Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 07:26:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472479.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_SRR3472479 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472479_1.fastq.gz SRR3472479_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 07:26:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472479.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	16,939,254
Mapped reads	16,638,638 / 98.23%
Unmapped reads	300,616 / 1.77%
Mapped paired reads	16,638,638 / 98.23%
Mapped reads, first in pair	8,365,189 / 49.38%
Mapped reads, second in pair	8,273,449 / 48.84%
Mapped reads, both in pair	16,487,336 / 97.33%
Mapped reads, singletons	151,302 / 0.89%
Secondary alignments	0
Supplementary alignments	69,887 / 0.41%
Read min/max/mean length	30 / 100 / 100.17
Duplicated reads (estimated)	10,472,059 / 61.82%
Duplication rate	46.44%
Clipped reads	1,426,101 / 8.42%

2.2. ACGT Content

Number/percentage of A's	450,274,427 / 27.54%
Number/percentage of C's	369,372,670 / 22.59%
Number/percentage of T's	447,853,135 / 27.4%
Number/percentage of G's	367,026,378 / 22.45%
Number/percentage of N's	248,748 / 0.02%

GC Percentage	45.05%

2.3. Coverage

Mean	0.5281
Standard Deviation	19.0175

2.4. Mapping Quality

Mean Mapping Quality	55.03

2.5. Insert size

Mean	32,603.33
Standard Deviation	1,792,216.12
P25/Median/P75	176 / 247 / 331

2.6. Mismatches and indels

General error rate	0.66%
Mismatches	10,673,002
Insertions	87,190
Mapped reads with at least one insertion	0.52%
Deletions	85,807
Mapped reads with at least one deletion	0.51%
Homopolymer indels	44.58%

