

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/28 01:01:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472575.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_SRR3472575 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472575_1.fastq.gz SRR3472575_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 28 01:01:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472575.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	9,173,020
Mapped reads	8,327,893 / 90.79%
Unmapped reads	845,127 / 9.21%
Mapped paired reads	8,327,893 / 90.79%
Mapped reads, first in pair	4,205,111 / 45.84%
Mapped reads, second in pair	4,122,782 / 44.94%
Mapped reads, both in pair	8,115,790 / 88.47%
Mapped reads, singletons	212,103 / 2.31%
Secondary alignments	0
Supplementary alignments	247,268 / 2.7%
Read min/max/mean length	30 / 100 / 101.05
Duplicated reads (estimated)	1,256,104 / 13.69%
Duplication rate	12.6%
Clipped reads	6,381,802 / 69.57%

2.2. ACGT Content

Number/percentage of A's	172,895,391 / 25.5%
Number/percentage of C's	135,447,435 / 19.98%
Number/percentage of T's	202,158,277 / 29.82%
Number/percentage of G's	166,951,760 / 24.63%
Number/percentage of N's	456,583 / 0.07%

GC Percentage	44.61%
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2.3. Coverage

Mean	0.2191
Standard Deviation	2.3865

2.4. Mapping Quality

Mean Mapping Quality	50.35
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2.5. Insert size

Mean	227,284
Standard Deviation	4,606,816.26
P25/Median/P75	94 / 131 / 179

2.6. Mismatches and indels

General error rate	1.24%
Mismatches	8,274,644
Insertions	66,444
Mapped reads with at least one insertion	0.78%
Deletions	155,374
Mapped reads with at least one deletion	1.83%
Homopolymer indels	42.17%

