

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/30 07:43:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472757.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_SRR3472757 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472757_1.fastq.gz SRR3472757_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 30 07:43:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472757.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	17,068,244
Mapped reads	16,887,781 / 98.94%
Unmapped reads	180,463 / 1.06%
Mapped paired reads	16,887,781 / 98.94%
Mapped reads, first in pair	8,487,530 / 49.73%
Mapped reads, second in pair	8,400,251 / 49.22%
Mapped reads, both in pair	16,766,954 / 98.23%
Mapped reads, singletons	120,827 / 0.71%
Secondary alignments	0
Supplementary alignments	125,526 / 0.74%
Read min/max/mean length	30 / 100 / 100.3
Duplicated reads (estimated)	10,511,166 / 61.58%
Duplication rate	47.51%
Clipped reads	1,415,068 / 8.29%

2.2. ACGT Content

Number/percentage of A's	465,101,761 / 27.91%
Number/percentage of C's	370,394,802 / 22.23%
Number/percentage of T's	462,973,651 / 27.79%
Number/percentage of G's	367,358,764 / 22.05%
Number/percentage of N's	320,213 / 0.02%

GC Percentage	44.28%
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2.3. Coverage

Mean	0.5383
Standard Deviation	16.5579

2.4. Mapping Quality

Mean Mapping Quality	55.39
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2.5. Insert size

Mean	56,016.29
Standard Deviation	2,316,313.9
P25/Median/P75	179 / 254 / 349

2.6. Mismatches and indels

General error rate	0.67%
Mismatches	10,983,249
Insertions	97,818
Mapped reads with at least one insertion	0.57%
Deletions	93,213
Mapped reads with at least one deletion	0.55%
Homopolymer indels	45.29%

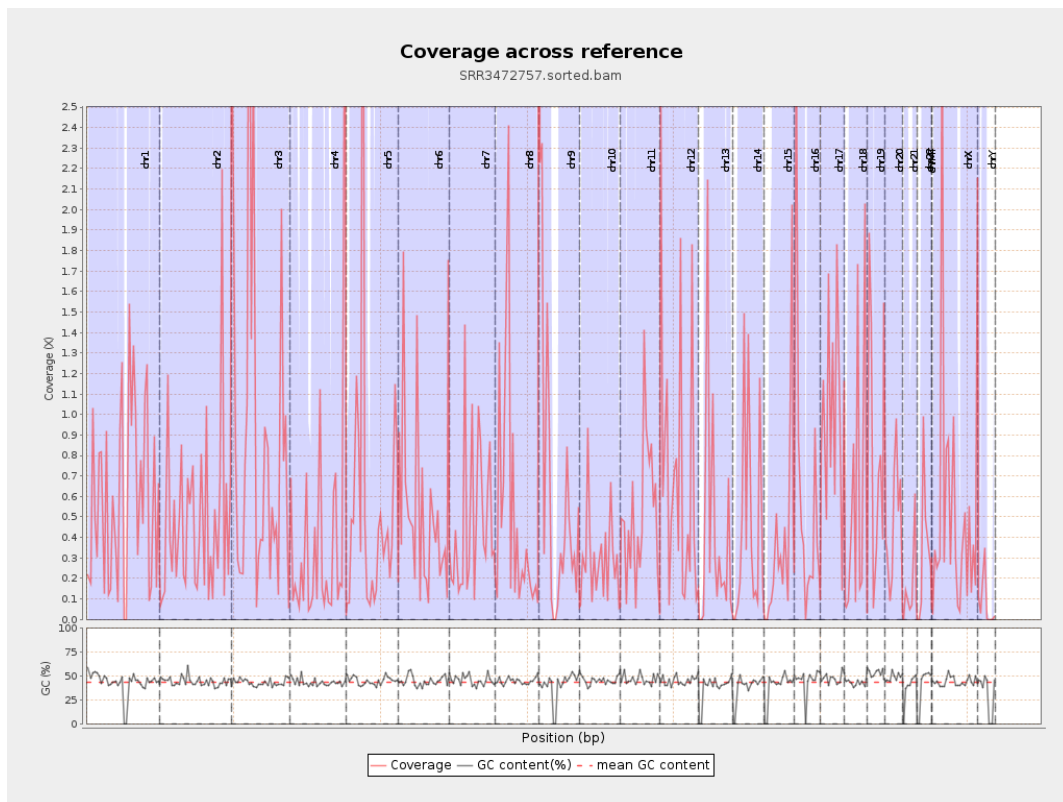
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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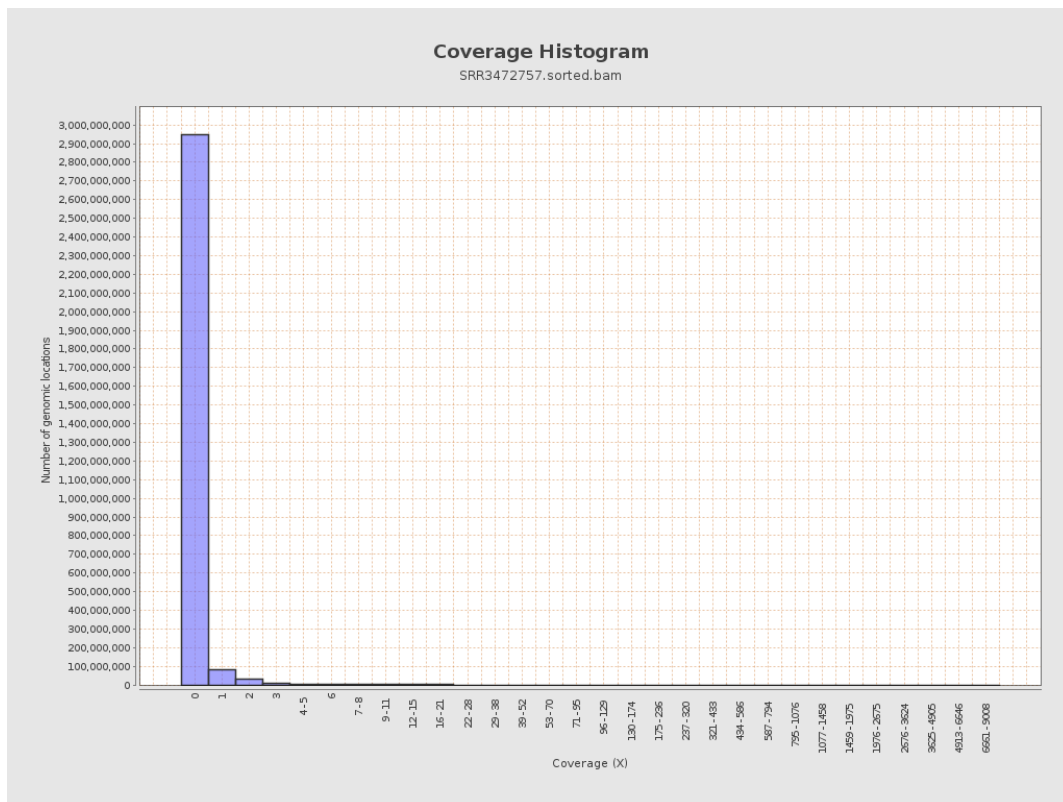
		bases	coverage	deviation
chr1	249250621	148251600	0.5948	19.3427
chr2	243199373	115964442	0.4768	16.3865
chr3	198022430	182315272	0.9207	20.3767
chr4	191154276	74506265	0.3898	16.1616
chr5	180915260	104195708	0.5759	17.7267
chr6	171115067	89275164	0.5217	14.1956
chr7	159138663	75177315	0.4724	15.4881
chr8	146364022	74038694	0.5059	15.8849
chr9	141213431	90489711	0.6408	14.9651
chr10	135534747	41145459	0.3036	11.2406
chr11	135006516	69408387	0.5141	14.0278
chr12	133851895	97374828	0.7275	19.6944
chr13	115169878	48436883	0.4206	15.364
chr14	107349540	46260751	0.4309	14.3031
chr15	102531392	40793905	0.3979	14.9211
chr16	90354753	52821938	0.5846	17.5614
chr17	81195210	80316064	0.9892	22.4542
chr18	78077248	47516926	0.6086	21.6786
chr19	59128983	46957019	0.7941	24.4247
chr20	63025520	29766472	0.4723	11.5414
chr21	48129895	8001376	0.1662	7.9434
chr22	51304566	16891768	0.3292	9.1716
chrMT	16571	5045	0.3044	0.7661
chrX	155270560	81271424	0.5234	14.8995

chrY	59373566	5208577	0.0877	4.6603
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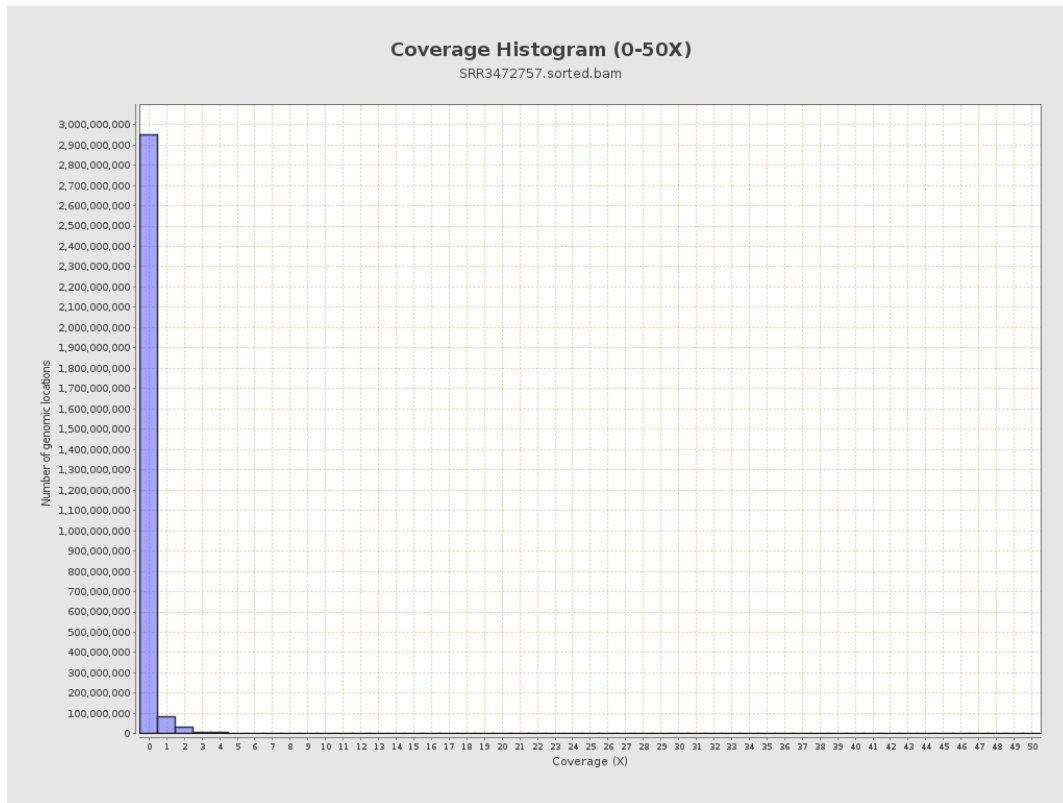
3. Results : Coverage across reference