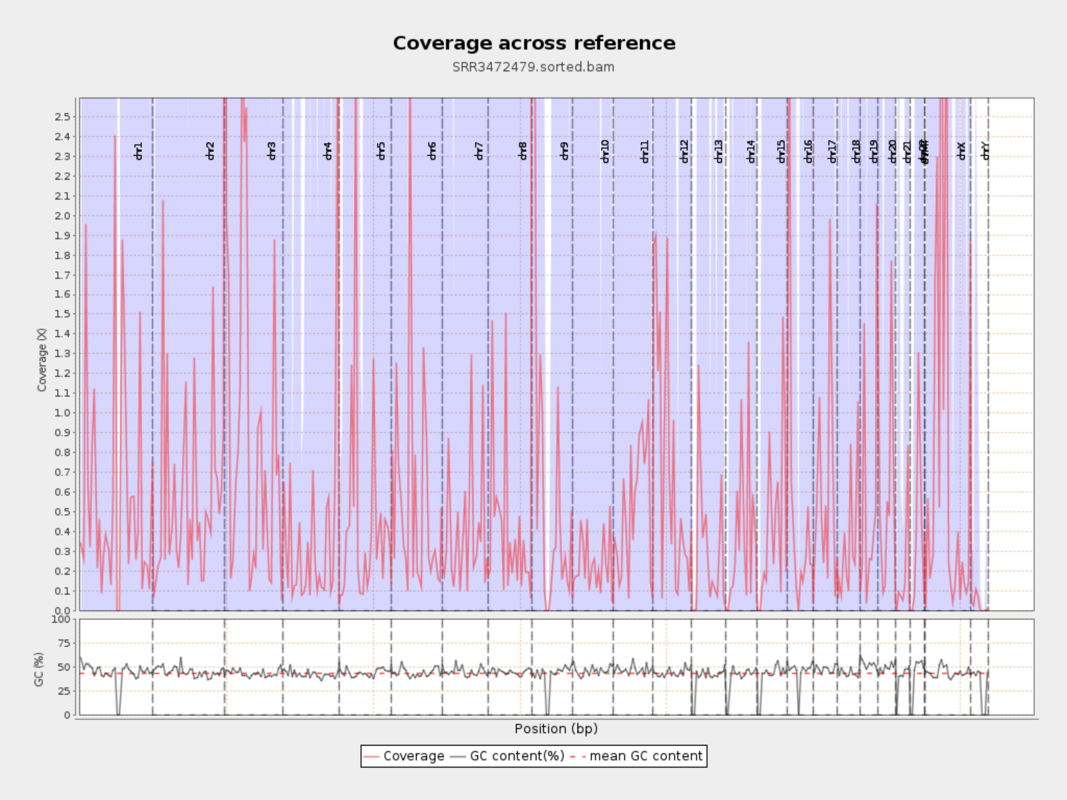
2.7. Chromosome stats

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

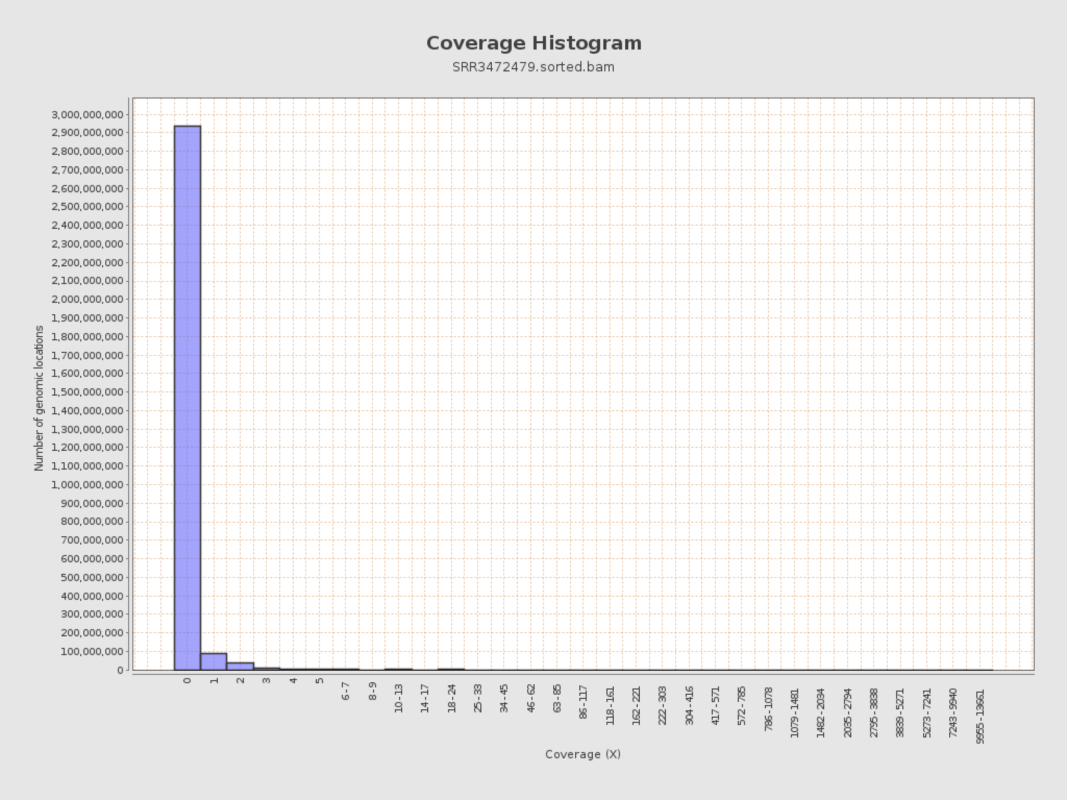
		bases	coverage	deviation
chr1	249250621	149730745	0.6007	22.0846
chr2	243199373	137806042	0.5666	20.2276
chr3	198022430	193904803	0.9792	21.1324
chr4	191154276	72954243	0.3817	13.6364
chr5	180915260	85154077	0.4707	15.0455
chr6	171115067	93636458	0.5472	14.7319
chr7	159138663	65047475	0.4087	12.3105
chr8	146364022	61219479	0.4183	12.7107
chr9	141213431	98843277	0.7	17.4962
chr10	135534747	33457264	0.2469	7.7358
chr11	135006516	71804992	0.5319	17.2962
chr12	133851895	99826024	0.7458	26.7569
chr13	115169878	35615717	0.3092	13.8524
chr14	107349540	40427379	0.3766	20.3495
chr15	102531392	45636797	0.4451	14.4652
chr16	90354753	47791018	0.5289	14.4184
chr17	81195210	47201044	0.5813	16.2728
chr18	78077248	28417803	0.364	12.6739
chr19	59128983	28940316	0.4894	12.6891
chr20	63025520	38233163	0.6066	24.8801
chr21	48129895	9419948	0.1957	8.5303
chr22	51304566	18341766	0.3575	11.6214
chrMT	16571	6462	0.39	1.2368
chrX	155270560	129603784	0.8347	41.0115

