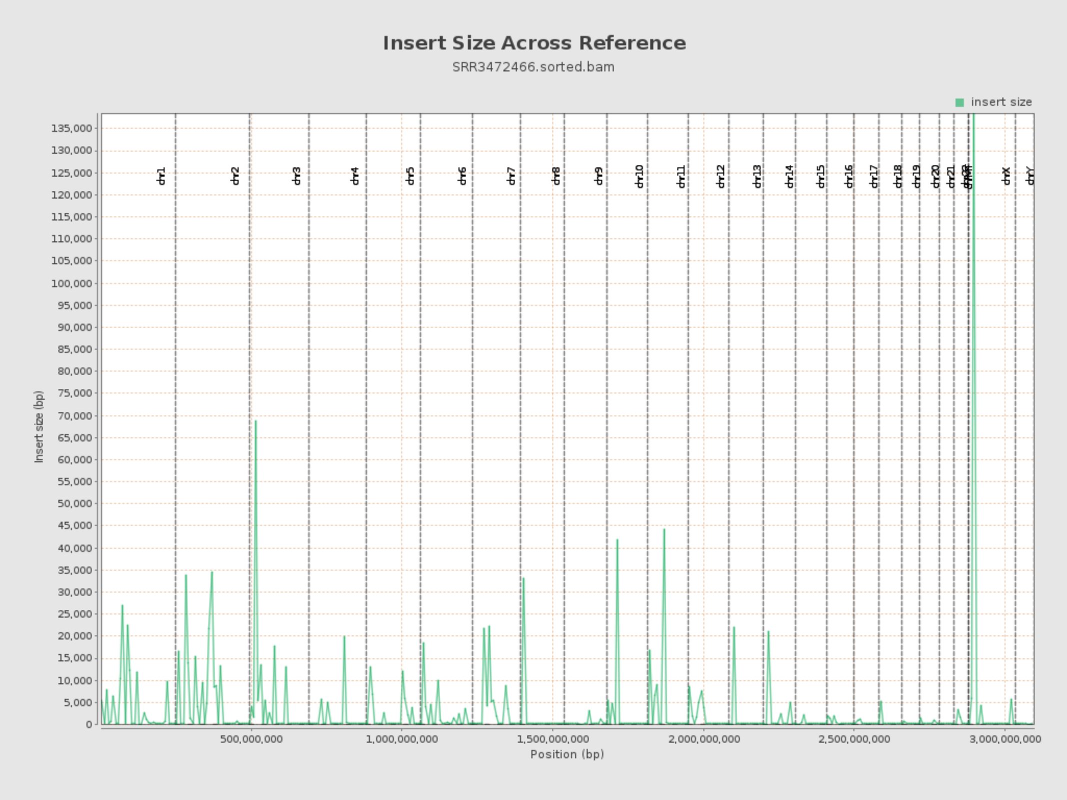
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram