

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 06:20:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472475.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_SRR3472475 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472475_1.fastq.gz SRR3472475_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 06:20:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472475.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	19,102,790
Mapped reads	18,892,013 / 98.9%
Unmapped reads	210,777 / 1.1%
Mapped paired reads	18,892,013 / 98.9%
Mapped reads, first in pair	9,469,695 / 49.57%
Mapped reads, second in pair	9,422,318 / 49.32%
Mapped reads, both in pair	18,787,612 / 98.35%
Mapped reads, singletons	104,401 / 0.55%
Secondary alignments	0
Supplementary alignments	74,678 / 0.39%
Read min/max/mean length	30 / 100 / 100.16
Duplicated reads (estimated)	12,274,012 / 64.25%
Duplication rate	47.49%
Clipped reads	1,816,467 / 9.51%

2.2. ACGT Content

Number/percentage of A's	496,171,809 / 26.77%
Number/percentage of C's	433,349,350 / 23.38%
Number/percentage of T's	494,054,078 / 26.65%
Number/percentage of G's	429,705,304 / 23.18%
Number/percentage of N's	291,874 / 0.02%

GC Percentage	46.56%
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2.3. Coverage

Mean	0.5988
Standard Deviation	20.4336

2.4. Mapping Quality

Mean Mapping Quality	55.02
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2.5. Insert size

Mean	29,739.11
Standard Deviation	1,680,197.2
P25/Median/P75	156 / 219 / 296

2.6. Mismatches and indels

General error rate	0.57%
Mismatches	10,341,399
Insertions	93,705
Mapped reads with at least one insertion	0.49%
Deletions	86,337
Mapped reads with at least one deletion	0.45%
Homopolymer indels	44.76%

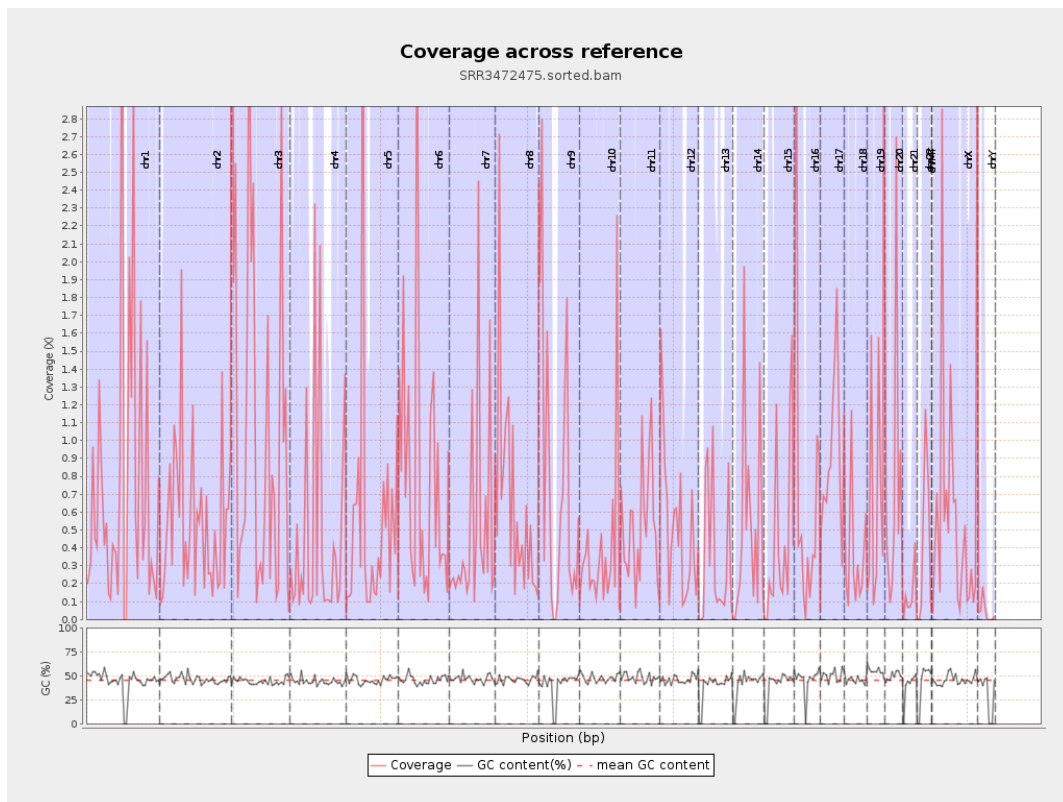
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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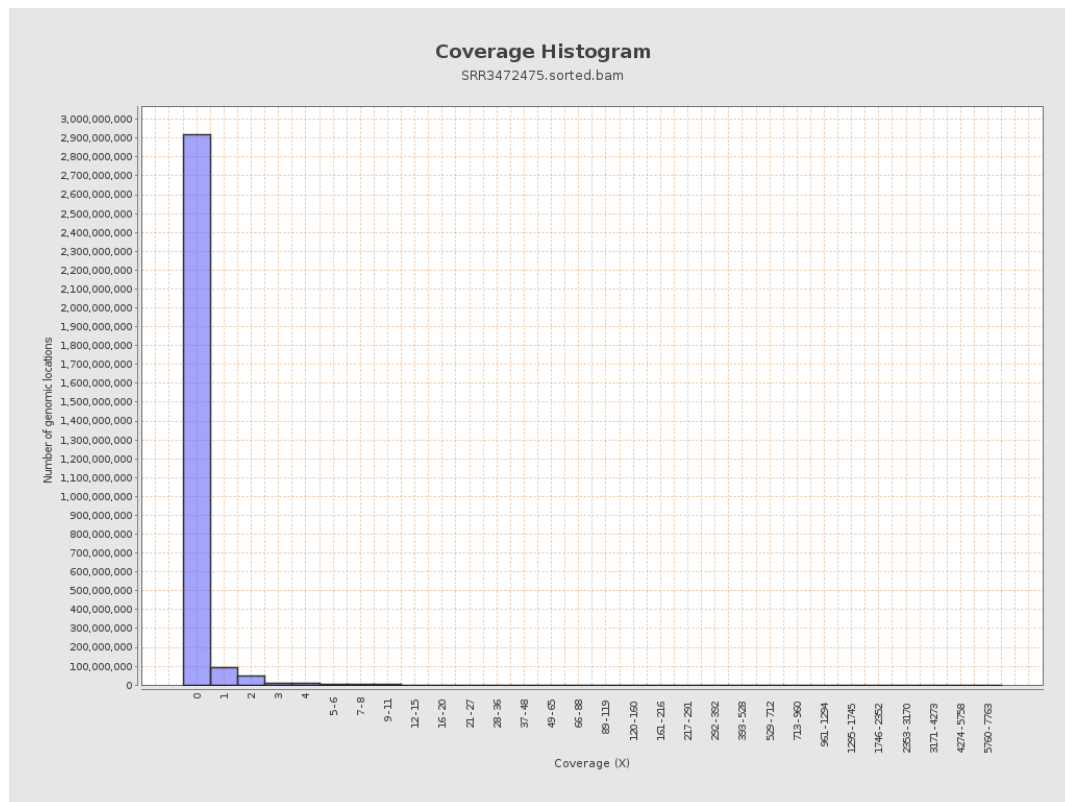
		bases	coverage	deviation
chr1	249250621	192511989	0.7724	28.5372
chr2	243199373	132516230	0.5449	18.2422
chr3	198022430	218548243	1.1037	25.6293
chr4	191154276	87447504	0.4575	23.4141
chr5	180915260	101747941	0.5624	19.7003
chr6	171115067	131329206	0.7675	20.5789
chr7	159138663	78552305	0.4936	16.1488
chr8	146364022	92113116	0.6293	21.3774
chr9	141213431	107257062	0.7595	20.9231
chr10	135534747	53410734	0.3941	16.3775
chr11	135006516	71109236	0.5267	15.8986
chr12	133851895	71129674	0.5314	16.1918
chr13	115169878	39227993	0.3406	13.1702
chr14	107349540	53348885	0.497	24.5118
chr15	102531392	45815049	0.4468	14.8255
chr16	90354753	64495966	0.7138	19.9772
chr17	81195210	75247949	0.9268	20.6135
chr18	78077248	26995898	0.3458	16.6906
chr19	59128983	44880962	0.759	24.1727
chr20	63025520	45872468	0.7278	24.9237
chr21	48129895	6574008	0.1366	4.9302
chr22	51304566	21016594	0.4096	13.978
chrMT	16571	1131	0.0683	0.3348
chrX	155270560	89905970	0.579	21.3484

chrY	59373566	2735680	0.0461	1.771
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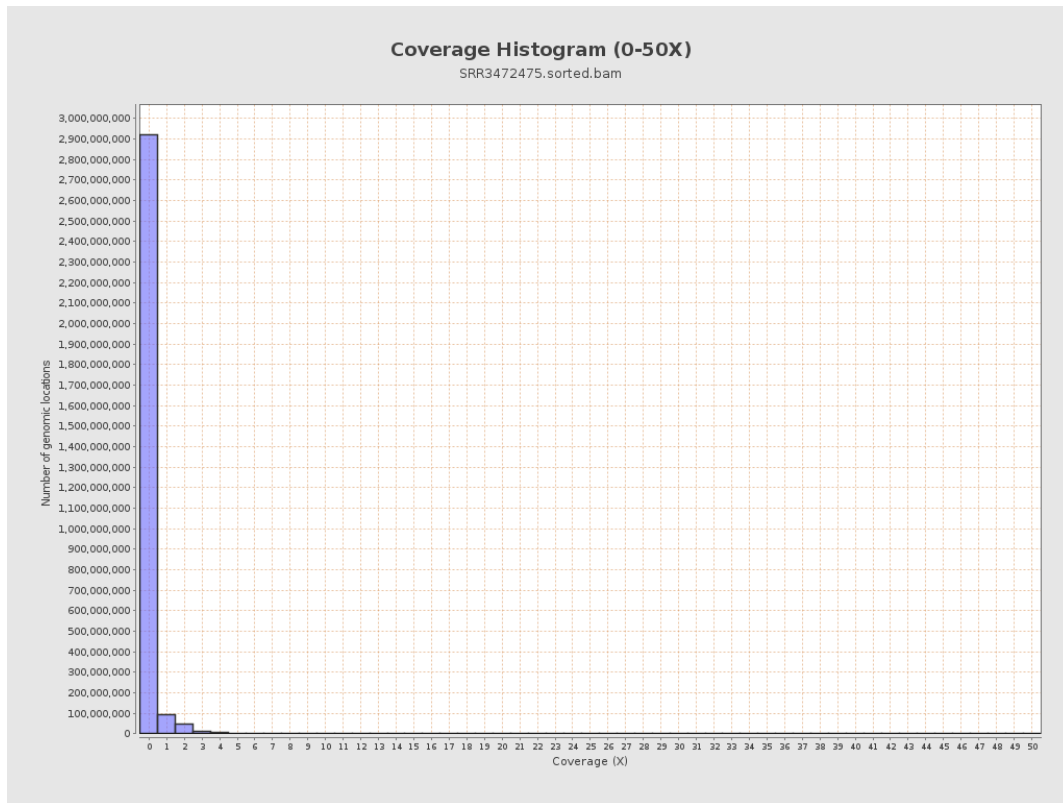
3. Results : Coverage across reference



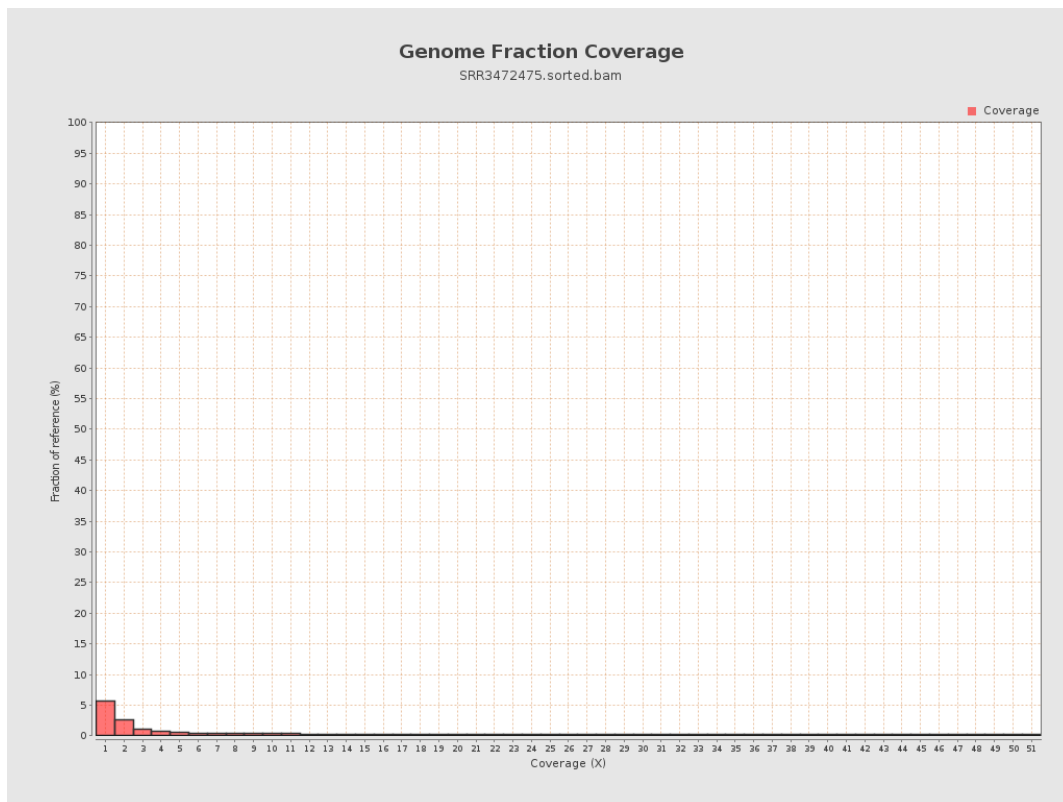
4. Results : Coverage Histogram



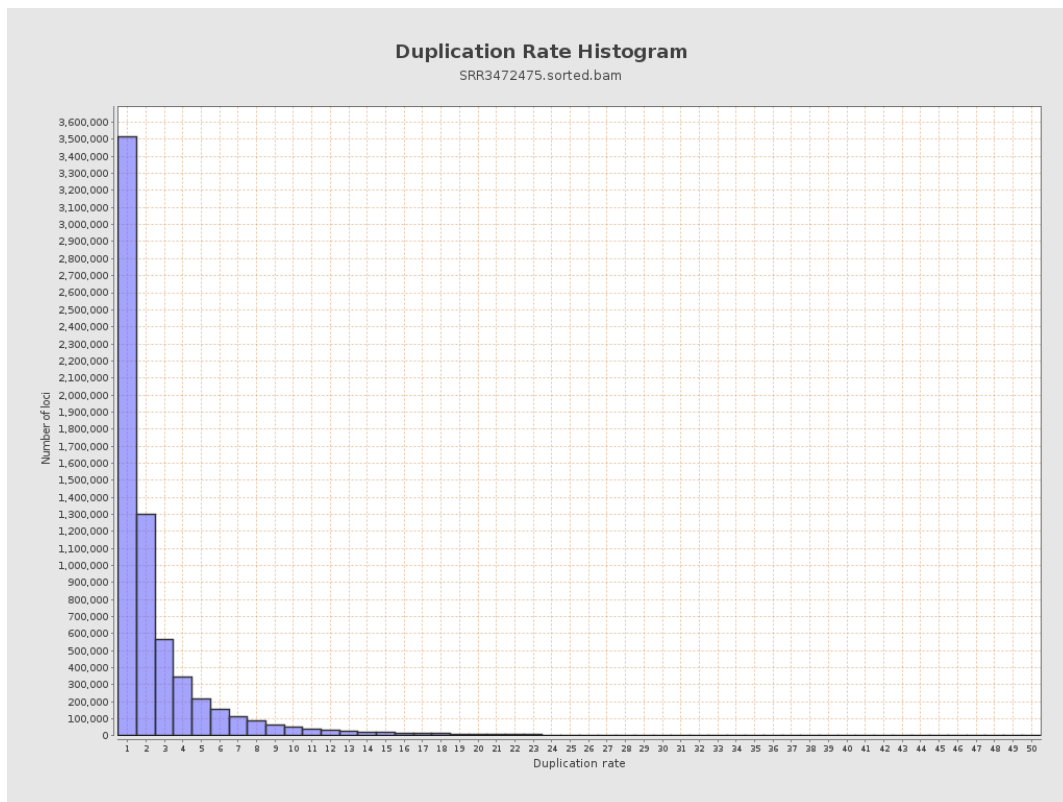
5. Results : Coverage Histogram (0-50X)



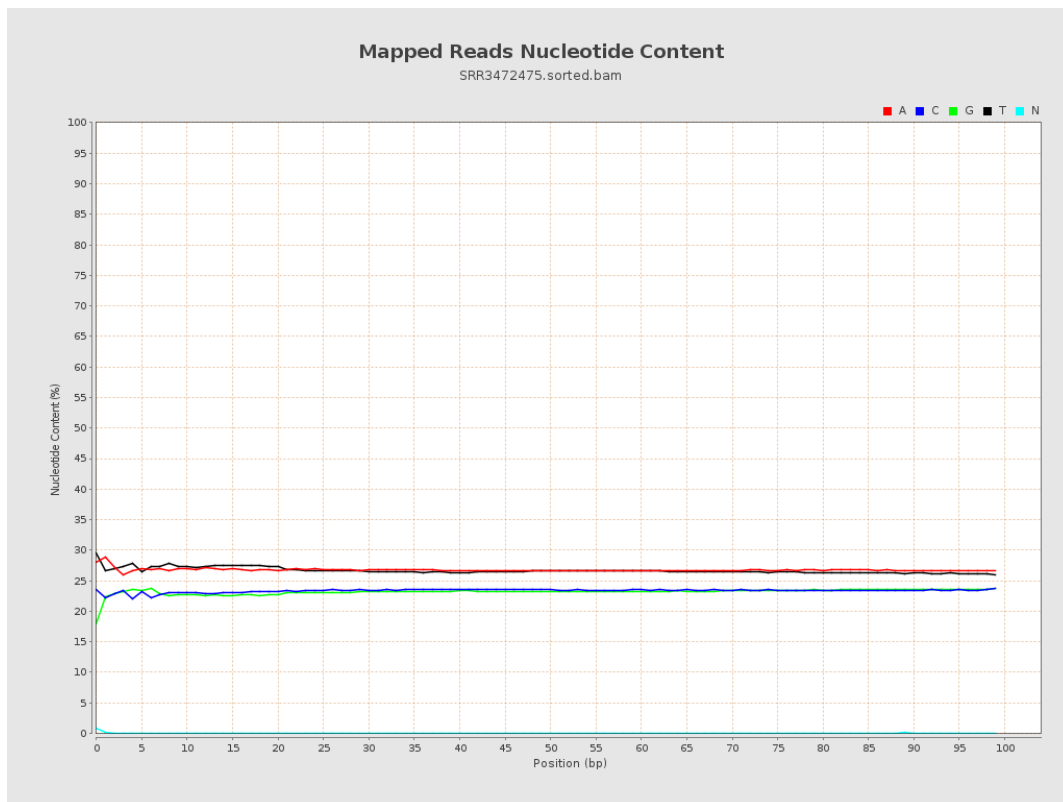
6. Results : Genome Fraction Coverage



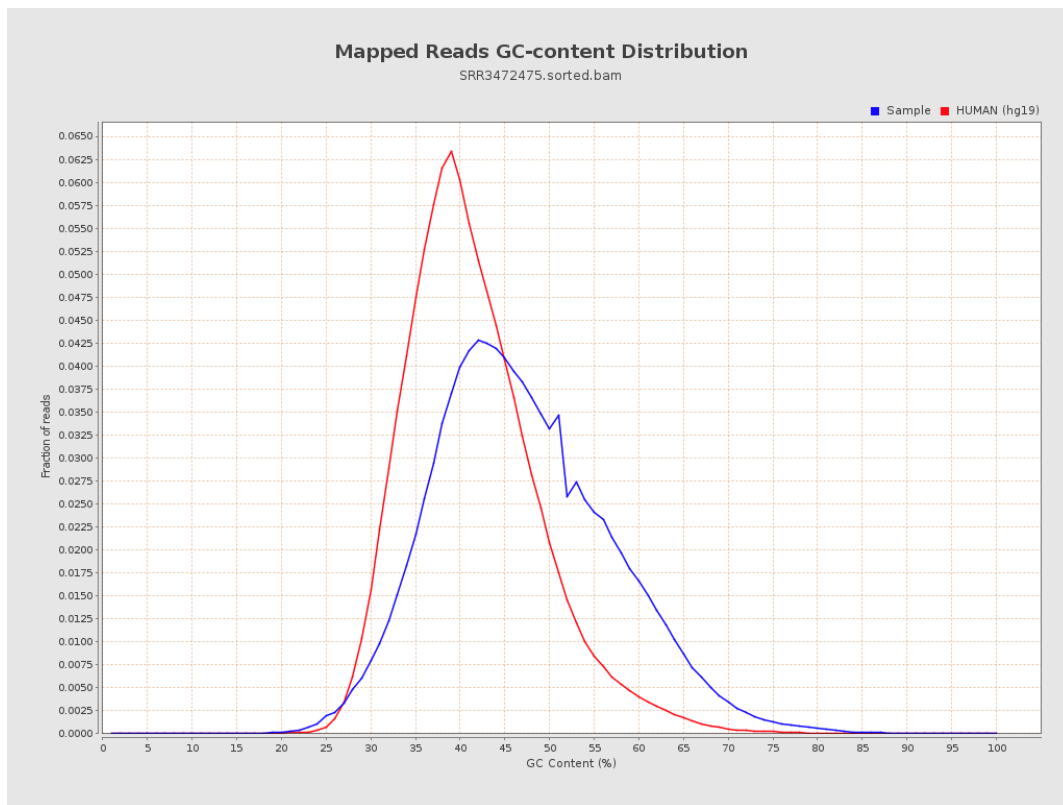
7. Results : Duplication Rate Histogram



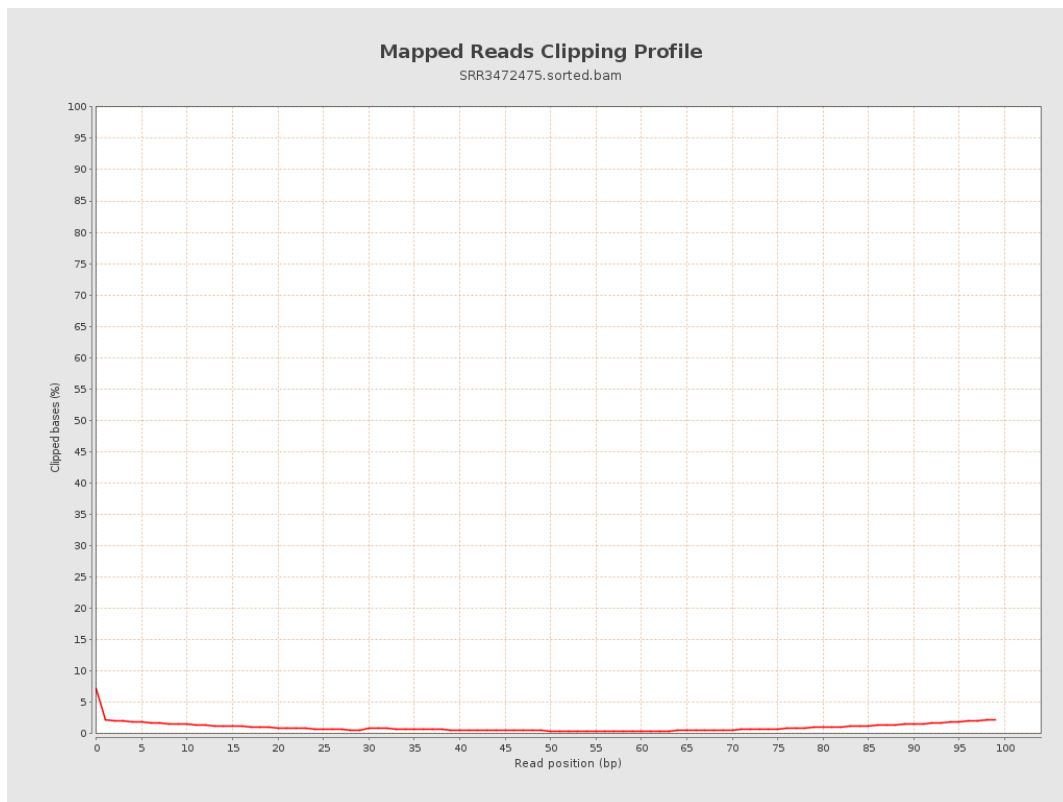
8. Results : Mapped Reads Nucleotide Content



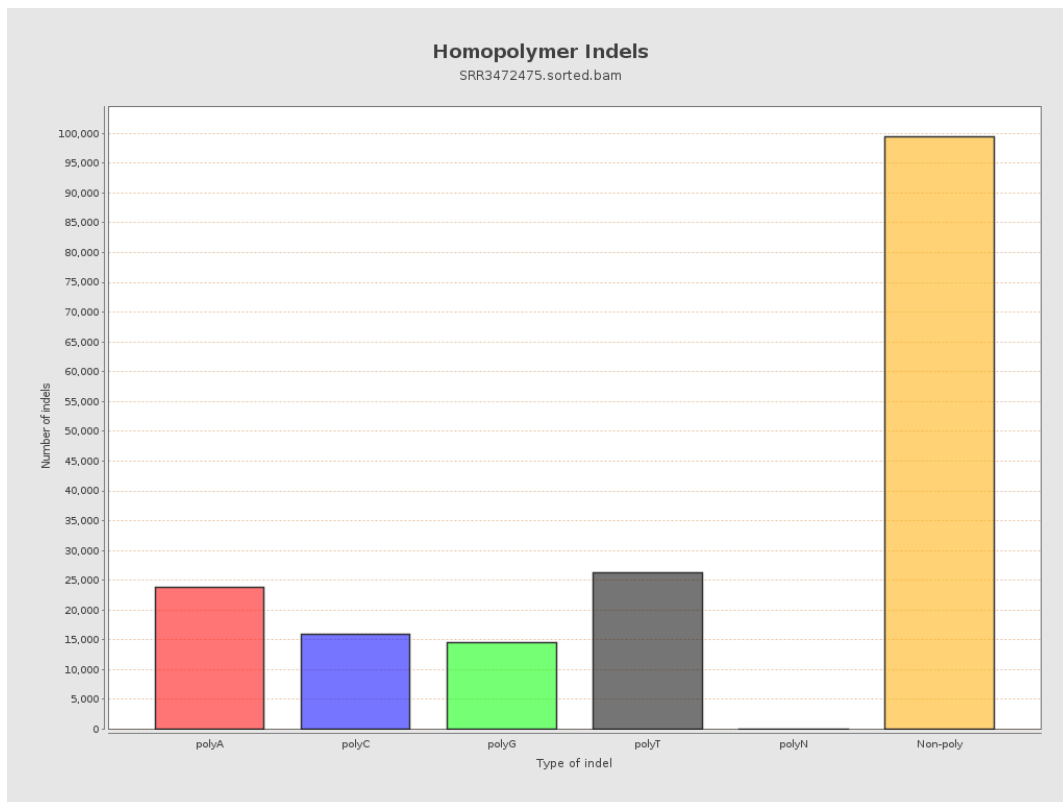
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



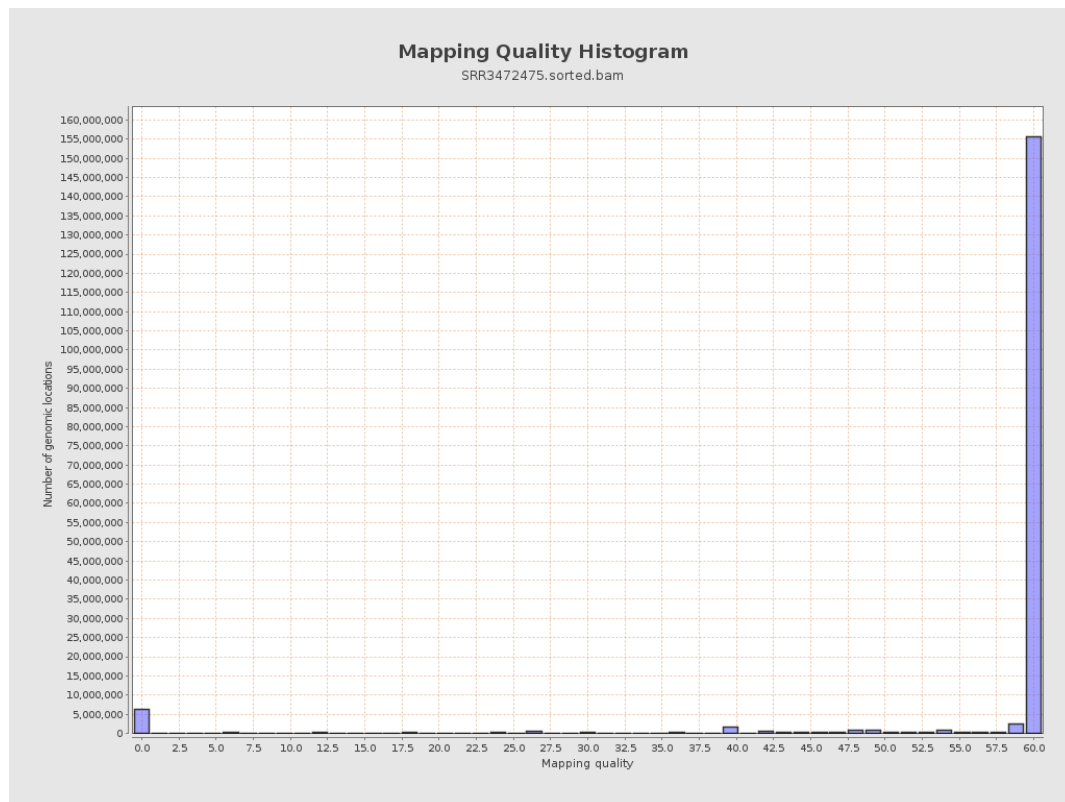
11. Results : Homopolymer Indels



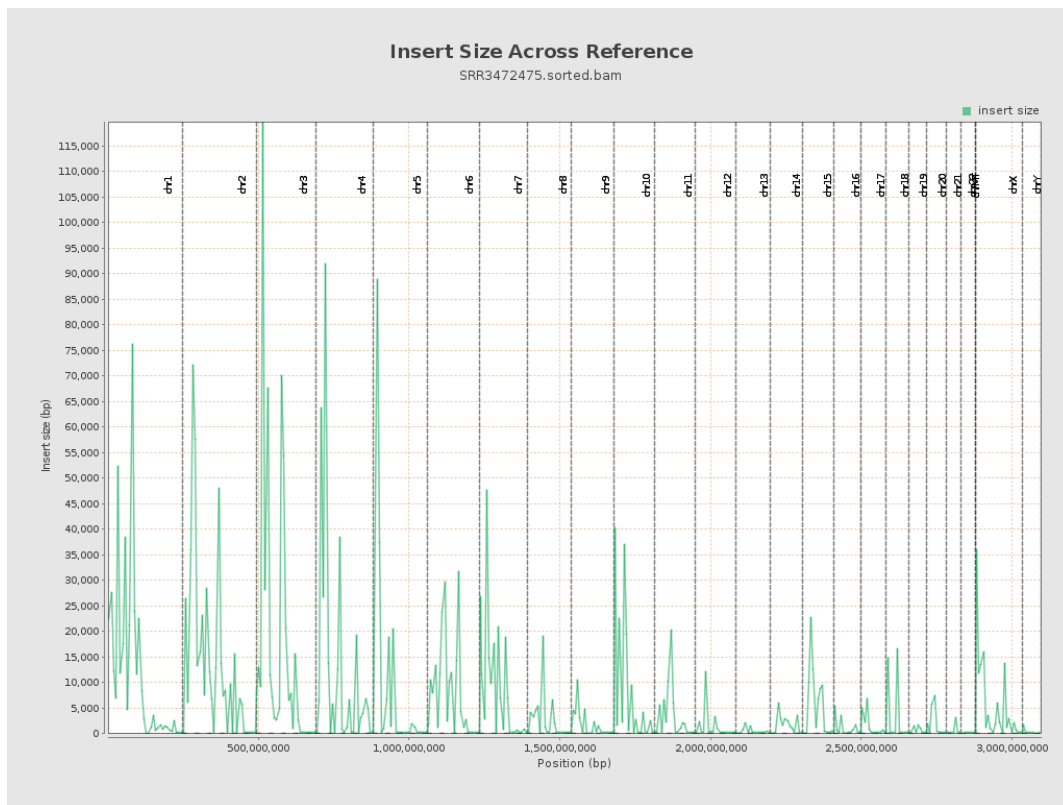
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