chrY	59373566	1966221	0.0331	1.1071

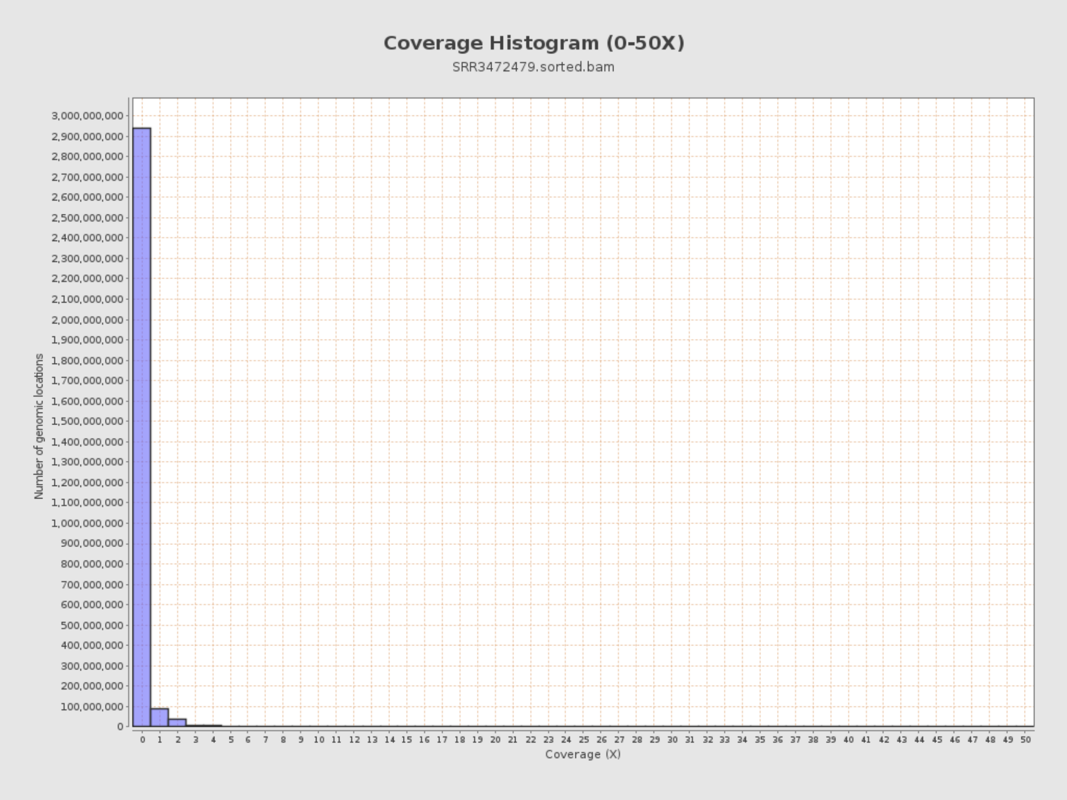
3. Results : Coverage across reference