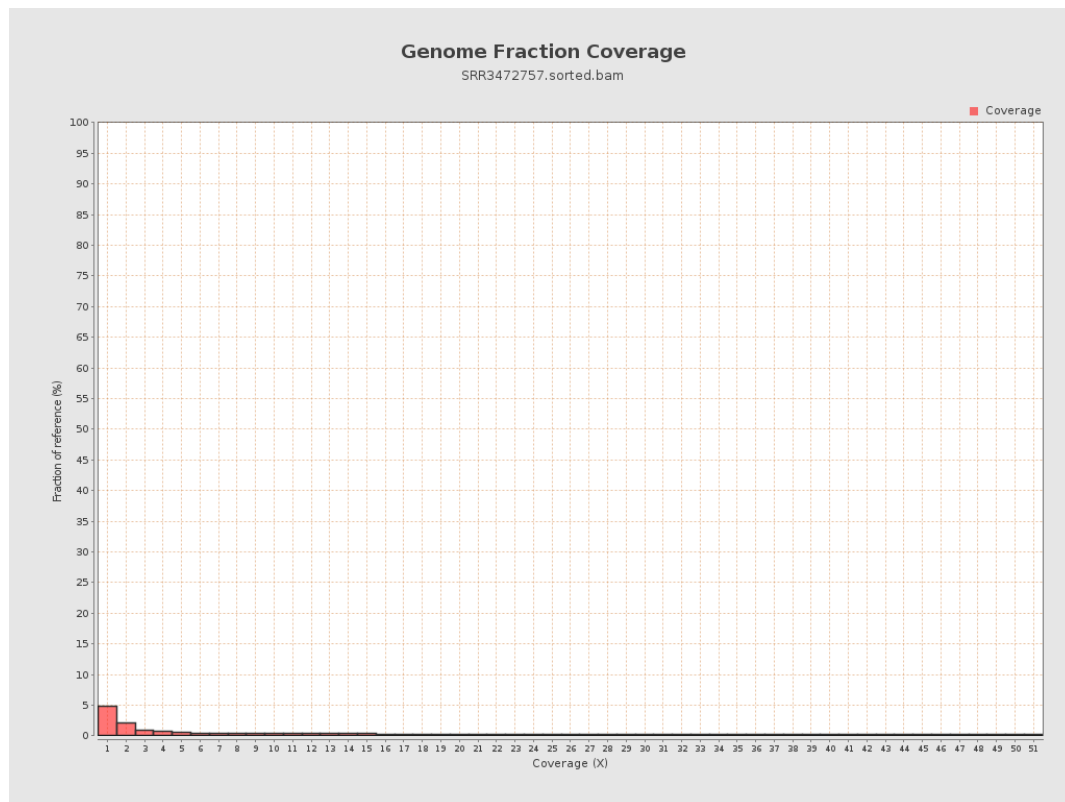
4. Results : Coverage Histogram



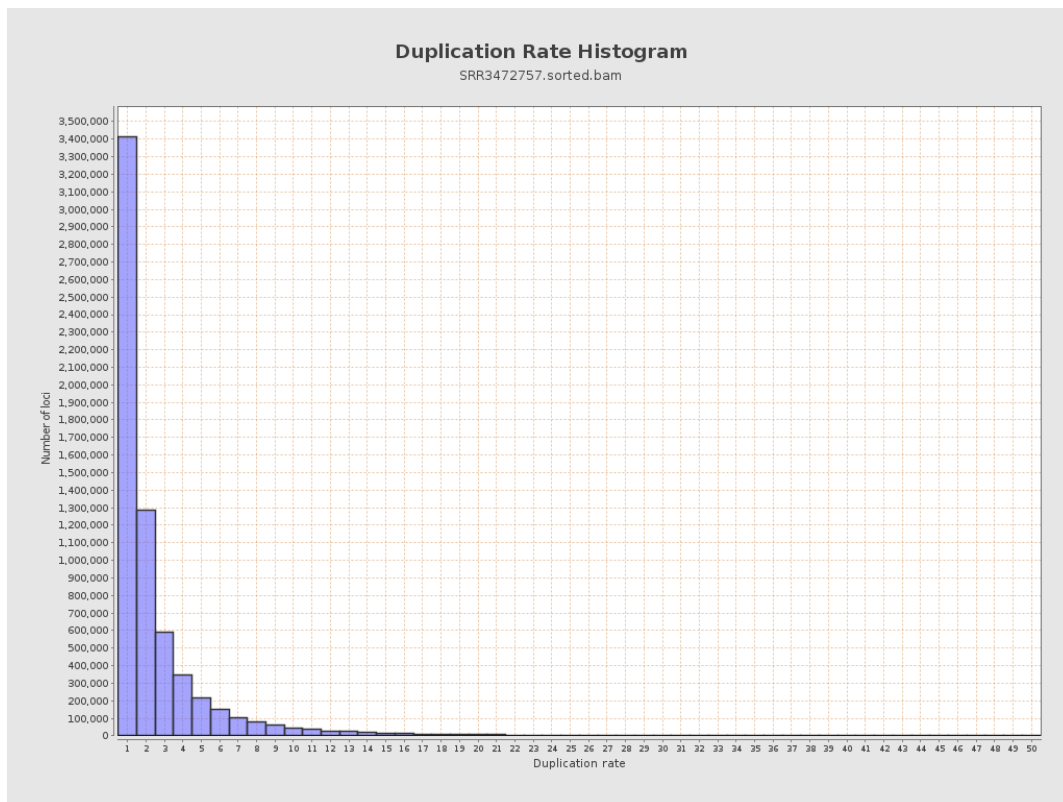
5. Results : Coverage Histogram (0-50X)



