

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 08:24:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472481.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_SRR3472481 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472481_1.fastq.gz SRR3472481_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 08:24:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472481.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	14,217,418
Mapped reads	13,951,660 / 98.13%
Unmapped reads	265,758 / 1.87%
Mapped paired reads	13,951,660 / 98.13%
Mapped reads, first in pair	7,013,797 / 49.33%
Mapped reads, second in pair	6,937,863 / 48.8%
Mapped reads, both in pair	13,825,536 / 97.24%
Mapped reads, singletons	126,124 / 0.89%
Secondary alignments	0
Supplementary alignments	47,586 / 0.33%
Read min/max/mean length	30 / 100 / 100.14
Duplicated reads (estimated)	8,476,364 / 59.62%
Duplication rate	45.27%
Clipped reads	1,186,289 / 8.34%

2.2. ACGT Content

Number/percentage of A's	371,719,295 / 27.11%
Number/percentage of C's	315,678,064 / 23.02%
Number/percentage of T's	369,612,408 / 26.96%
Number/percentage of G's	313,892,609 / 22.89%
Number/percentage of N's	213,060 / 0.02%

GC Percentage	45.92%
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2.3. Coverage

Mean	0.443
Standard Deviation	16.3721

2.4. Mapping Quality

Mean Mapping Quality	54.97
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2.5. Insert size

Mean	26,566.34
Standard Deviation	1,608,447.07
P25/Median/P75	165 / 229 / 307

2.6. Mismatches and indels

General error rate	0.6%
Mismatches	8,062,330
Insertions	72,882
Mapped reads with at least one insertion	0.52%
Deletions	67,289
Mapped reads with at least one deletion	0.48%
Homopolymer indels	45.74%

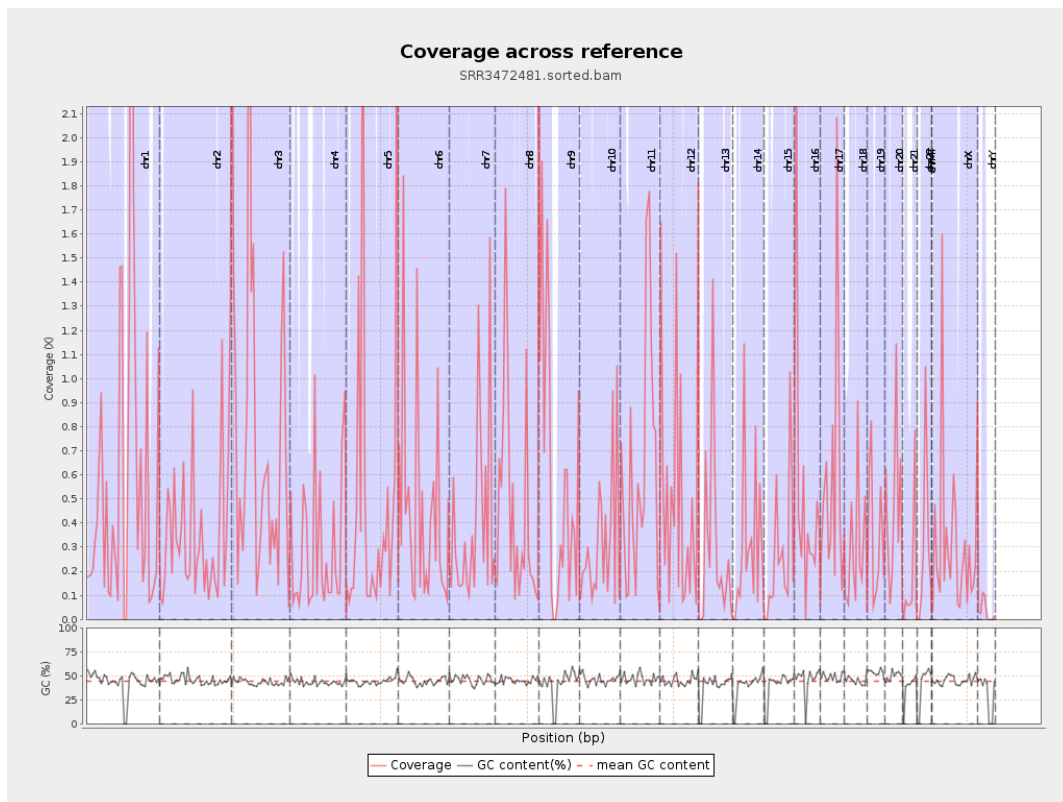
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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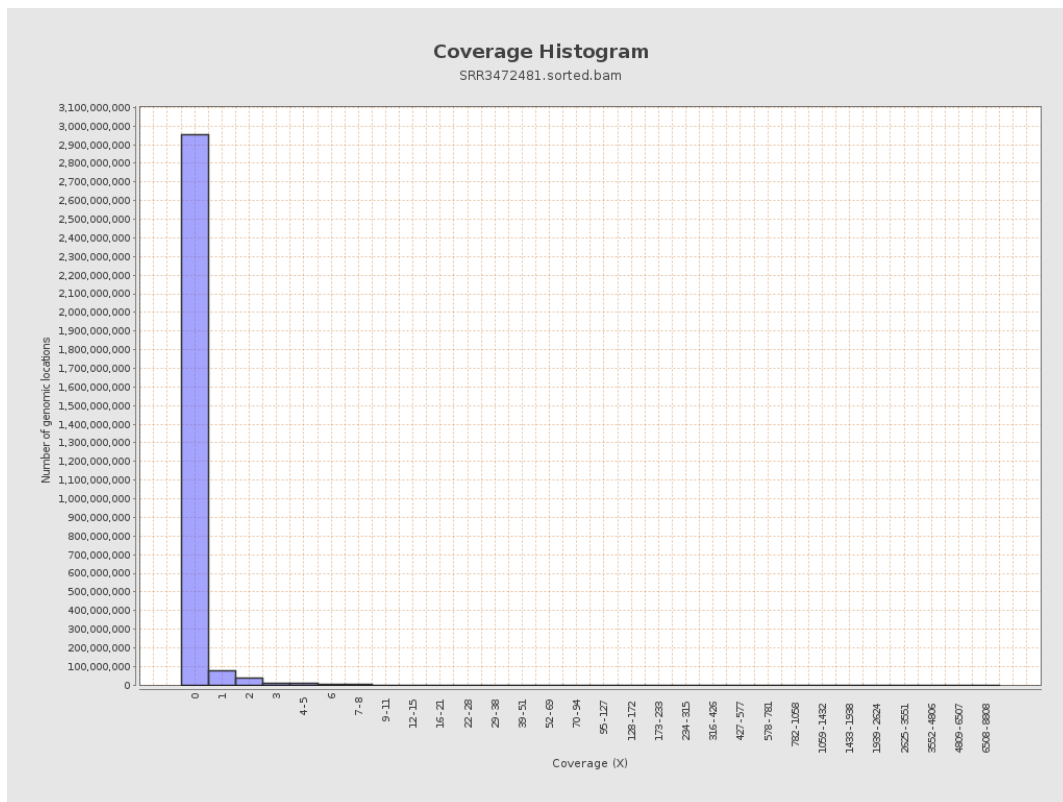
		bases	coverage	deviation
chr1	249250621	158934560	0.6376	30.8441
chr2	243199373	86630938	0.3562	11.4692
chr3	198022430	156095139	0.7883	18.8455
chr4	191154276	54947422	0.2875	11.0895
chr5	180915260	98140739	0.5425	22.8982
chr6	171115067	75549540	0.4415	13.5836
chr7	159138663	63837496	0.4011	13.8358
chr8	146364022	66149473	0.452	15.243
chr9	141213431	83772868	0.5932	15.4995
chr10	135534747	43557117	0.3214	13.4614
chr11	135006516	84267164	0.6242	21.4091
chr12	133851895	67718770	0.5059	13.6644
chr13	115169878	33033694	0.2868	13.044
chr14	107349540	32451976	0.3023	13.1352
chr15	102531392	27804146	0.2712	9.1382
chr16	90354753	46307976	0.5125	15.4945
chr17	81195210	44459698	0.5476	13.8582
chr18	78077248	23302753	0.2985	10.5921
chr19	59128983	21498006	0.3636	10.4395
chr20	63025520	29397079	0.4664	11.8861
chr21	48129895	8512806	0.1769	8.7515
chr22	51304566	14496198	0.2826	10.1078
chrMT	16571	2216	0.1337	0.4594
chrX	155270560	48312644	0.3112	9.2869

chrY	59373566	2104798	0.0355	1.3243
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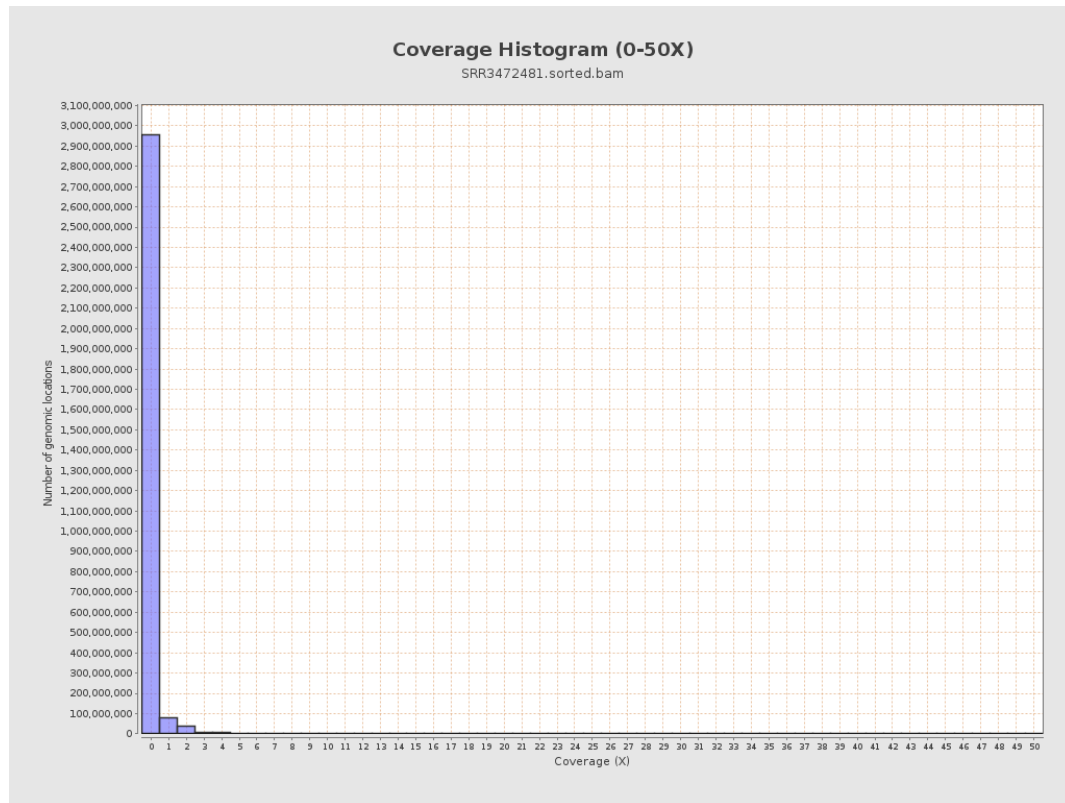
3. Results : Coverage across reference



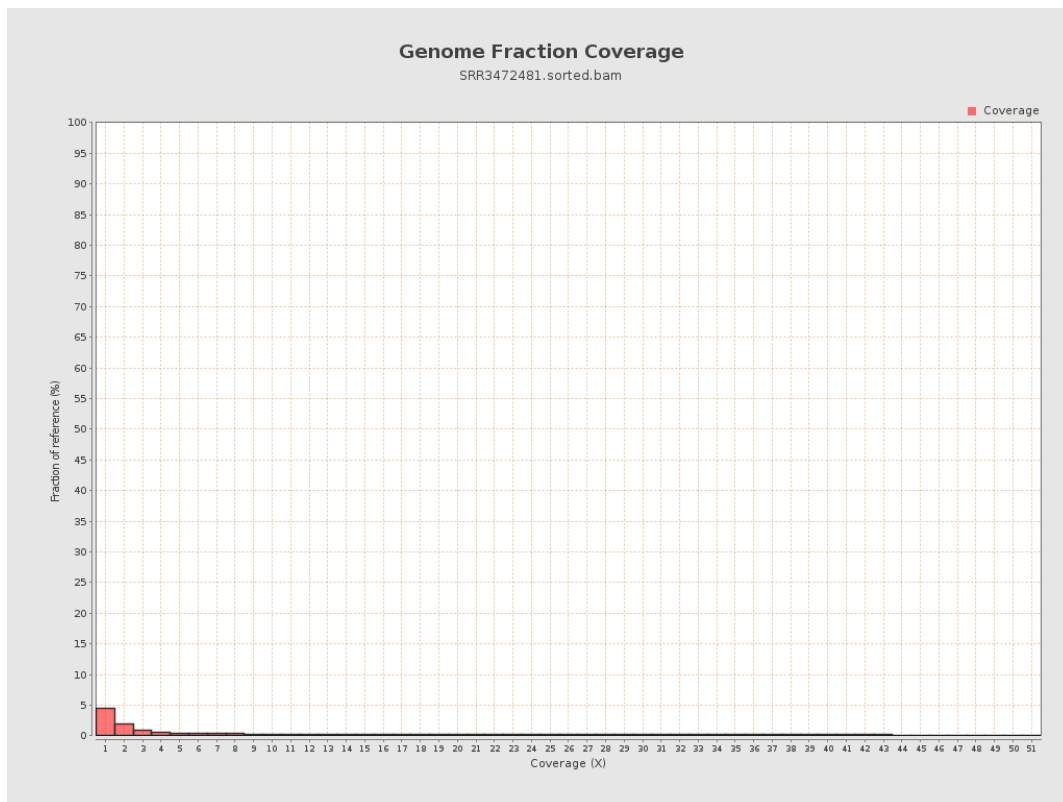
4. Results : Coverage Histogram



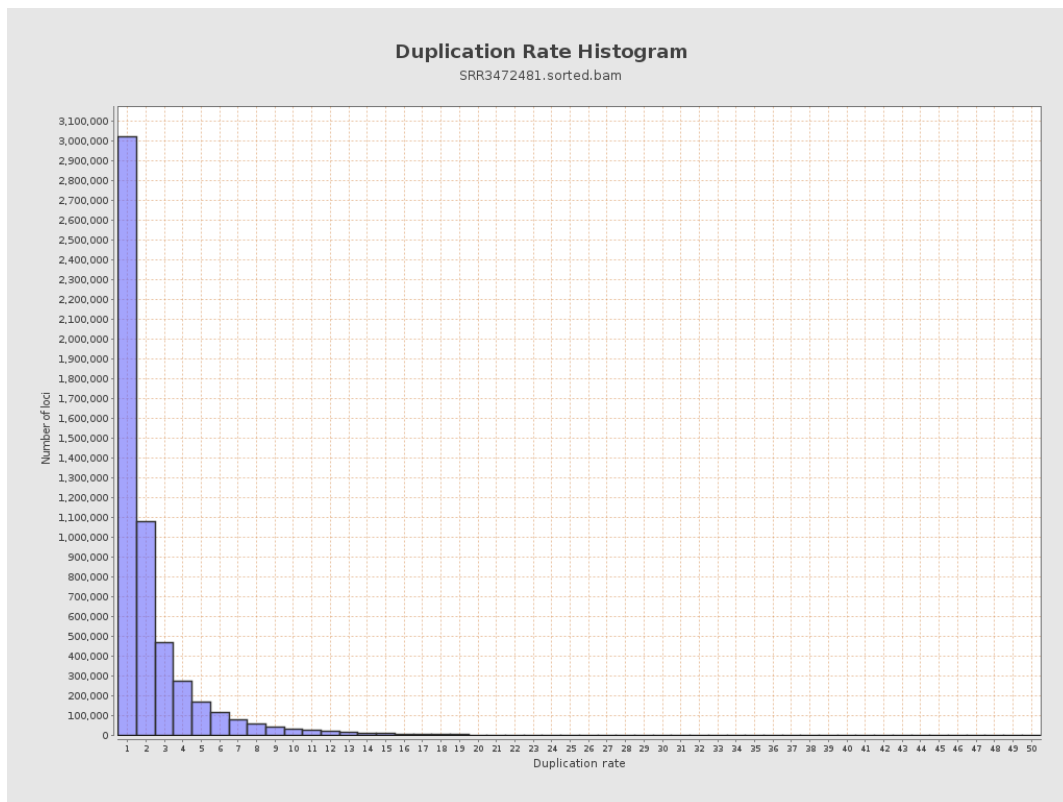
5. Results : Coverage Histogram (0-50X)



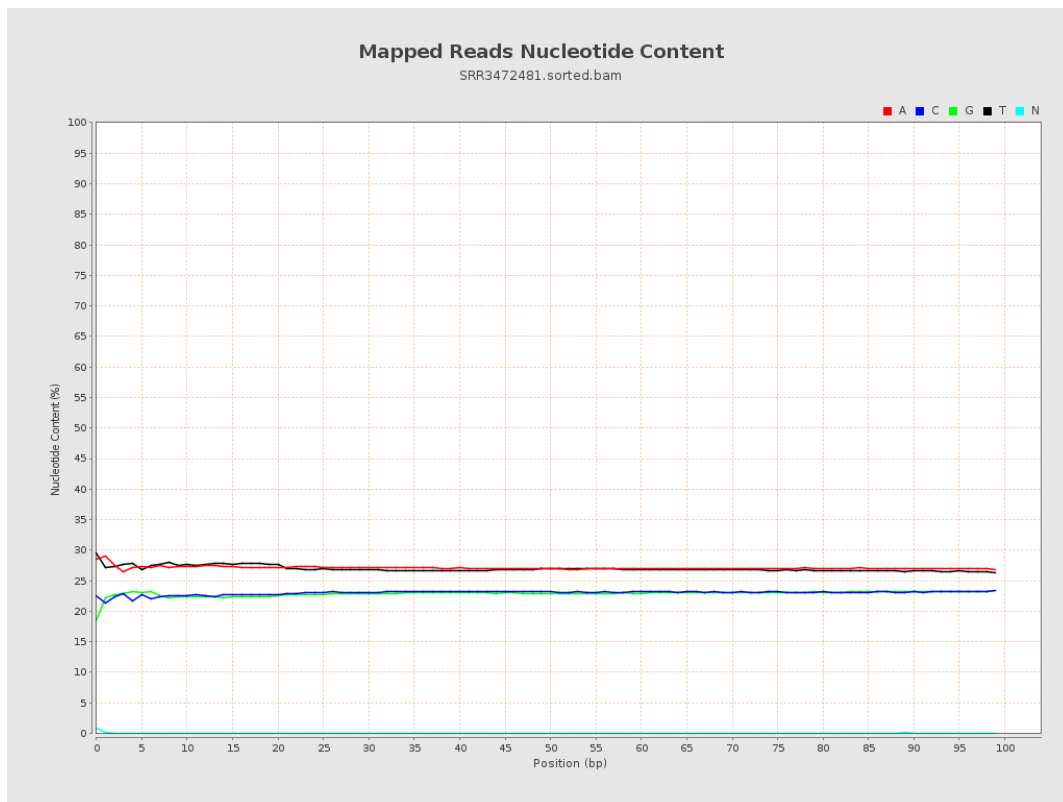
6. Results : Genome Fraction Coverage



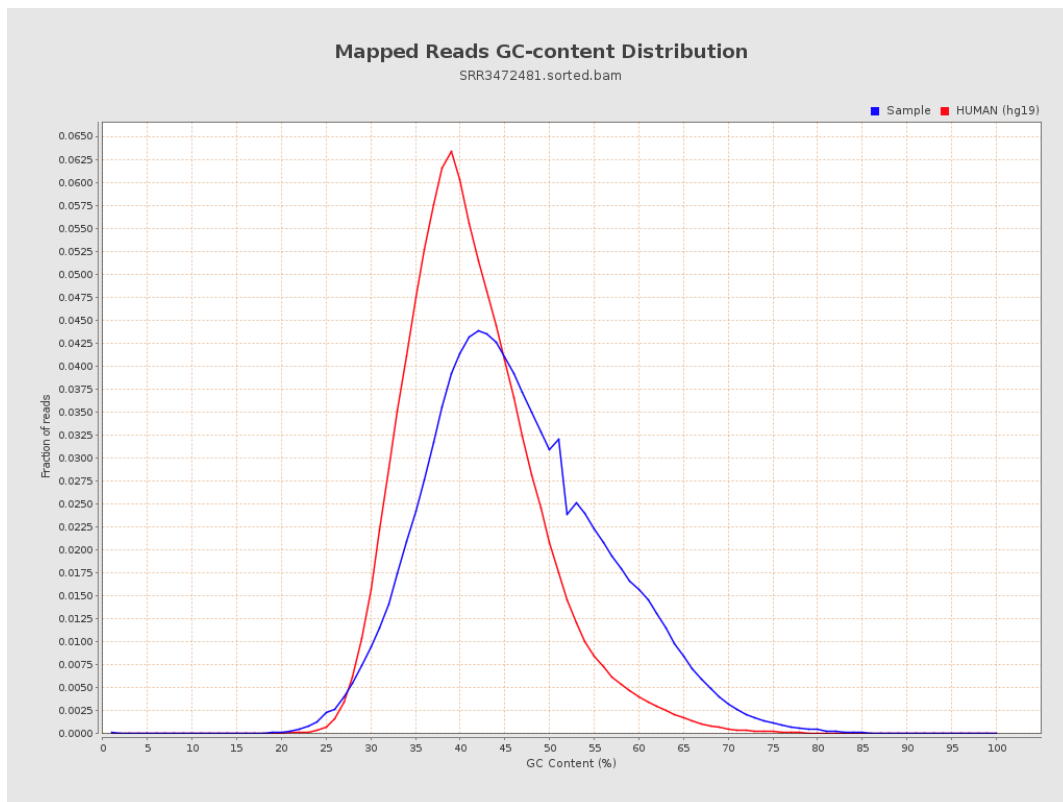
7. Results : Duplication Rate Histogram



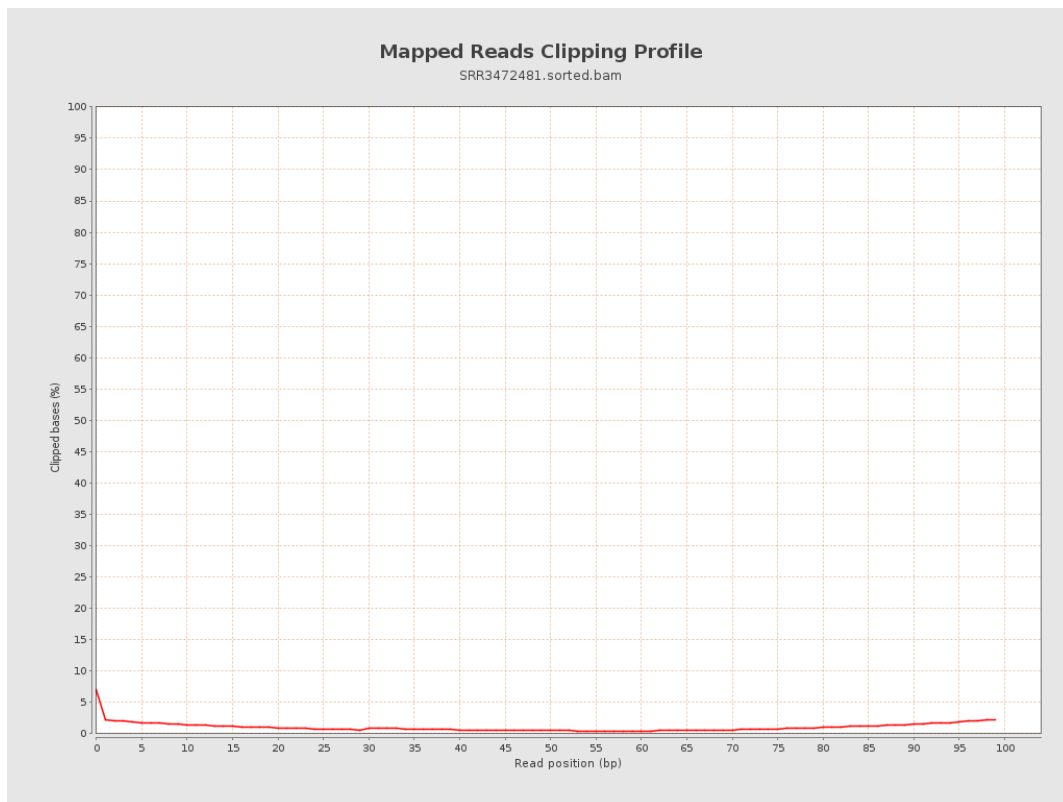
8. Results : Mapped Reads Nucleotide Content



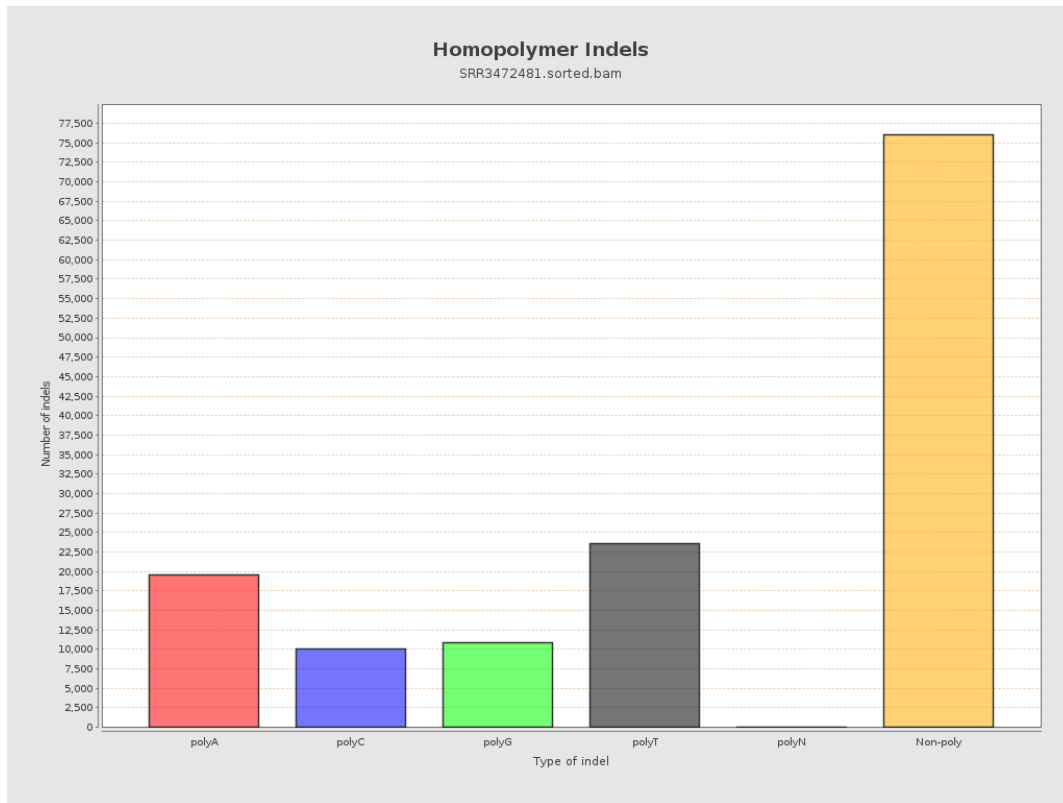
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



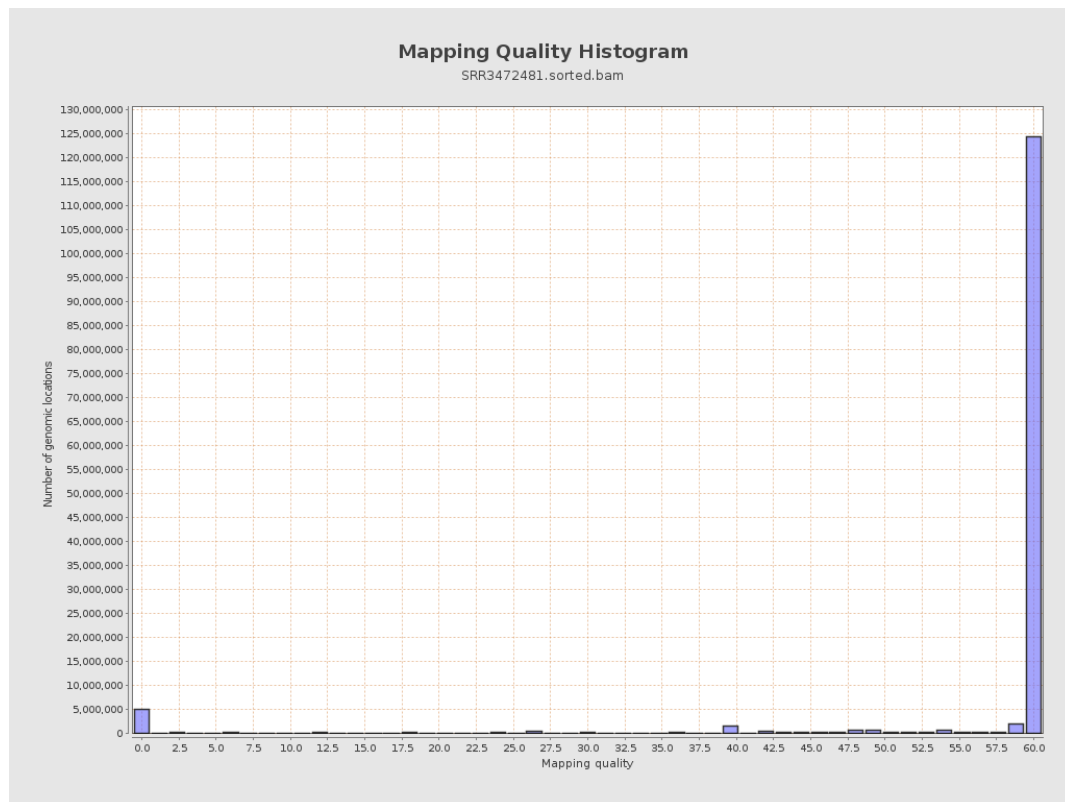
11. Results : Homopolymer Indels



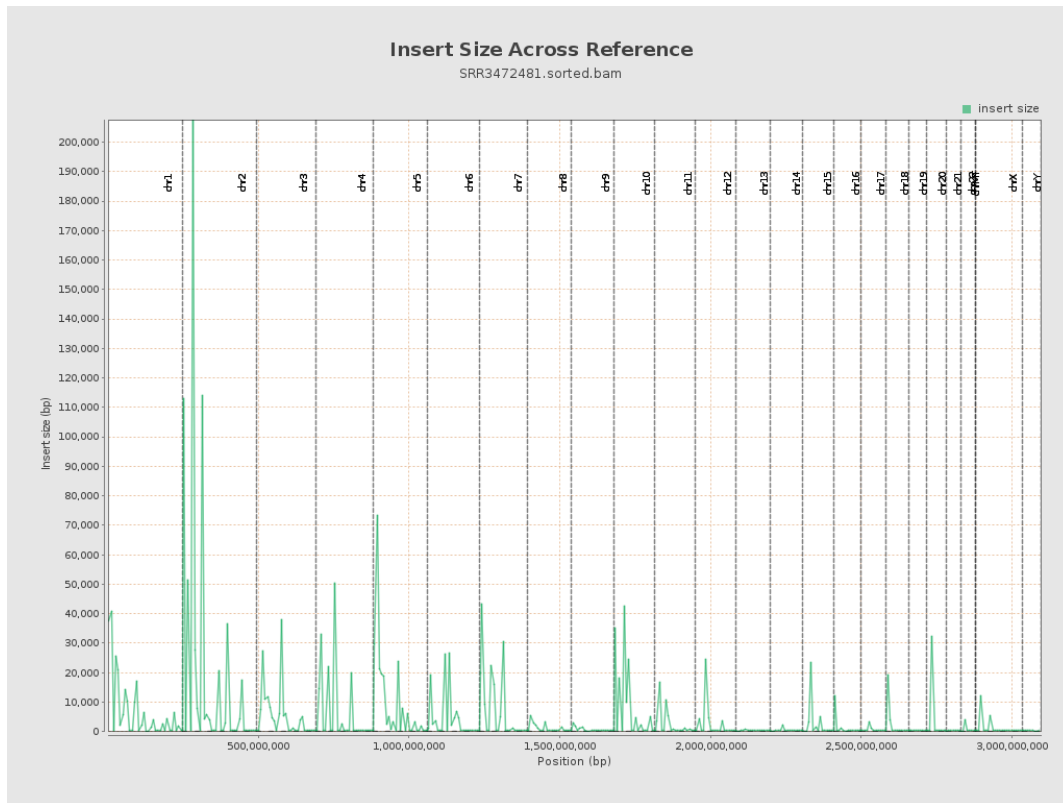
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