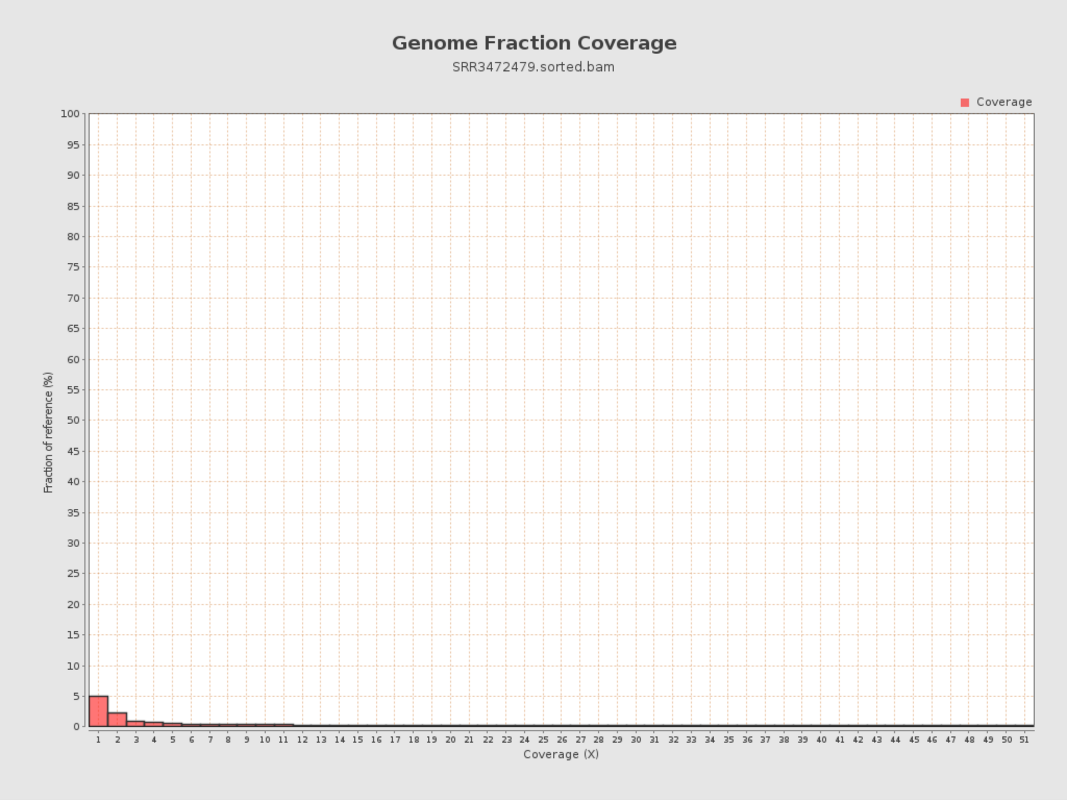
4. Results : Coverage Histogram



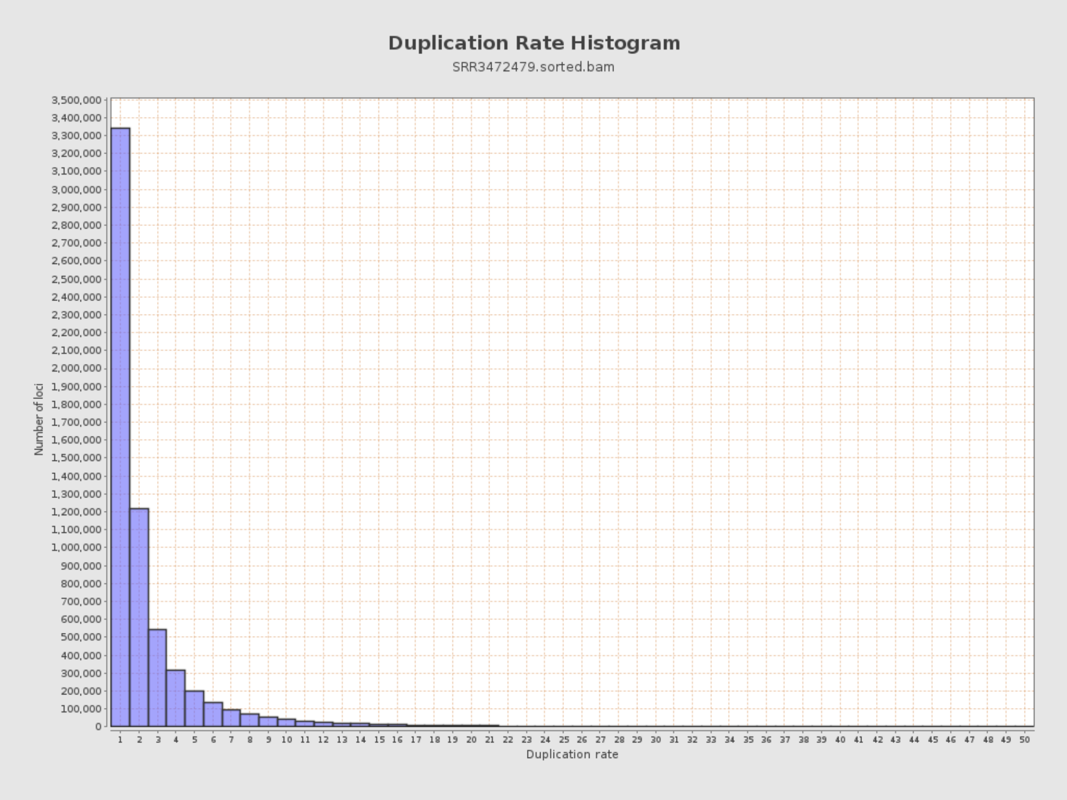
5. Results : Coverage Histogram (0-50X)



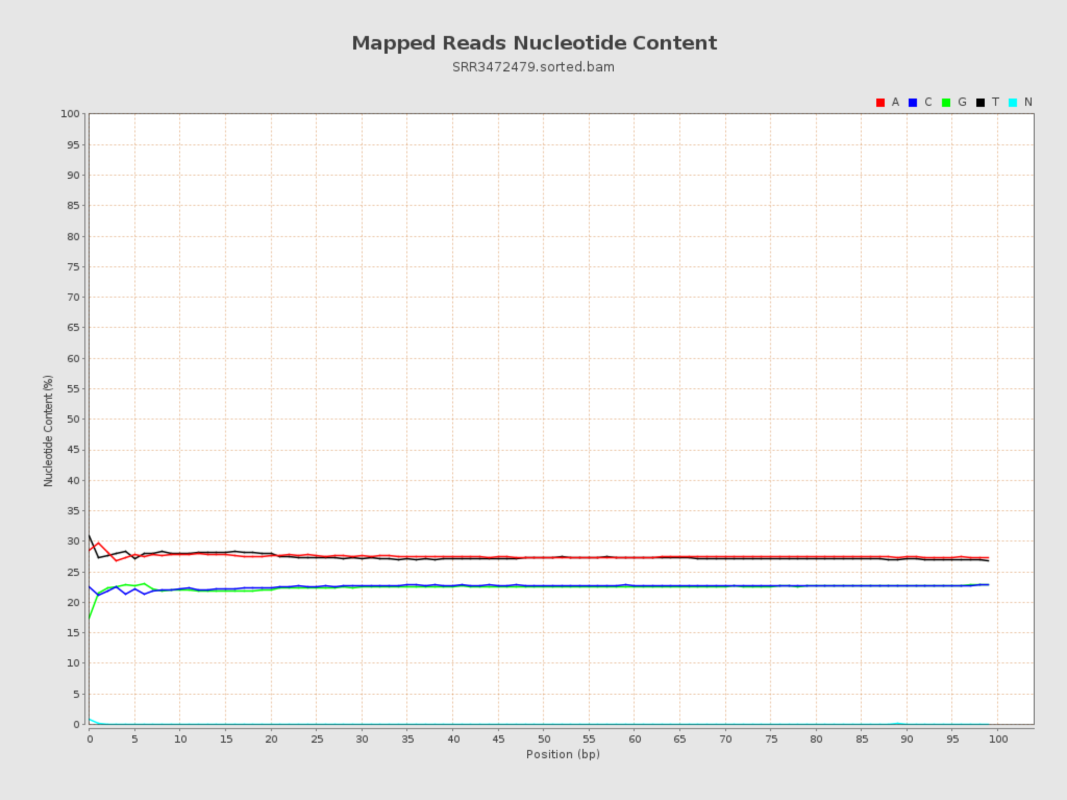
6. Results : Genome Fraction Coverage



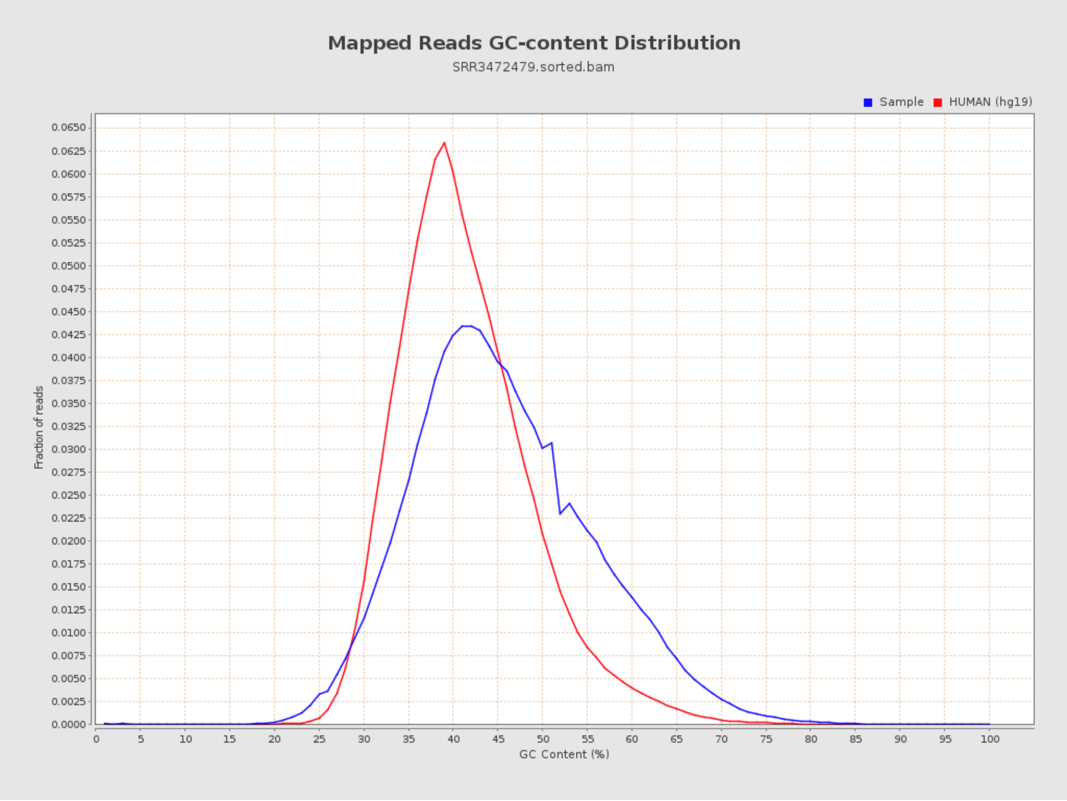
7. Results : Duplication Rate Histogram



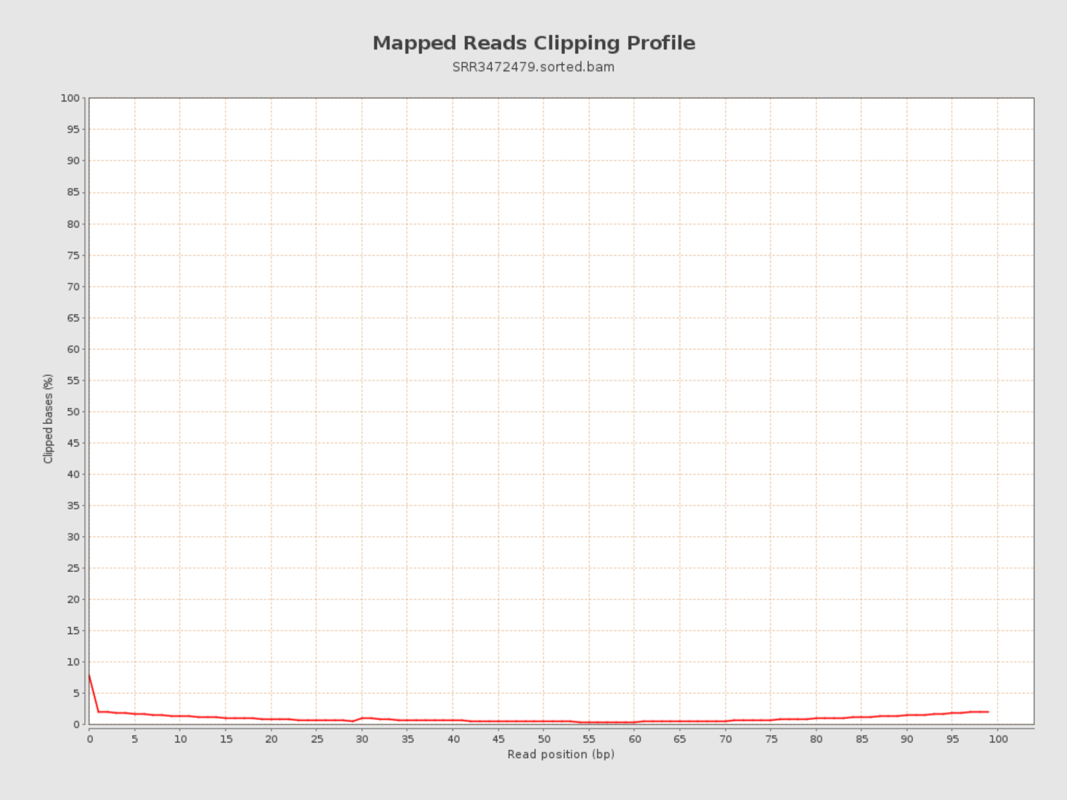
8. Results : Mapped Reads Nucleotide Content



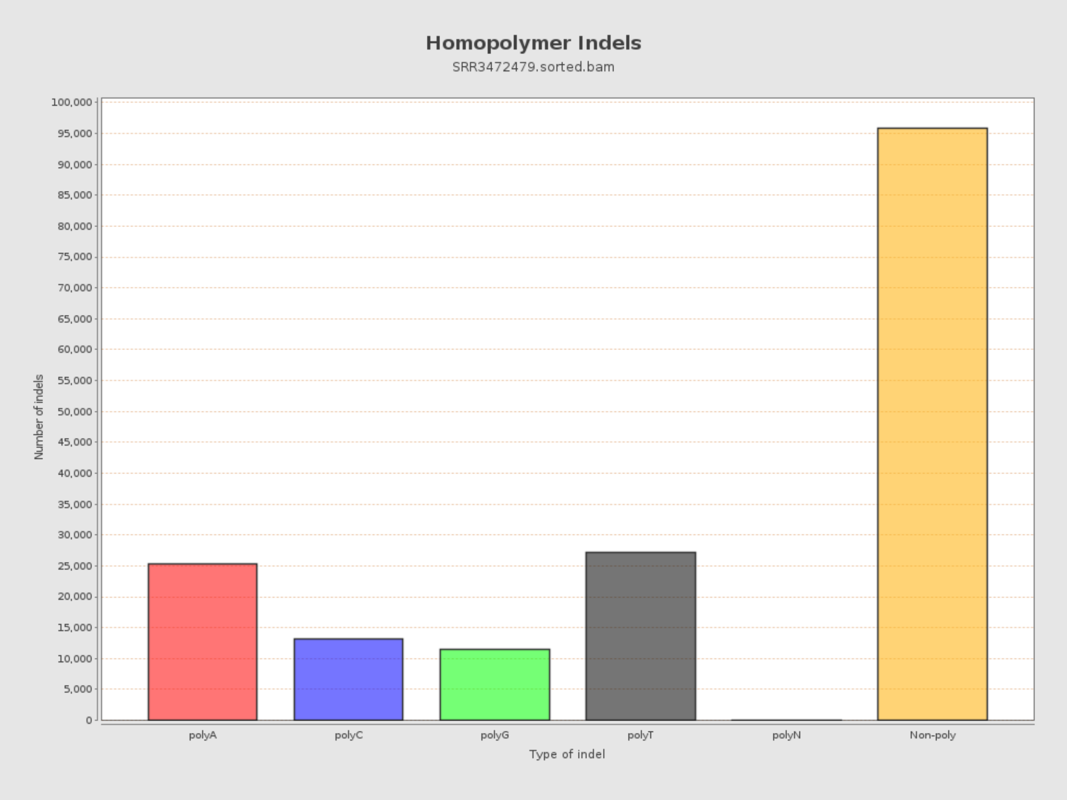
9. Results : Mapped Reads GC-content Distribution



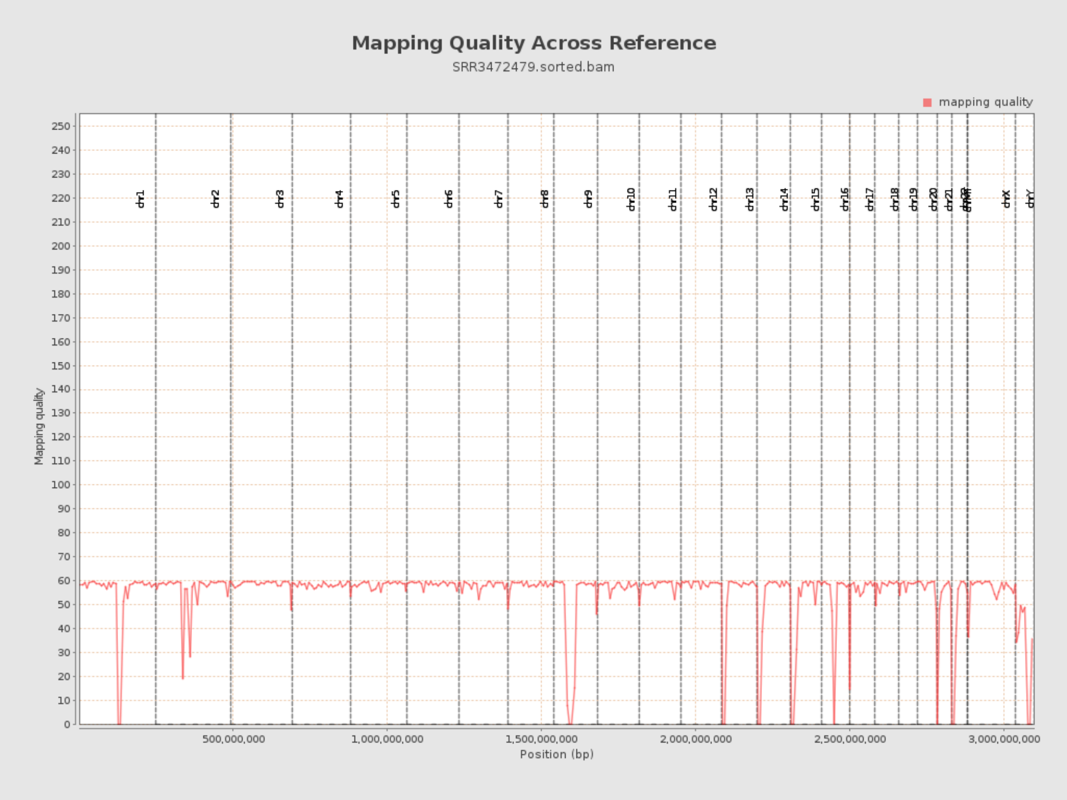
10. Results : Mapped Reads Clipping Profile



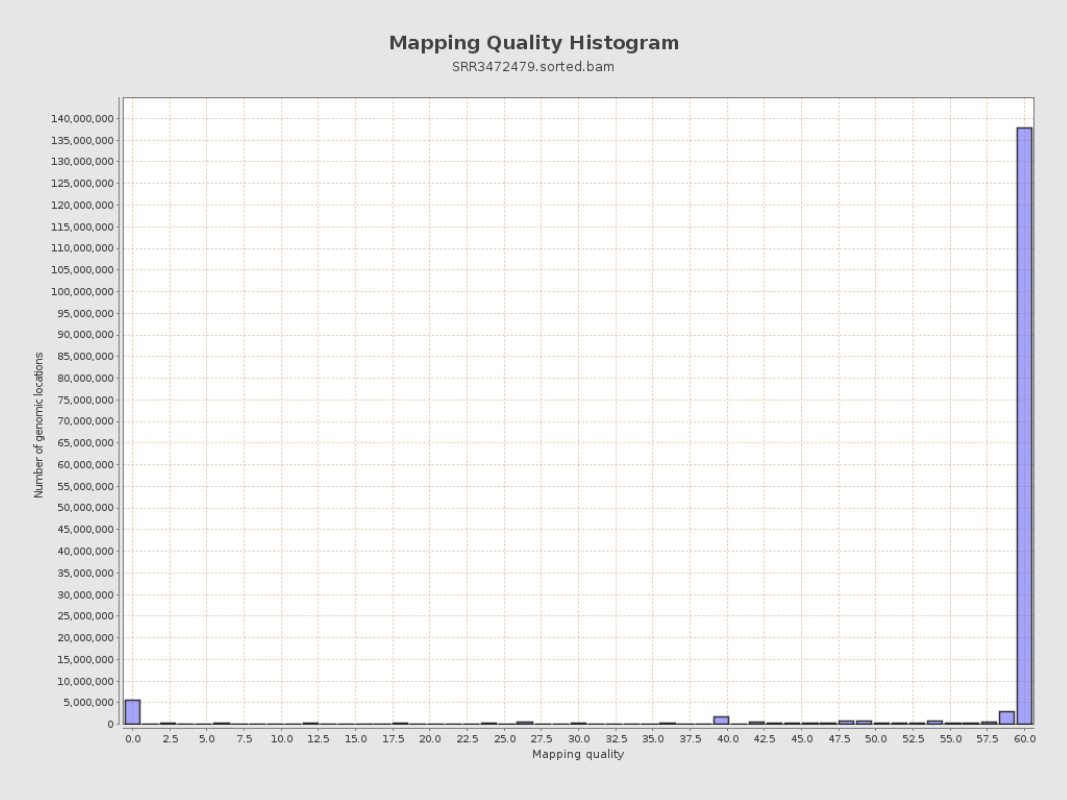
11. Results : Homopolymer Indels



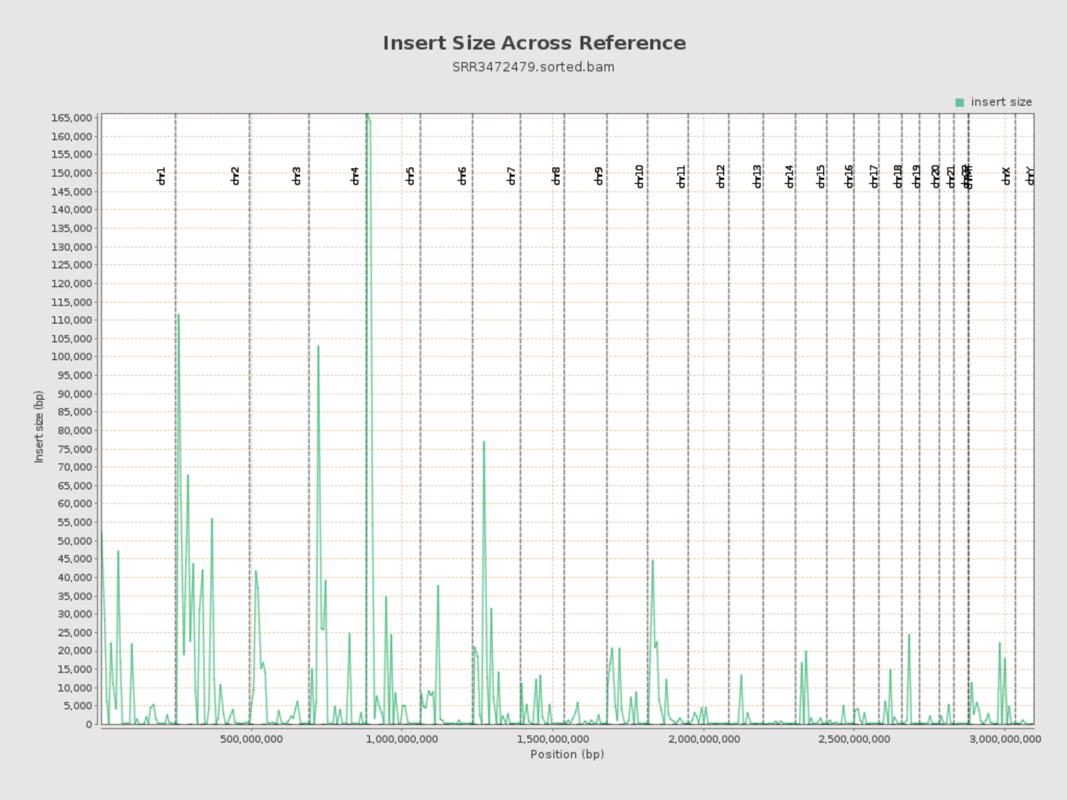
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram