

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 16:15:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472567.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_SRR3472567 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472567_1.fastq.gz SRR3472567_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 16:15:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472567.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	207,827,342
Mapped reads	205,317,284 / 98.79%
Unmapped reads	2,510,058 / 1.21%
Mapped paired reads	205,317,284 / 98.79%
Mapped reads, first in pair	102,857,499 / 49.49%
Mapped reads, second in pair	102,459,785 / 49.3%
Mapped reads, both in pair	204,734,168 / 98.51%
Mapped reads, singletons	583,116 / 0.28%
Secondary alignments	0
Supplementary alignments	94,329 / 0.05%
Read min/max/mean length	30 / 100 / 100.02
Duplicated reads (estimated)	133,093,335 / 64.04%
Duplication rate	47.95%
Clipped reads	57,969,983 / 27.89%

2.2. ACGT Content

Number/percentage of A's	4,368,720,268 / 23.22%
Number/percentage of C's	5,062,027,967 / 26.9%
Number/percentage of T's	4,465,798,782 / 23.73%
Number/percentage of G's	4,919,003,464 / 26.14%
Number/percentage of N's	2,276,880 / 0.01%

GC Percentage	53.04%
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2.3. Coverage

Mean	6.0797
Standard Deviation	76.9967

2.4. Mapping Quality

Mean Mapping Quality	51.68
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2.5. Insert size

Mean	4,220.16
Standard Deviation	606,292.15
P25/Median/P75	95 / 155 / 239

2.6. Mismatches and indels

General error rate	0.51%
Mismatches	94,481,149
Insertions	984,807
Mapped reads with at least one insertion	0.46%
Deletions	1,228,313
Mapped reads with at least one deletion	0.58%
Homopolymer indels	38.23%