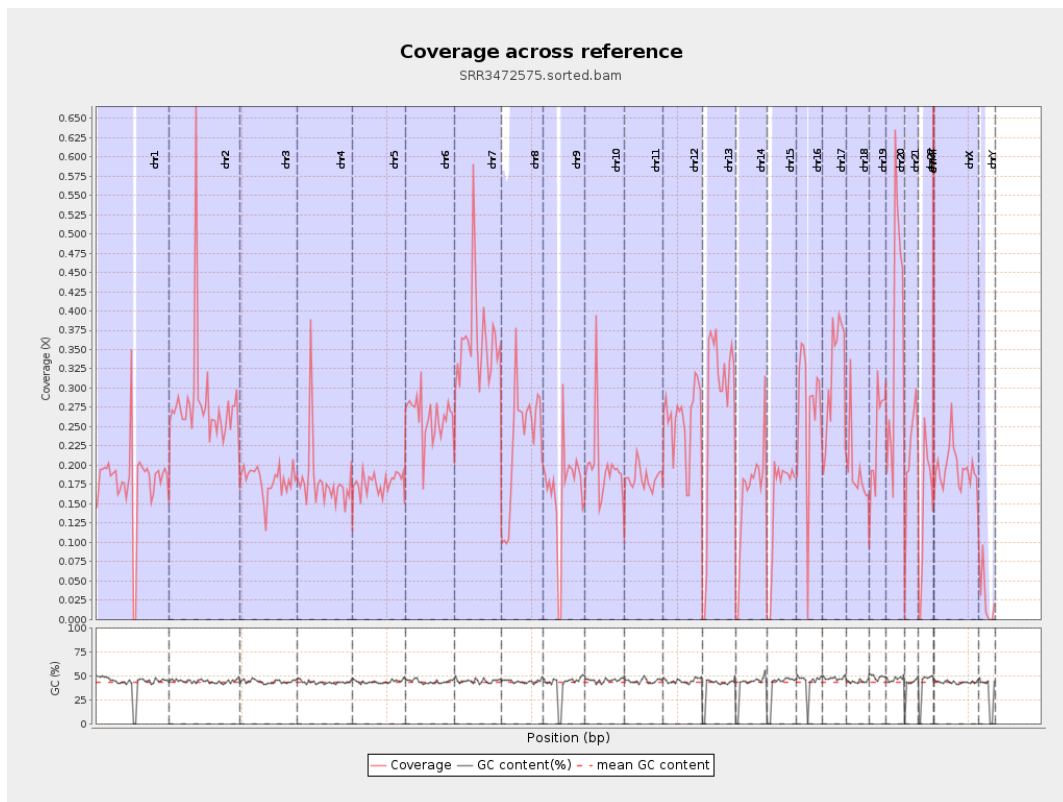
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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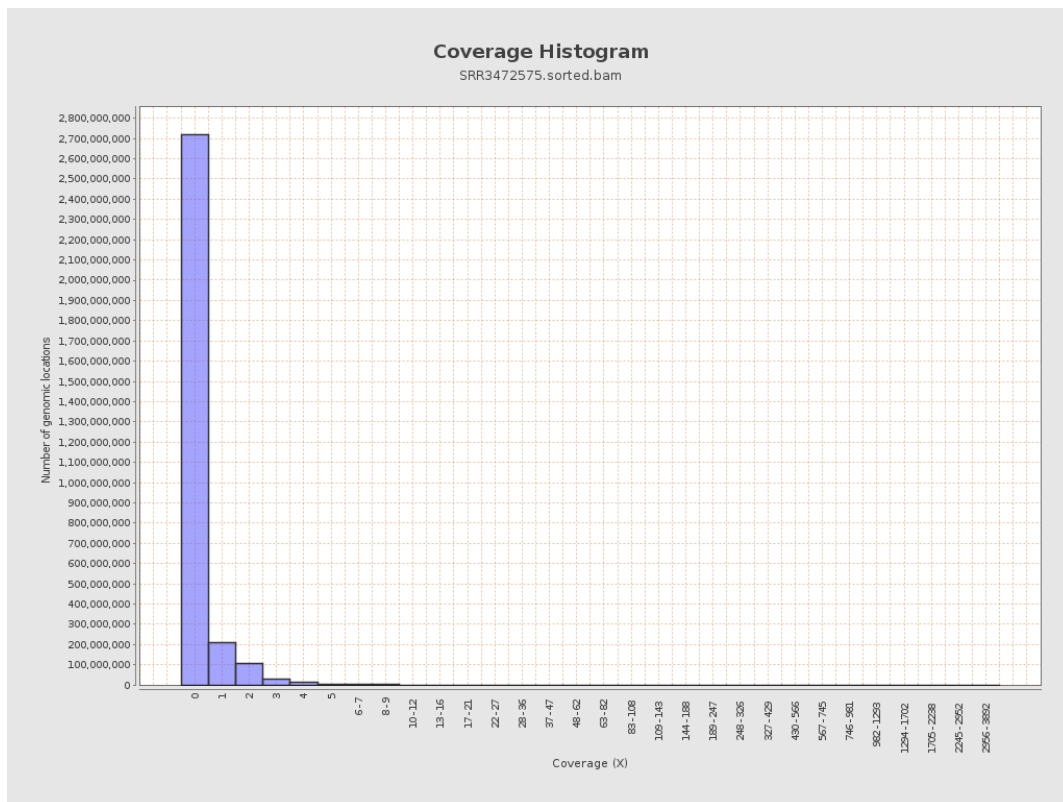
		bases	coverage	deviation
chr1	249250621	44347033	0.1779	3.0121
chr2	243199373	68232124	0.2806	3.2702
chr3	198022430	35664239	0.1801	0.6327
chr4	191154276	34277673	0.1793	1.3202
chr5	180915260	32001492	0.1769	0.6802
chr6	171115067	44807708	0.2619	1.2705
chr7	159138663	57808292	0.3633	4.3906
chr8	146364022	33447444	0.2285	1.8929
chr9	141213431	23552238	0.1668	2.4193
chr10	135534747	26823433	0.1979	2.1016
chr11	135006516	24543979	0.1818	1.7133
chr12	133851895	34648413	0.2589	0.7982
chr13	115169878	31947038	0.2774	0.8361
chr14	107349540	17487019	0.1629	6.0212
chr15	102531392	15820391	0.1543	0.6011
chr16	90354753	24803476	0.2745	1.22
chr17	81195210	25724372	0.3168	1.9685
chr18	78077248	15127548	0.1938	4.1781
chr19	59128983	14169876	0.2396	2.0718
chr20	63025520	23329024	0.3702	1.3641
chr21	48129895	10282376	0.2136	0.9204
chr22	51304566	7359854	0.1435	0.5832
chrMT	16571	31685	1.9121	2.4085
chrX	155270560	30410019	0.1959	1.0615

chrY	59373566	1557530	0.0262	0.9987
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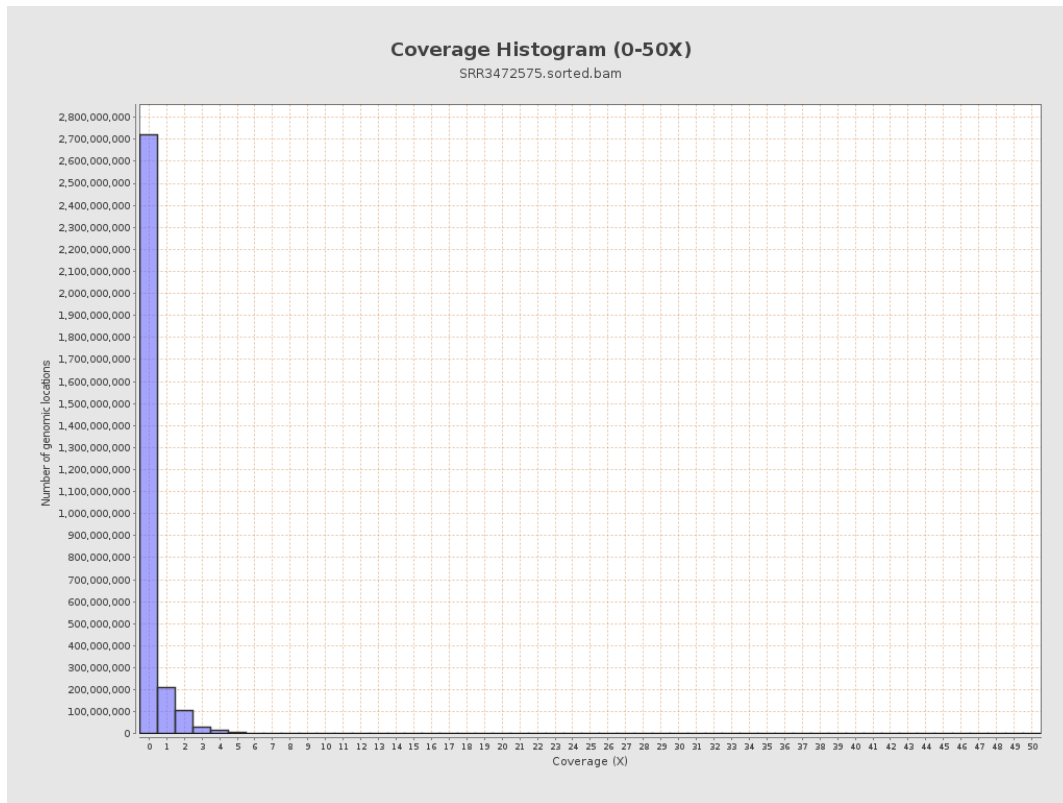
3. Results : Coverage across reference



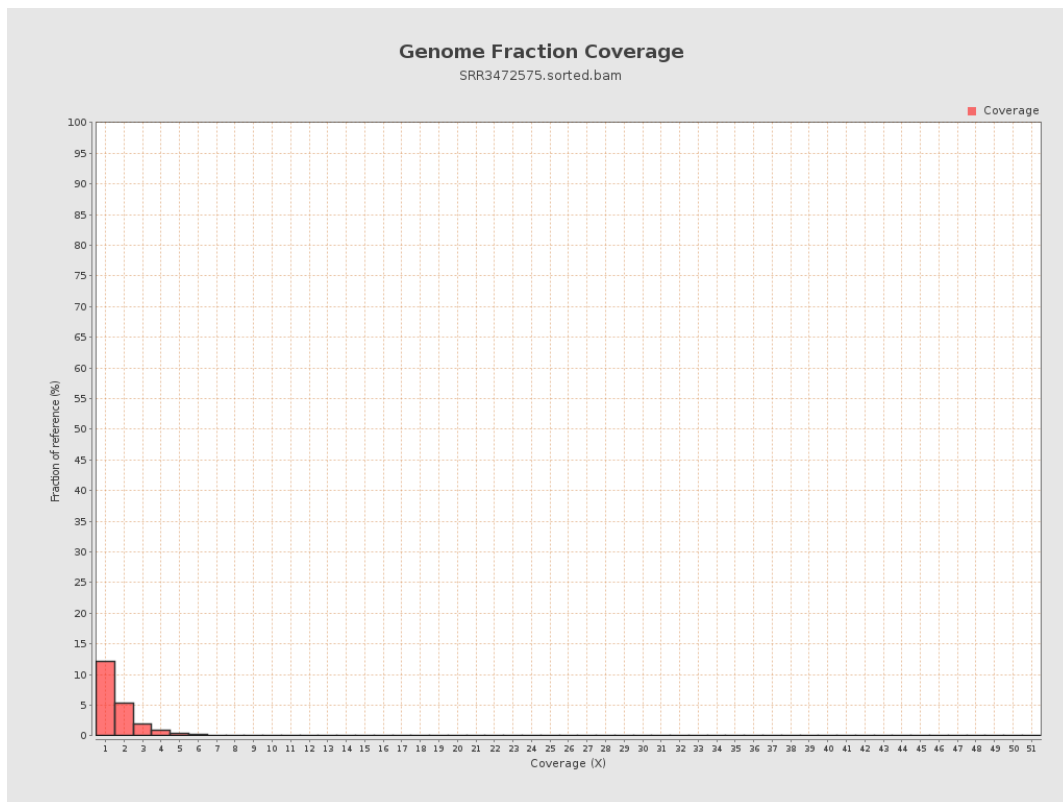
4. Results : Coverage Histogram



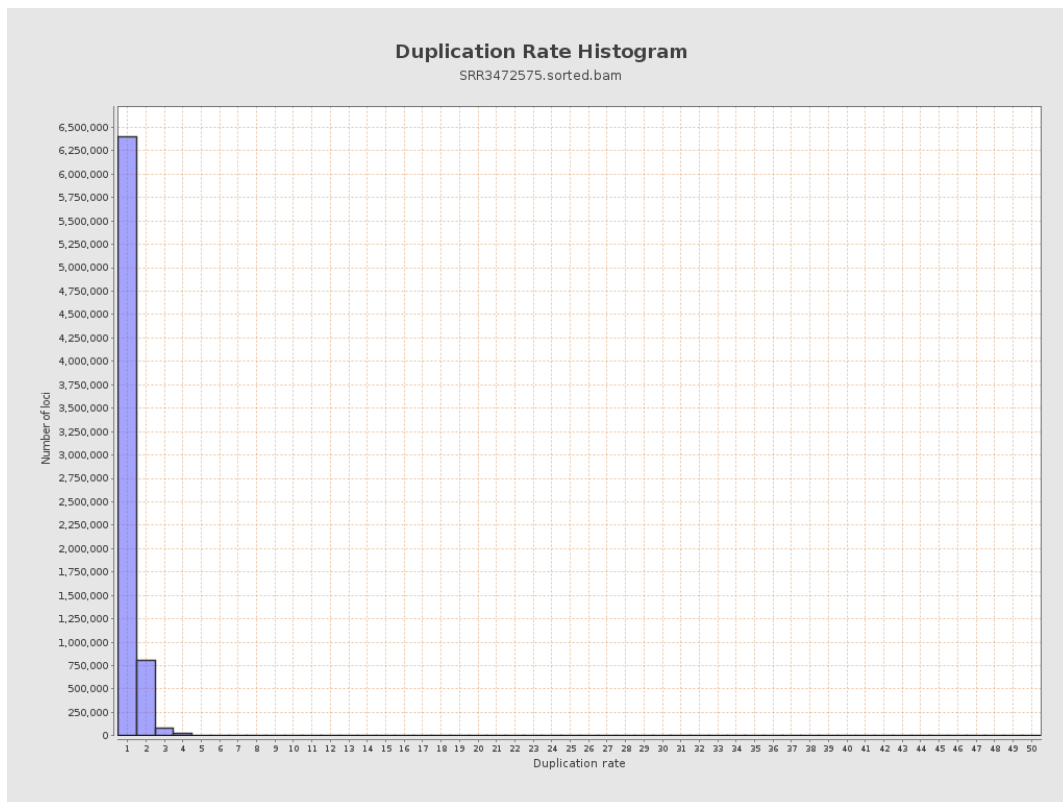
5. Results : Coverage Histogram (0-50X)



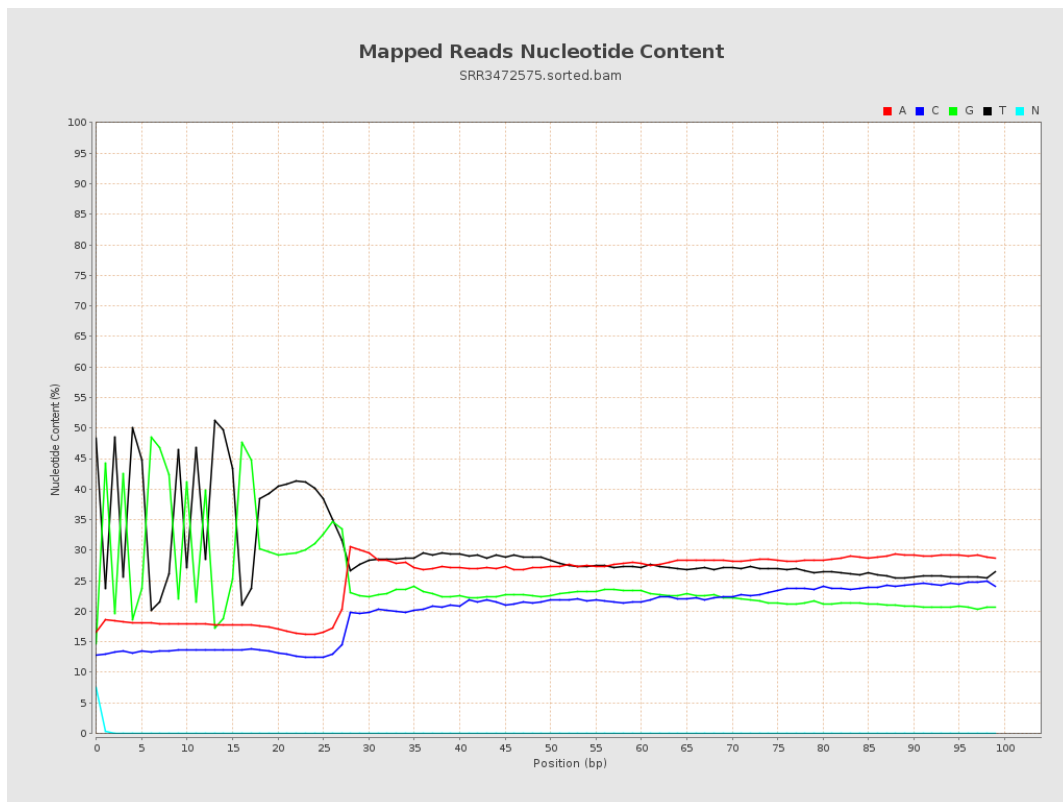
6. Results : Genome Fraction Coverage



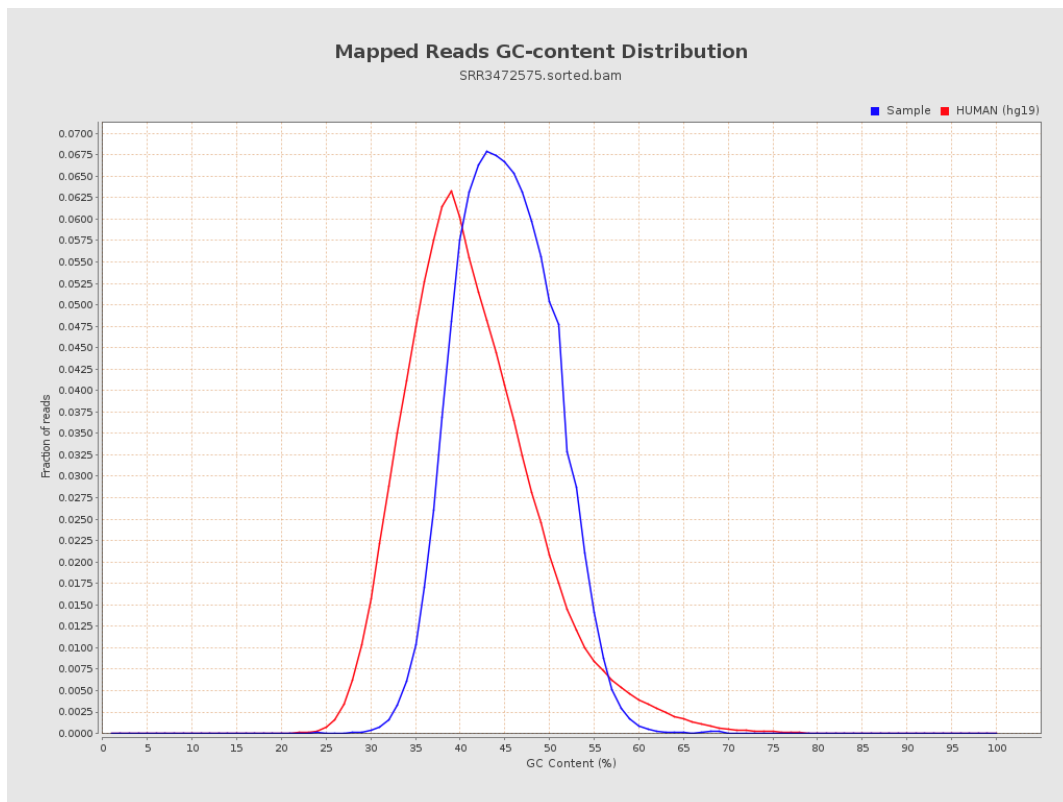
