

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 10:04:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124957.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_SRR3124957 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124957_1.fastq.gz SRR3124957_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 10:04:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124957.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,053,000
Mapped reads	5,848,977 / 96.63%
Unmapped reads	204,023 / 3.37%
Mapped paired reads	5,848,977 / 96.63%
Mapped reads, first in pair	2,980,246 / 49.24%
Mapped reads, second in pair	2,868,731 / 47.39%
Mapped reads, both in pair	5,718,578 / 94.48%
Mapped reads, singletons	130,399 / 2.15%
Secondary alignments	0
Supplementary alignments	5,731 / 0.09%
Read min/max/mean length	30 / 76 / 76.03
Duplicated reads (estimated)	426,729 / 7.05%
Duplication rate	5.02%
Clipped reads	2,641,362 / 43.64%

2.2. ACGT Content

Number/percentage of A's	100,708,955 / 27.63%
Number/percentage of C's	64,578,406 / 17.72%
Number/percentage of T's	110,302,075 / 30.26%
Number/percentage of G's	88,876,372 / 24.39%
Number/percentage of N's	3,167 / 0%

GC Percentage	42.1%
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2.3. Coverage

Mean	0.1178
Standard Deviation	1.0321

2.4. Mapping Quality

Mean Mapping Quality	51.83
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2.5. Insert size

Mean	25,658.19
Standard Deviation	1,510,694.47
P25/Median/P75	147 / 197 / 274

2.6. Mismatches and indels

General error rate	0.67%
Mismatches	2,386,986
Insertions	37,438
Mapped reads with at least one insertion	0.64%
Deletions	97,503
Mapped reads with at least one deletion	1.65%
Homopolymer indels	49.49%

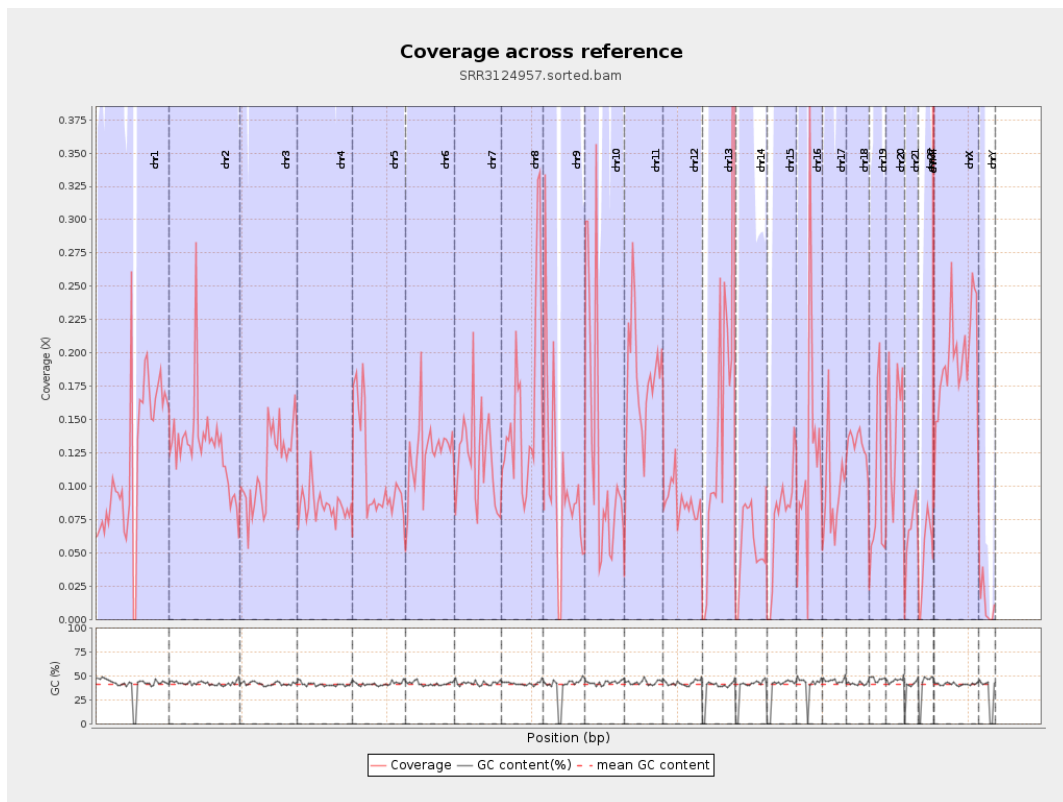
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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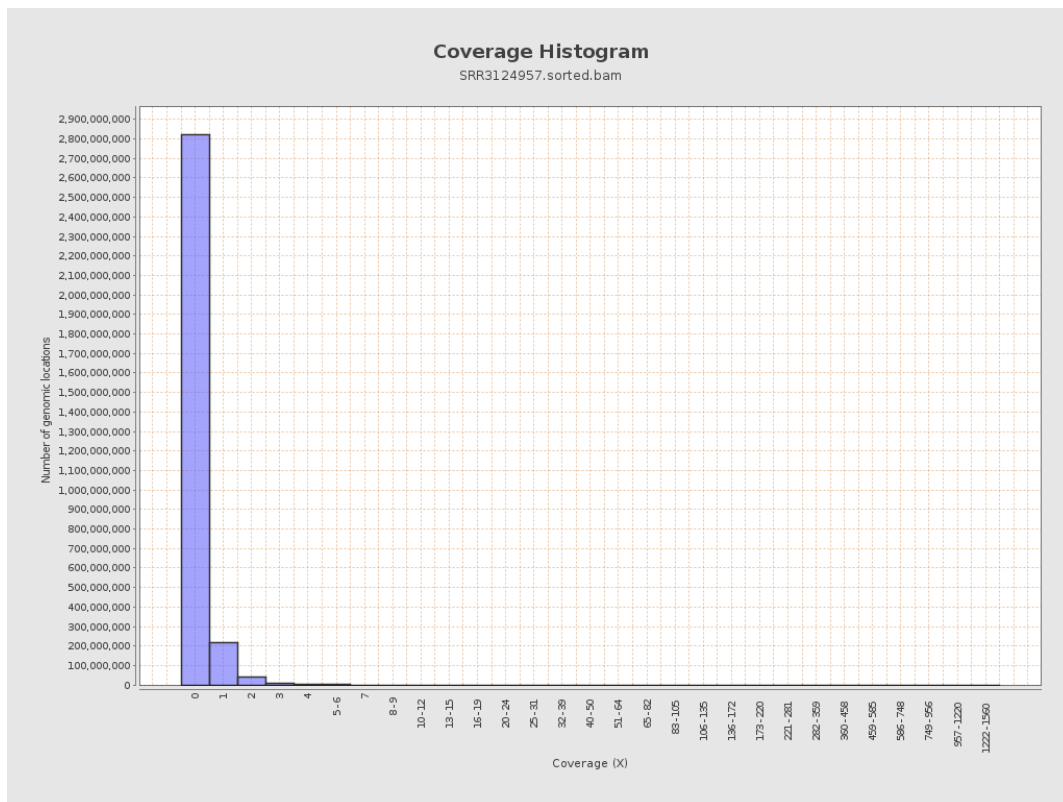
		bases	coverage	deviation
chr1	249250621	29862058	0.1198	1.471
chr2	243199373	31545125	0.1297	1.0931
chr3	198022430	22621615	0.1142	0.4196
chr4	191154276	16310036	0.0853	0.4462
chr5	180915260	19633414	0.1085	0.405
chr6	171115067	21318884	0.1246	0.84
chr7	159138663	19342581	0.1215	1.389
chr8	146364022	23373661	0.1597	0.6506
chr9	141213431	14469758	0.1025	0.8622
chr10	135534747	16939599	0.125	2.3794
chr11	135006516	24085125	0.1784	0.8929
chr12	133851895	11767370	0.0879	0.368
chr13	115169878	19369692	0.1682	0.696
chr14	107349540	5875285	0.0547	0.3536
chr15	102531392	7721099	0.0753	0.3511
chr16	90354753	10872542	0.1203	1.8553
chr17	81195210	7627262	0.0939	1.1194
chr18	78077248	10279314	0.1317	1.3976
chr19	59128983	5516202	0.0933	1.102
chr20	63025520	9176341	0.1456	0.4829
chr21	48129895	3124437	0.0649	0.3535
chr22	51304566	2469227	0.0481	0.2608
chrMT	16571	112948	6.816	5.7629
chrX	155270560	30487318	0.1963	0.8659

chrY	59373566	710524	0.012	0.4579
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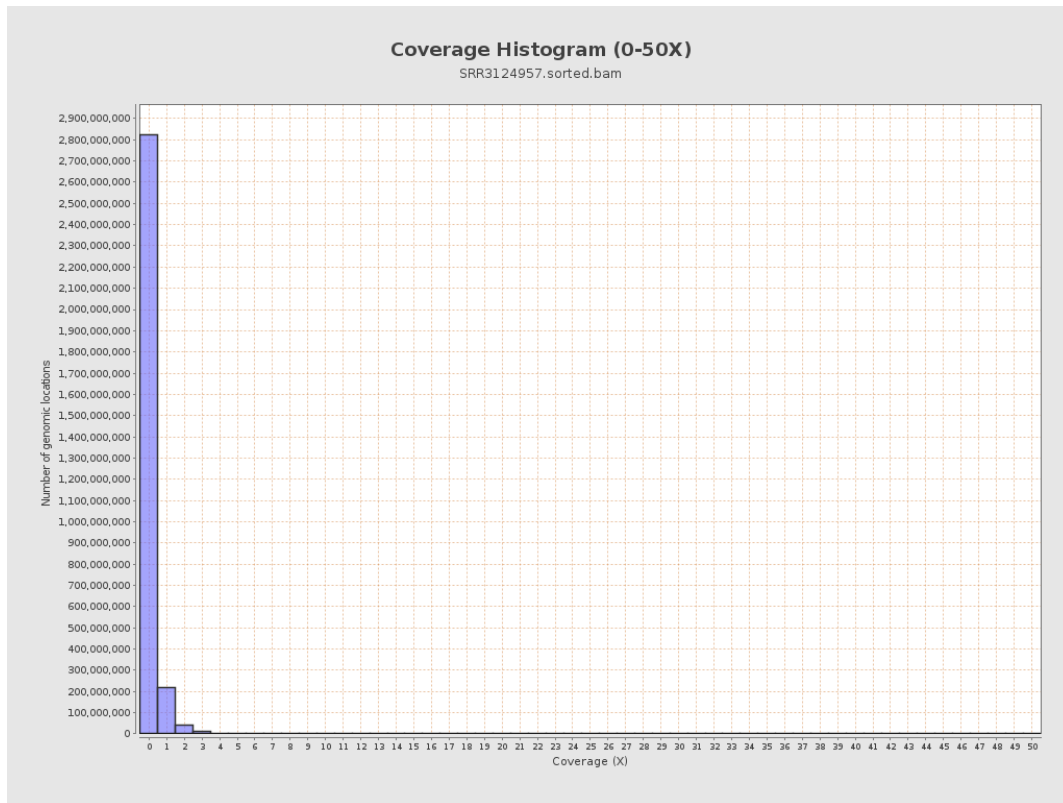
3. Results : Coverage across reference