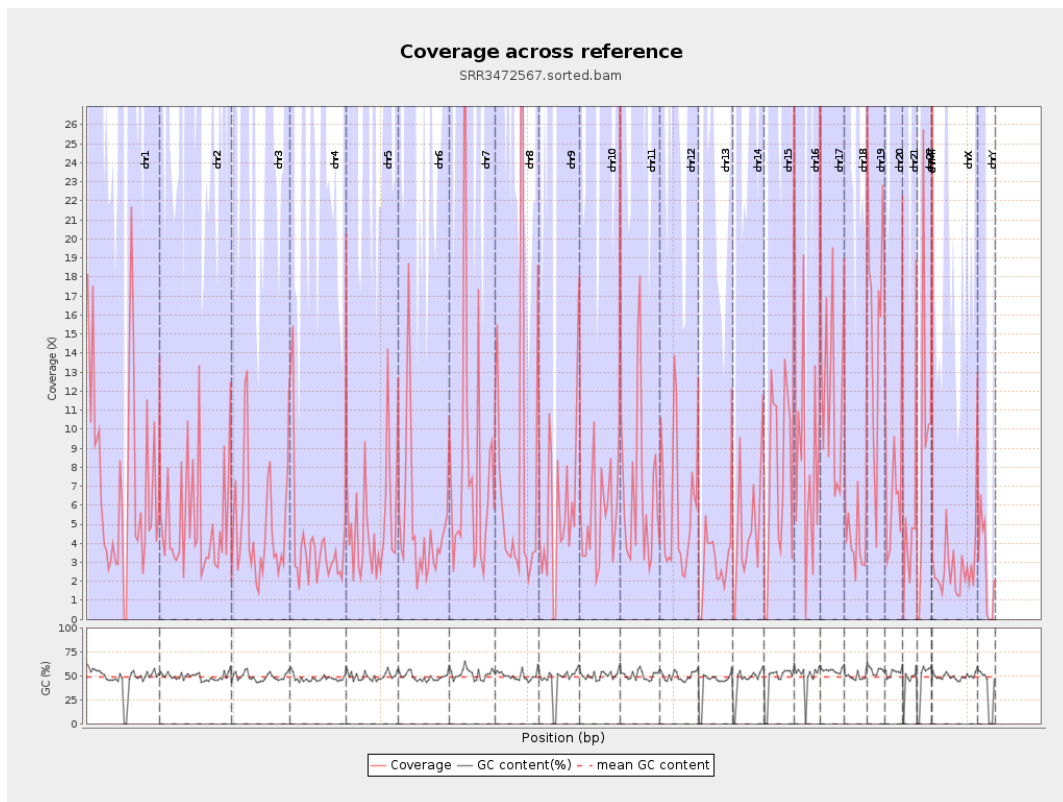
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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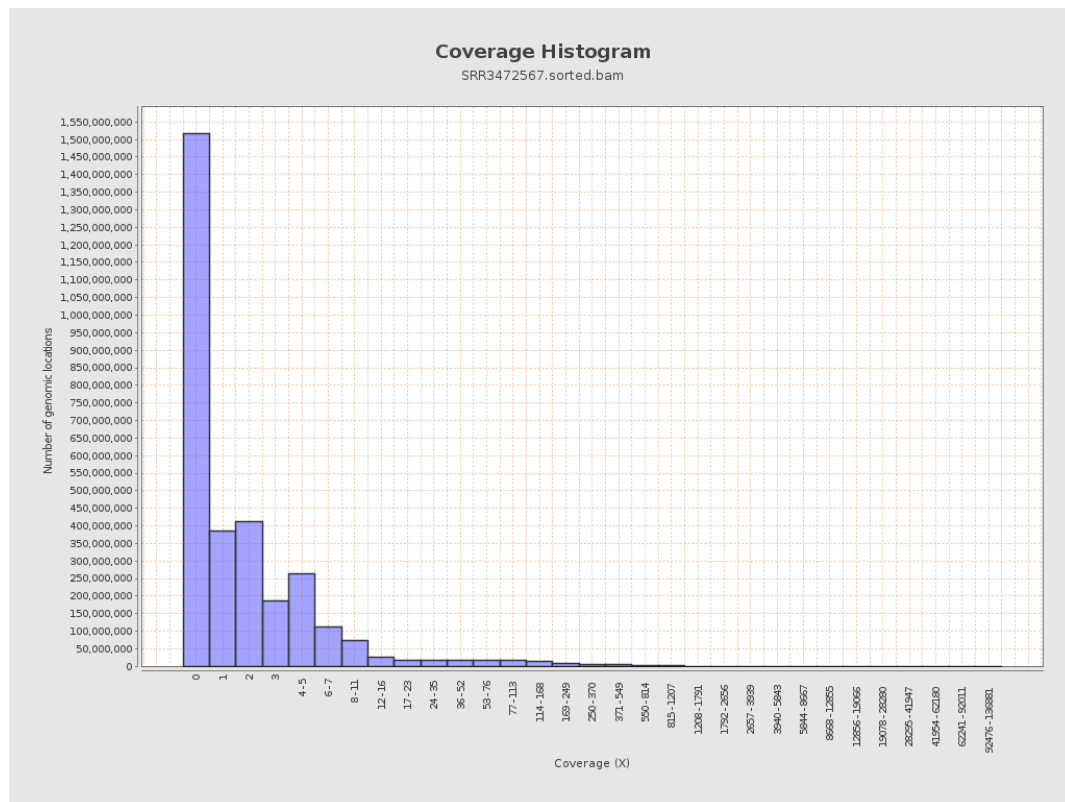
		bases	coverage	deviation
chr1	249250621	1805903031	7.2453	50.4264
chr2	243199373	1241852332	5.1063	42.3738
chr3	198022430	982055074	4.9593	34.1714
chr4	191154276	766633141	4.0105	39.1965
chr5	180915260	934224799	5.1639	51.2995
chr6	171115067	836483080	4.8884	30.878
chr7	159138663	1271674924	7.991	258.0289
chr8	146364022	1068945194	7.3033	134.6769
chr9	141213431	836241945	5.9218	39.3216
chr10	135534747	755628312	5.5752	36.1498
chr11	135006516	1005652356	7.4489	42.7486
chr12	133851895	785953230	5.8718	32.0757
chr13	115169878	348215614	3.0235	19.7948
chr14	107349540	510780430	4.7581	31.1919
chr15	102531392	768650996	7.4967	47.9698
chr16	90354753	850347752	9.4112	49.6343
chr17	81195210	961476843	11.8415	65.7137
chr18	78077248	326960793	4.1877	39.6851
chr19	59128983	938946839	15.8796	62.928
chr20	63025520	443552402	7.0377	45.3212
chr21	48129895	248927012	5.172	46.8674
chr22	51304566	502728614	9.7989	60.1518
chrMT	16571	48070232	2,900.8649	973.1936
chrX	155270560	420053114	2.7053	17.6903