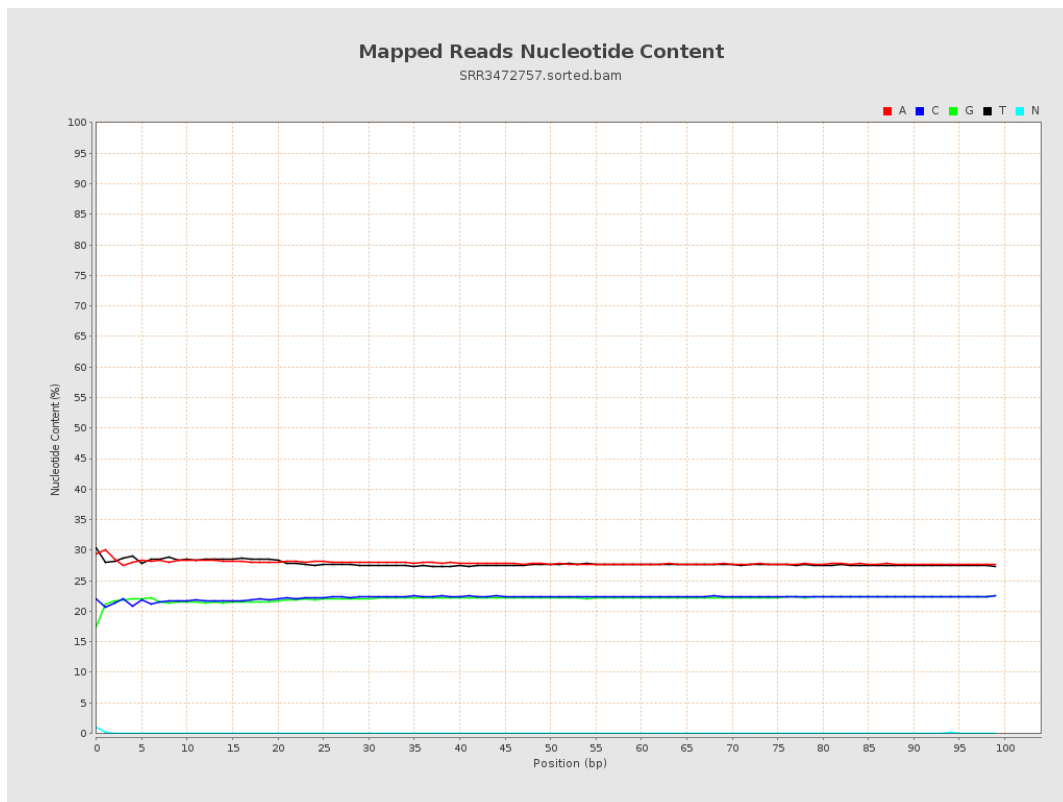
6. Results : Genome Fraction Coverage



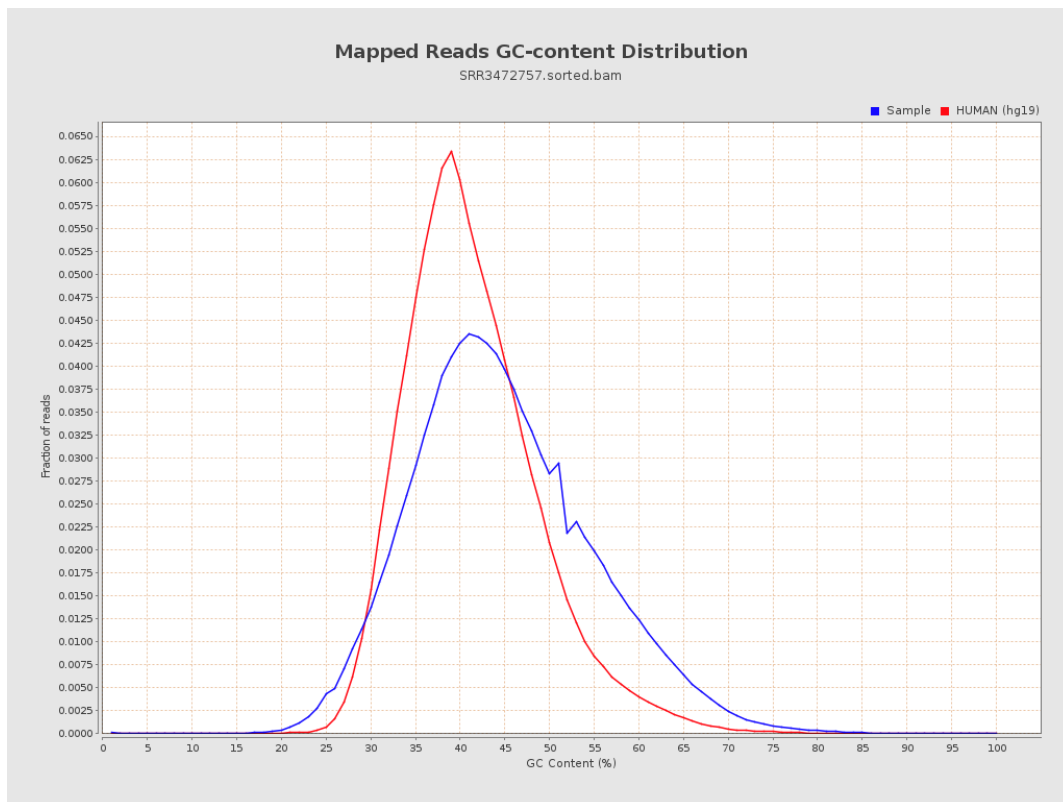
7. Results : Duplication Rate Histogram



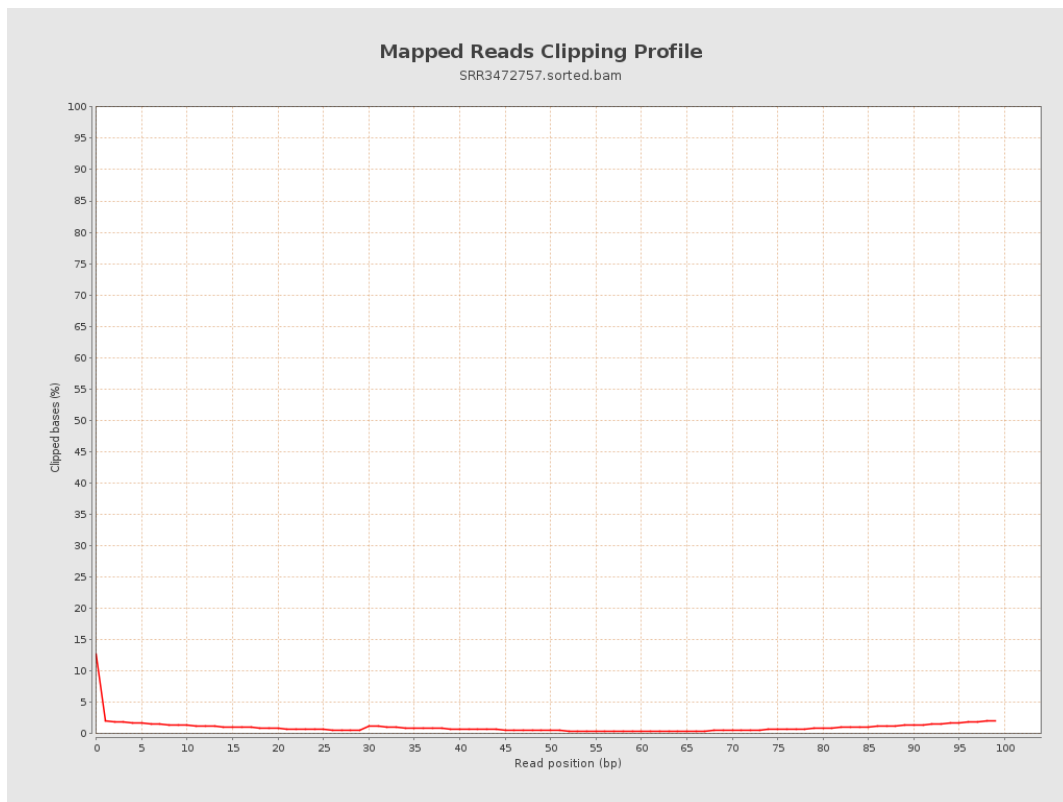
8. Results : Mapped Reads Nucleotide Content



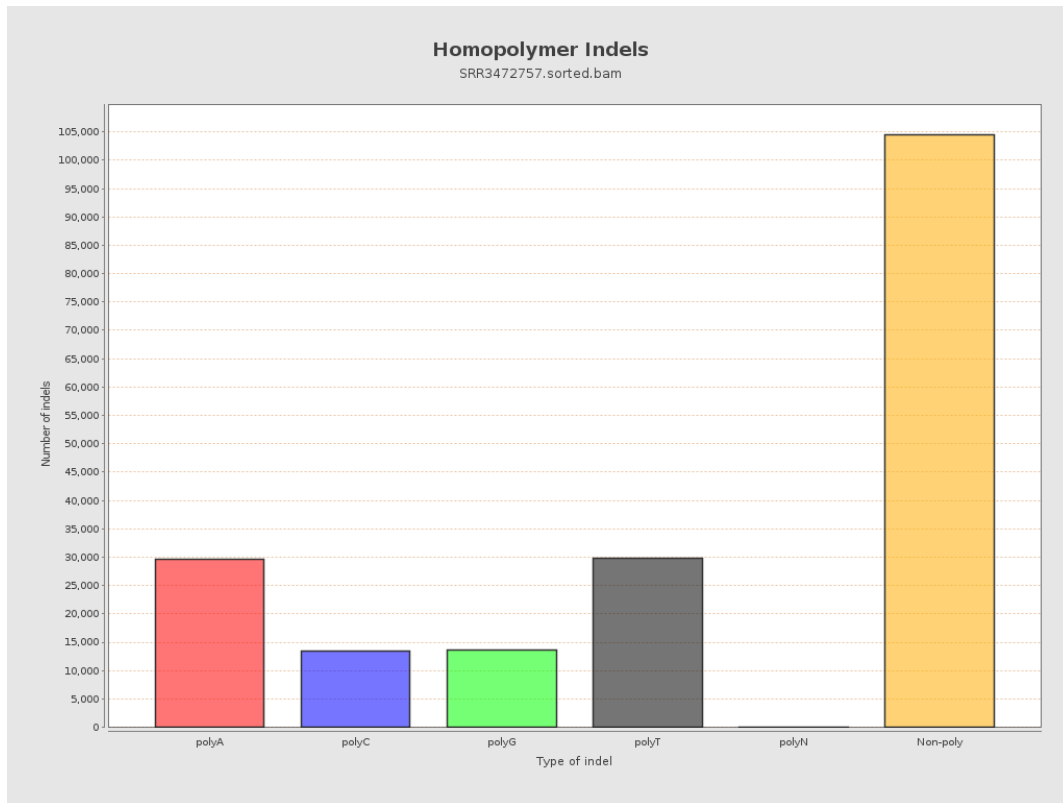
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