7. Results : Duplication Rate Histogram



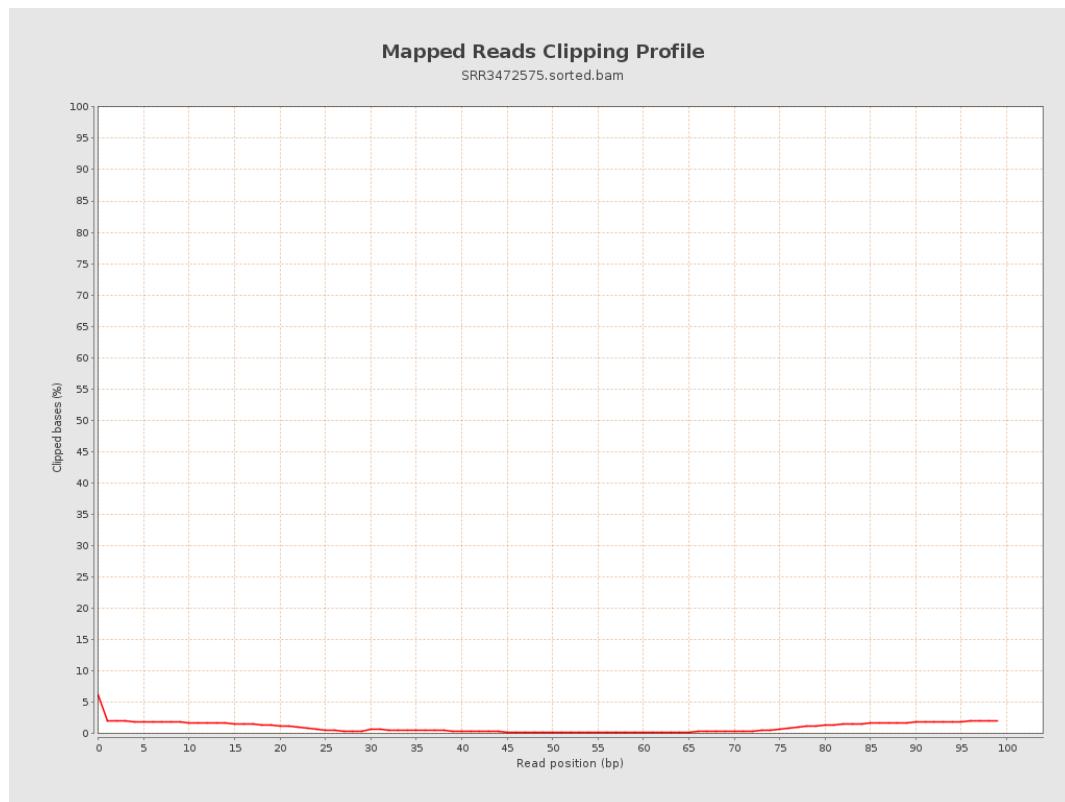
8. Results : Mapped Reads Nucleotide Content