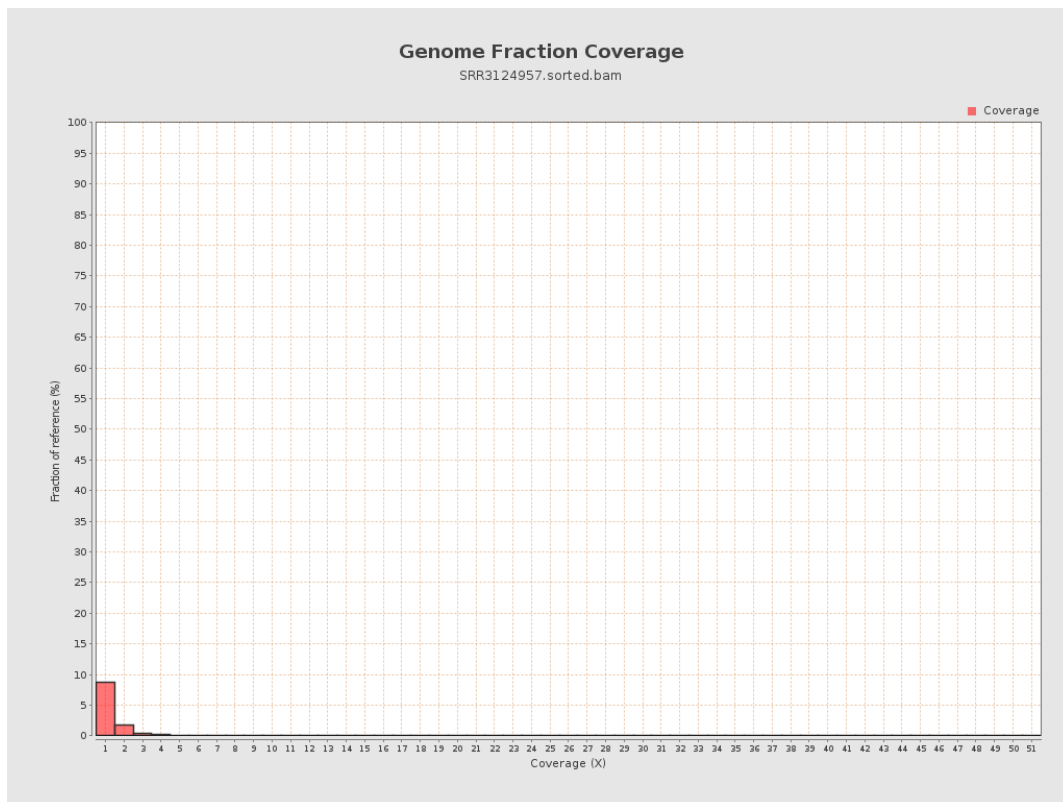
4. Results : Coverage Histogram



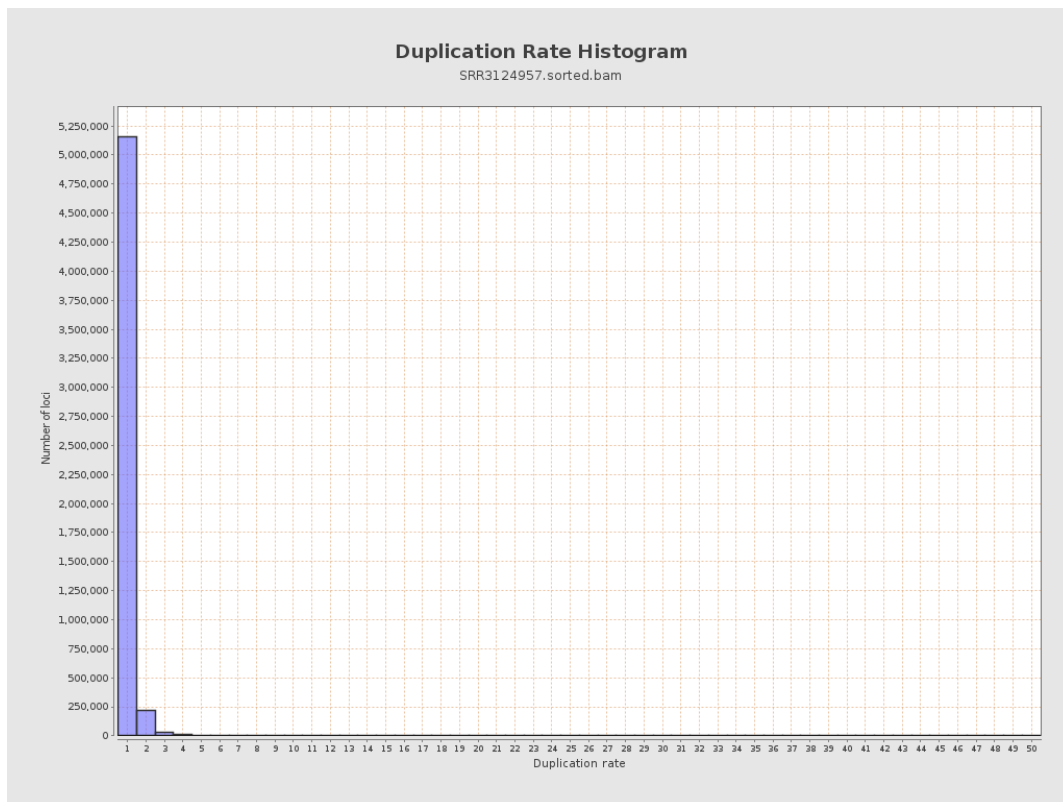
5. Results : Coverage Histogram (0-50X)