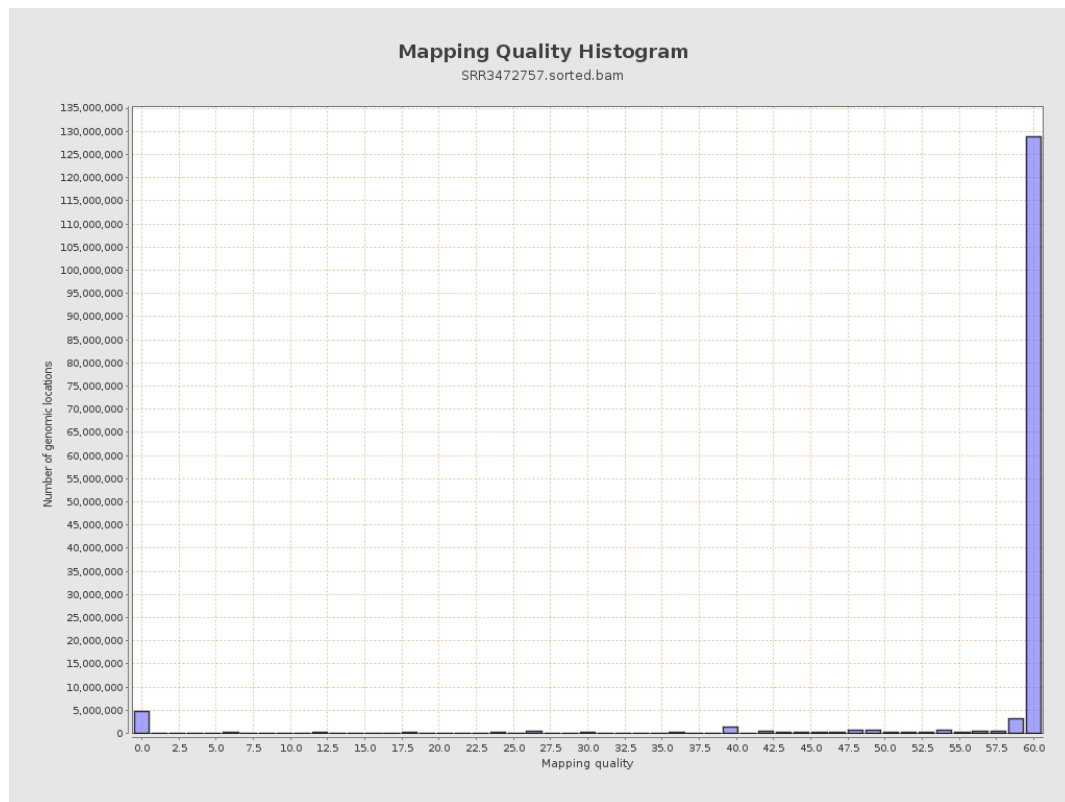
11. Results : Homopolymer Indels



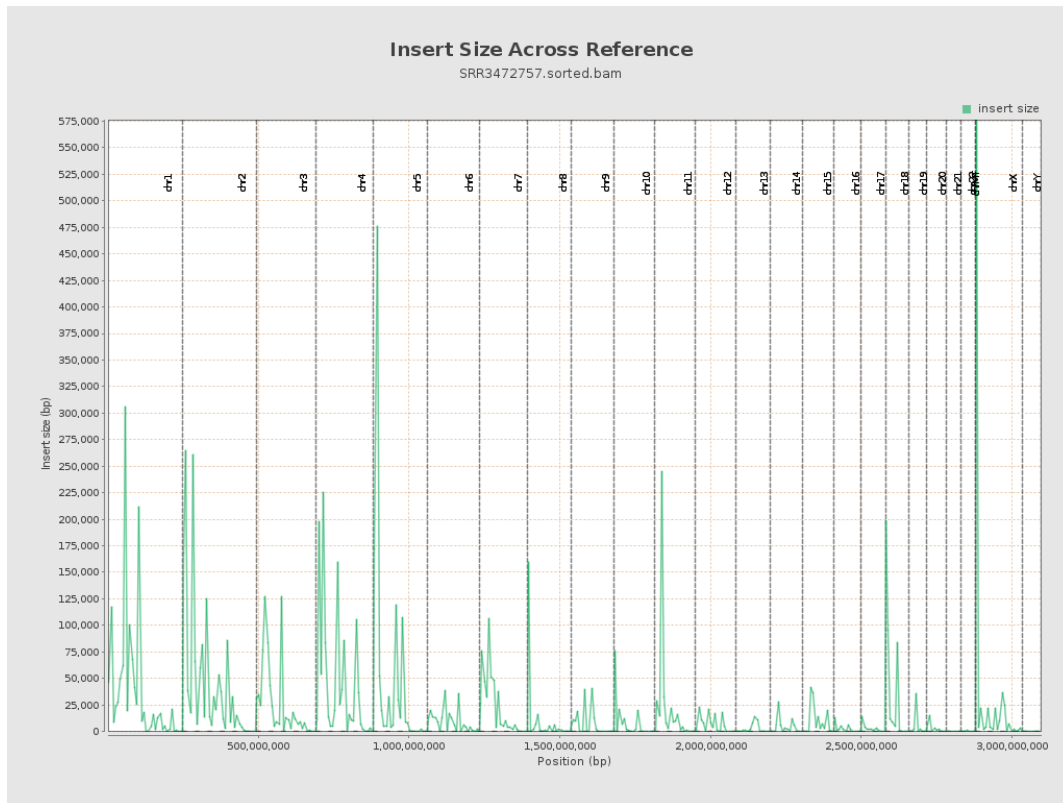
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