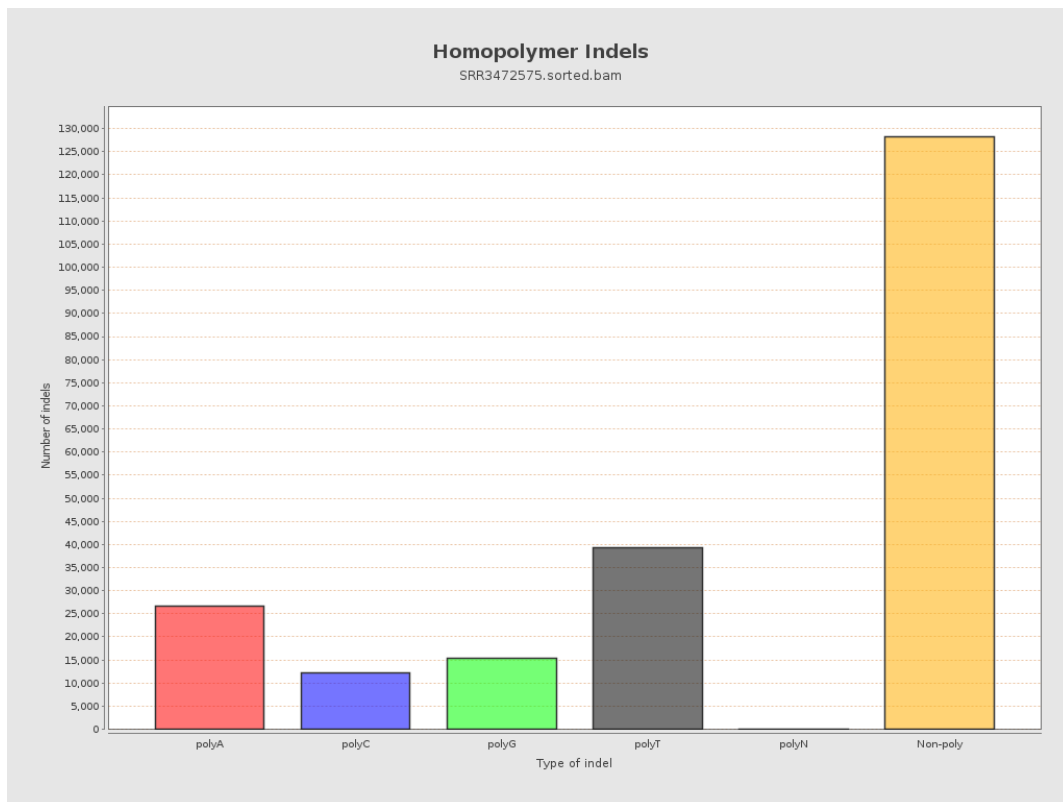
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