chrY	59373566	160794521	2.7082	46.9691
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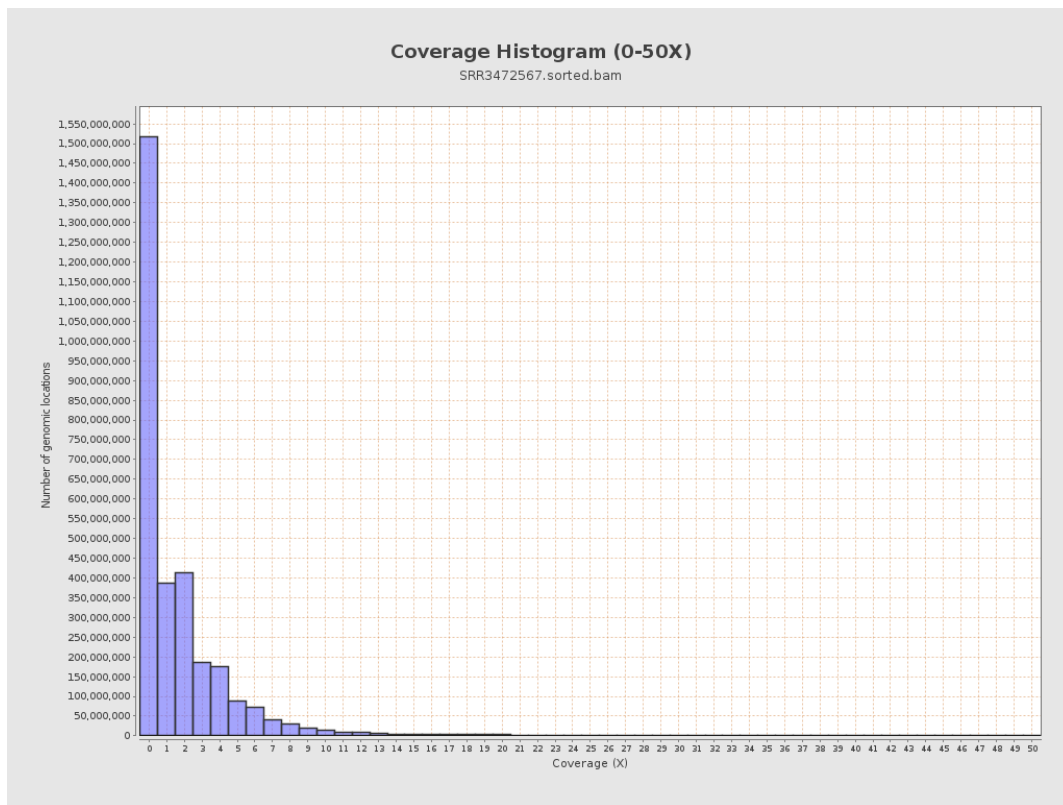
3. Results : Coverage across reference



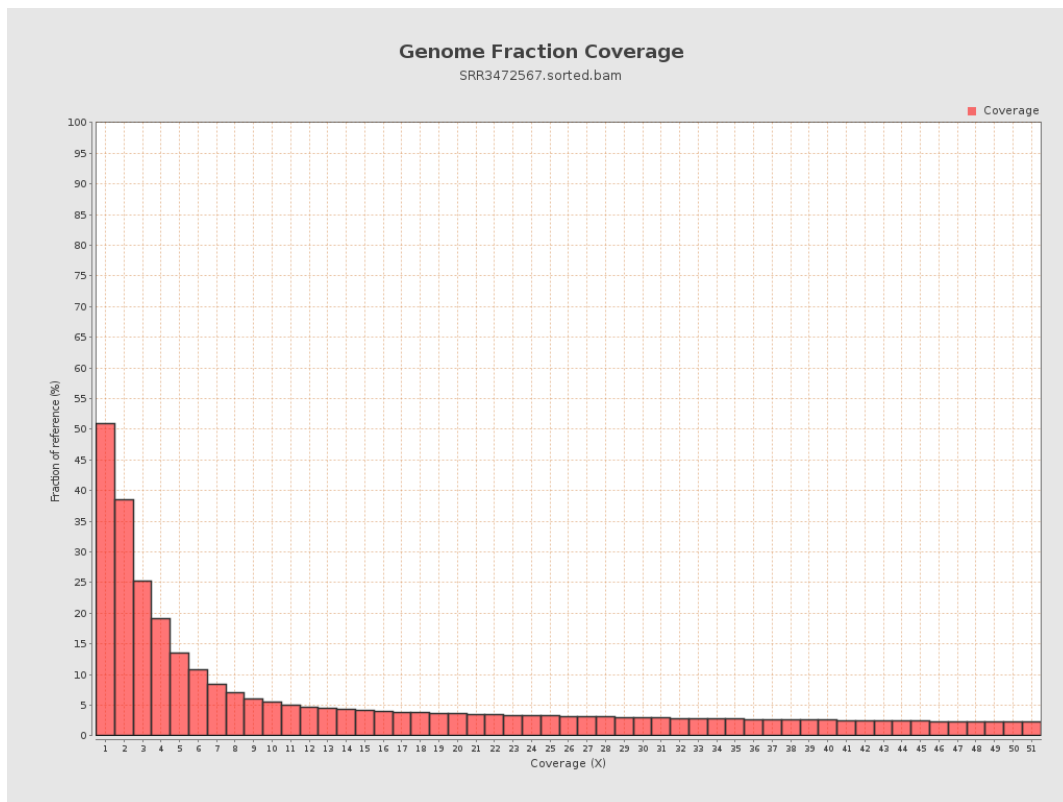
4. Results : Coverage Histogram



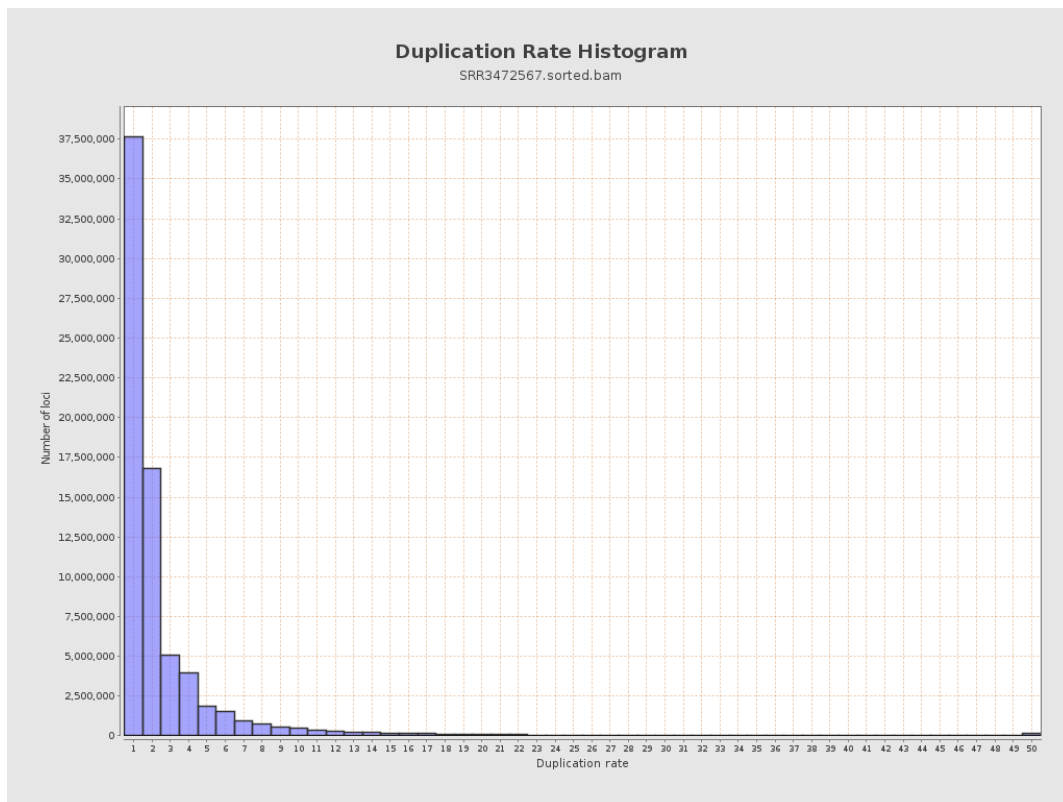
5. Results : Coverage Histogram (0-50X)



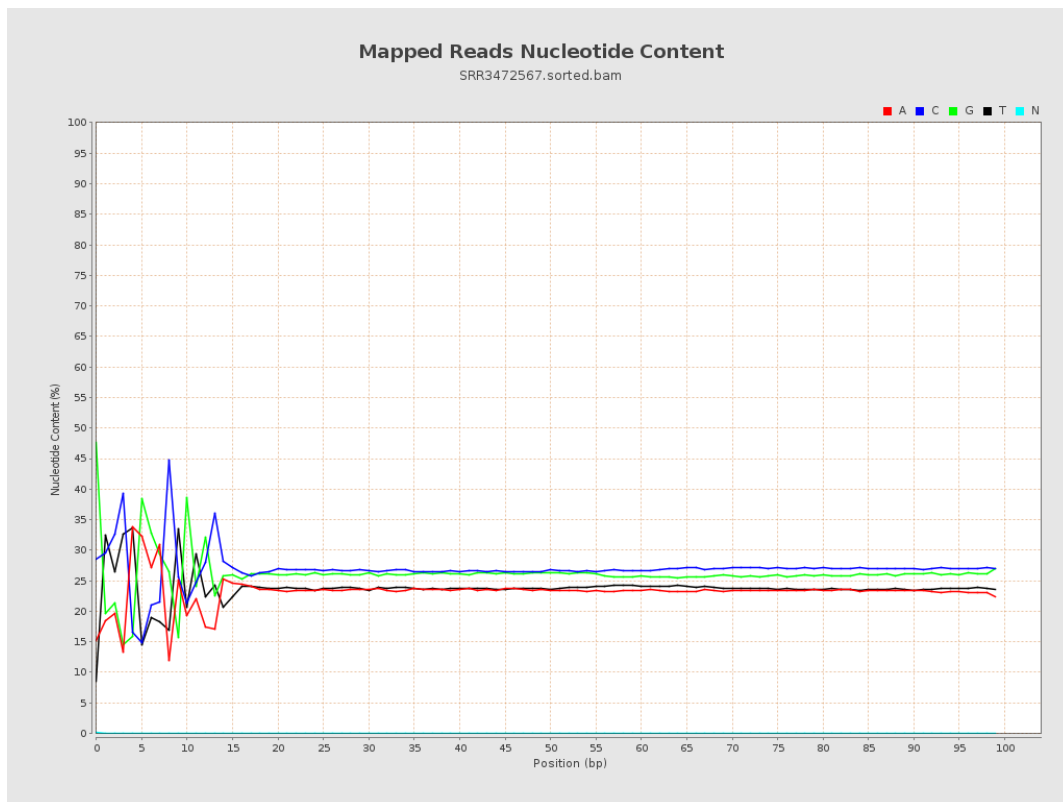
6. Results : Genome Fraction Coverage



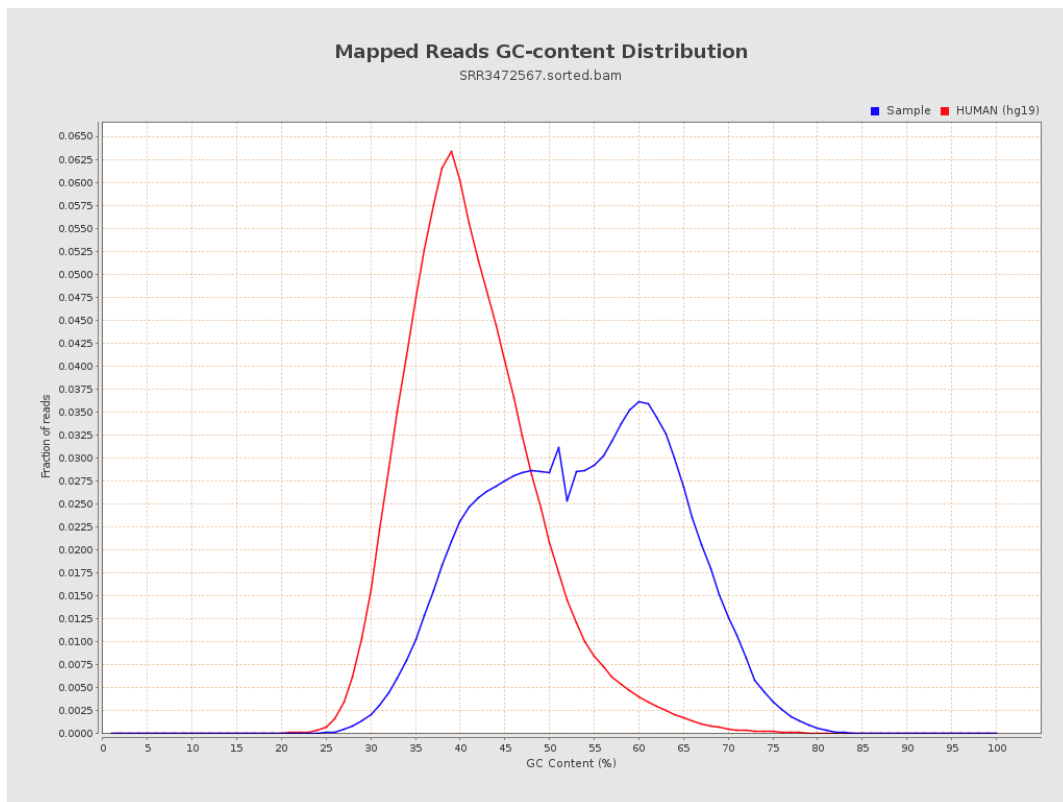
7. Results : Duplication Rate Histogram



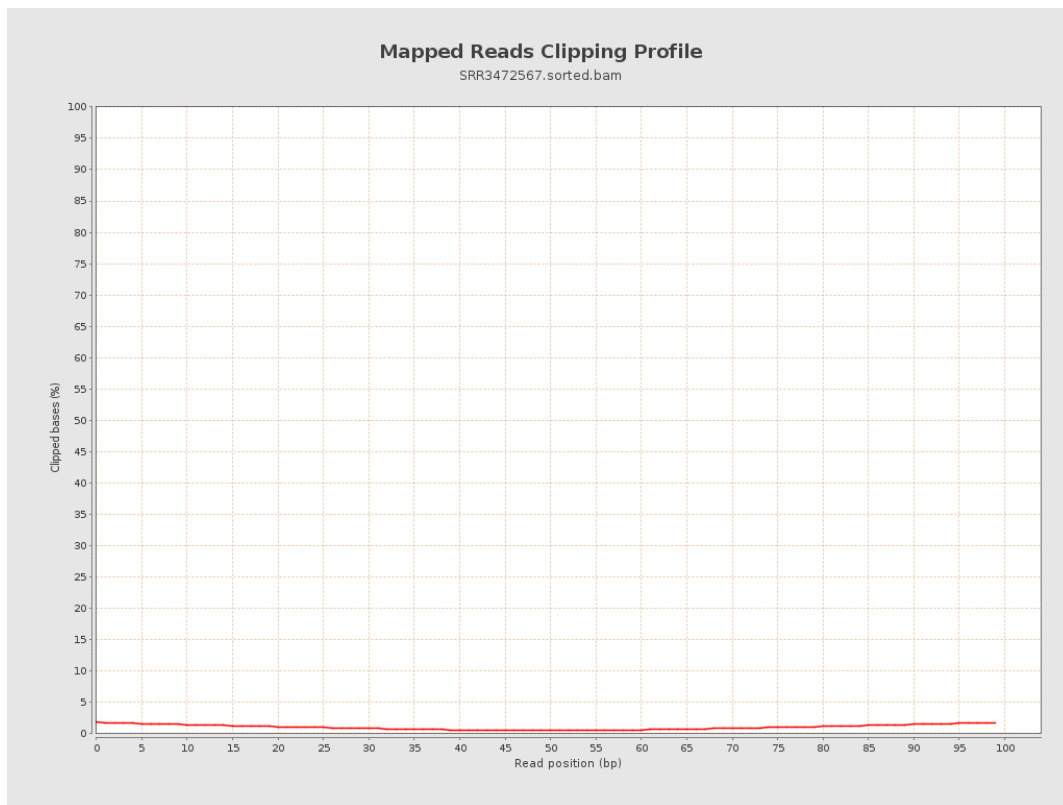
8. Results : Mapped Reads Nucleotide Content



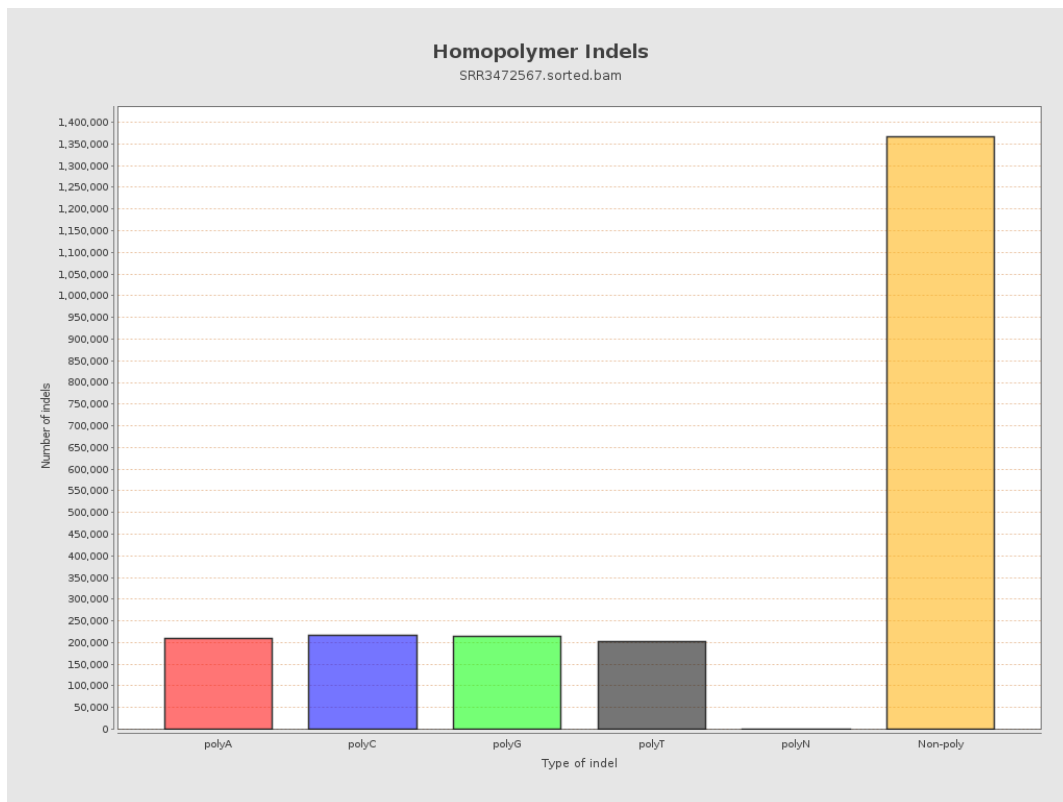
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



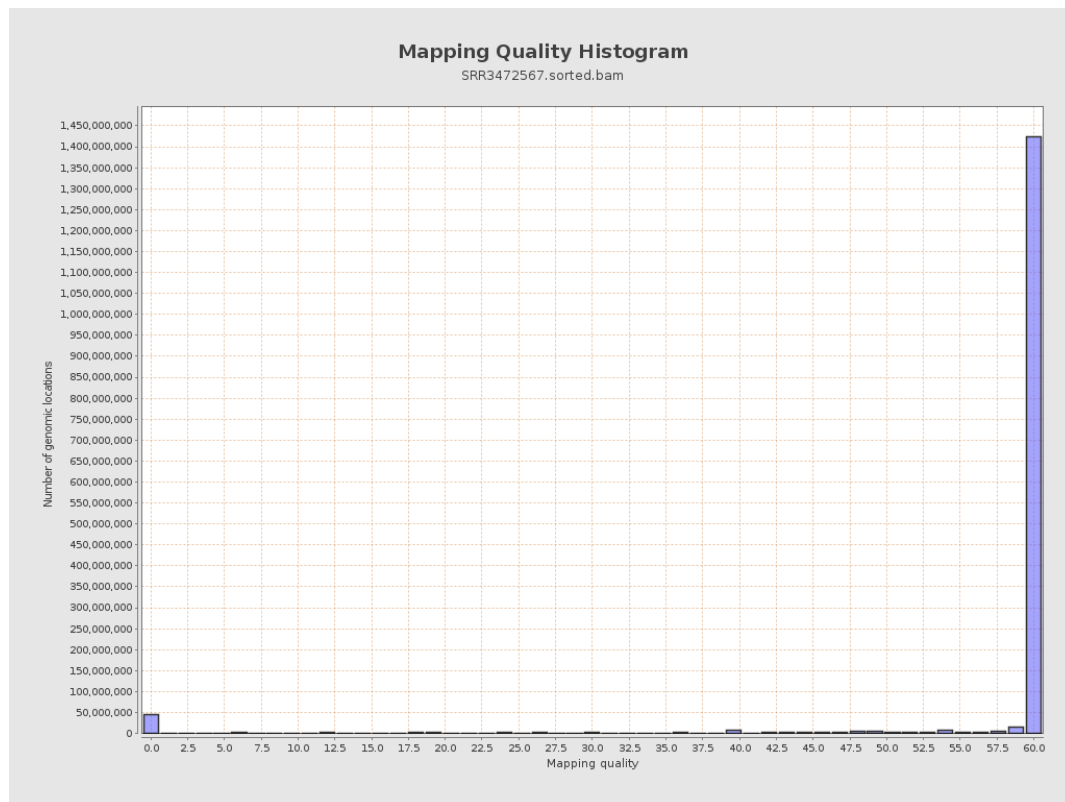
11. Results : Homopolymer Indels



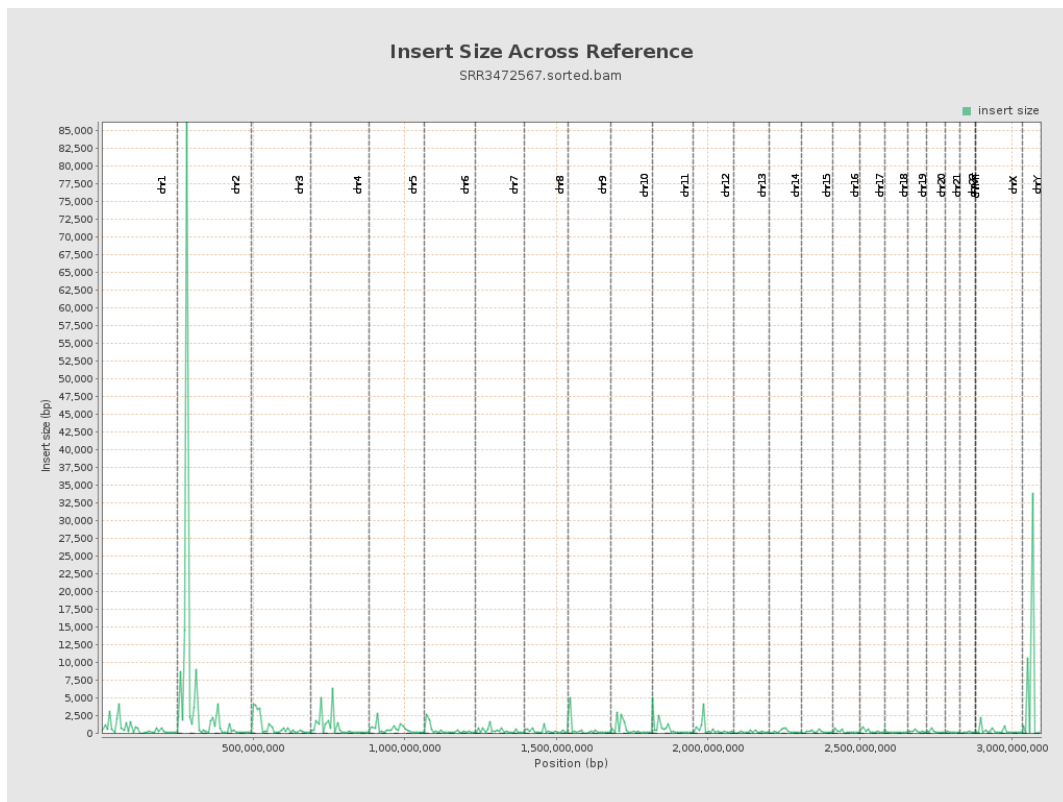
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