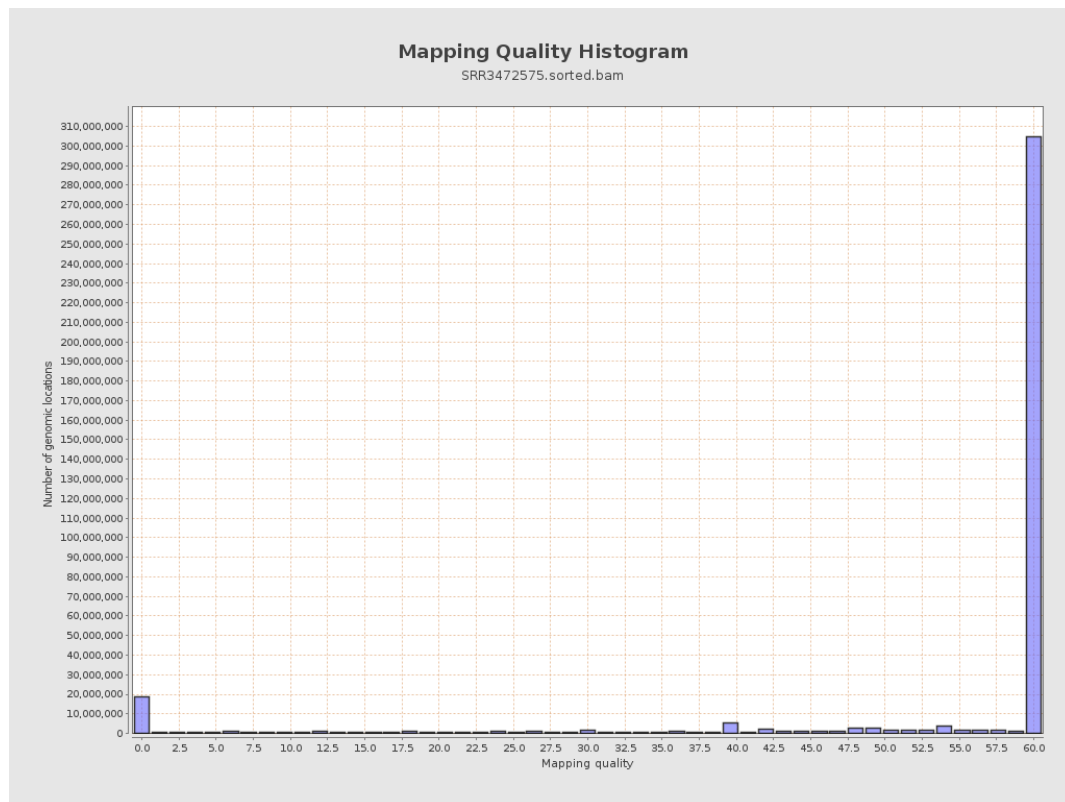
11. Results : Homopolymer Indels



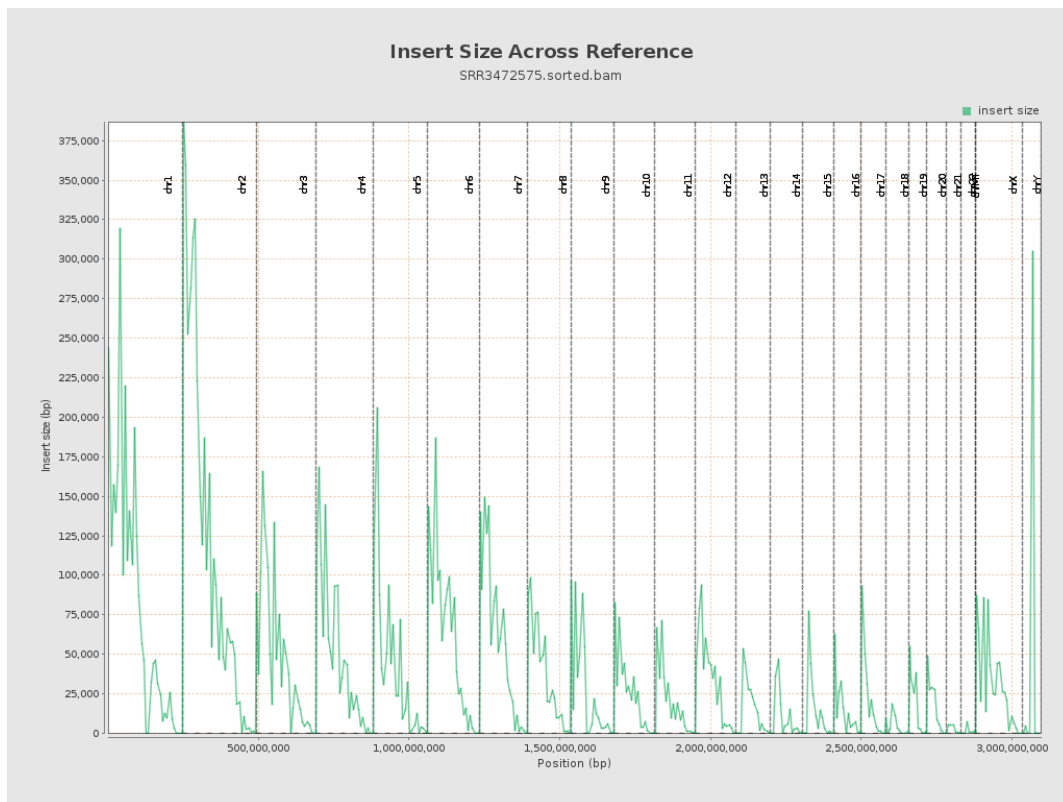
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