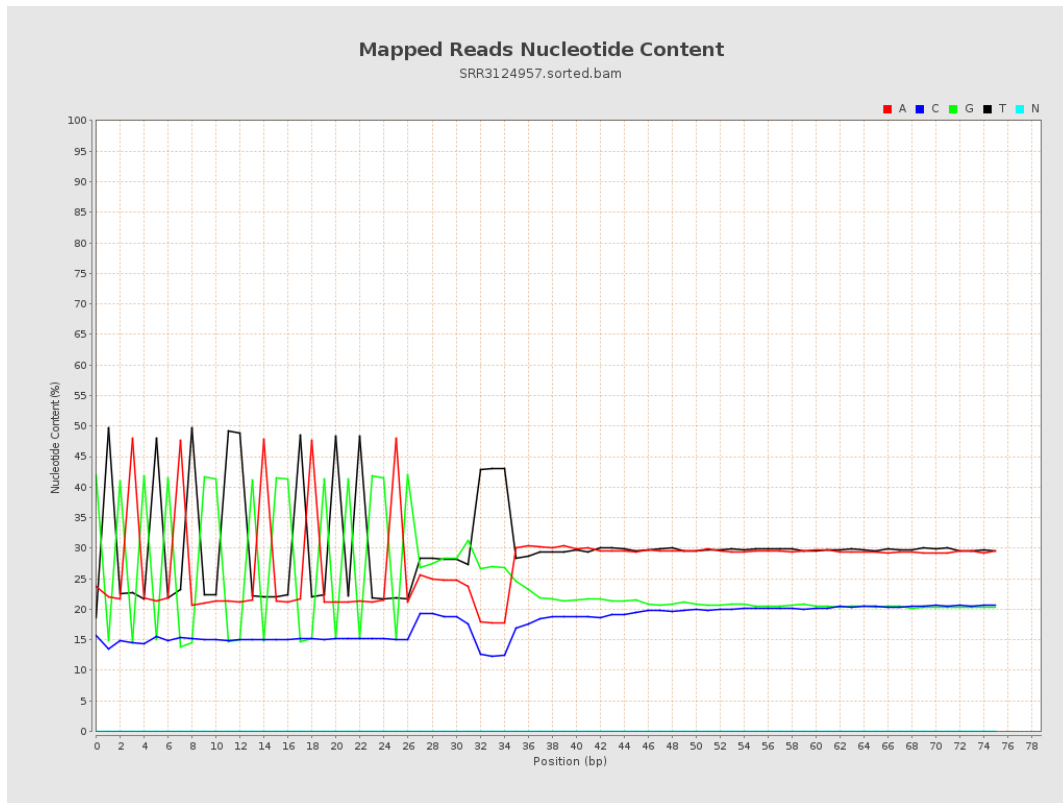
6. Results : Genome Fraction Coverage



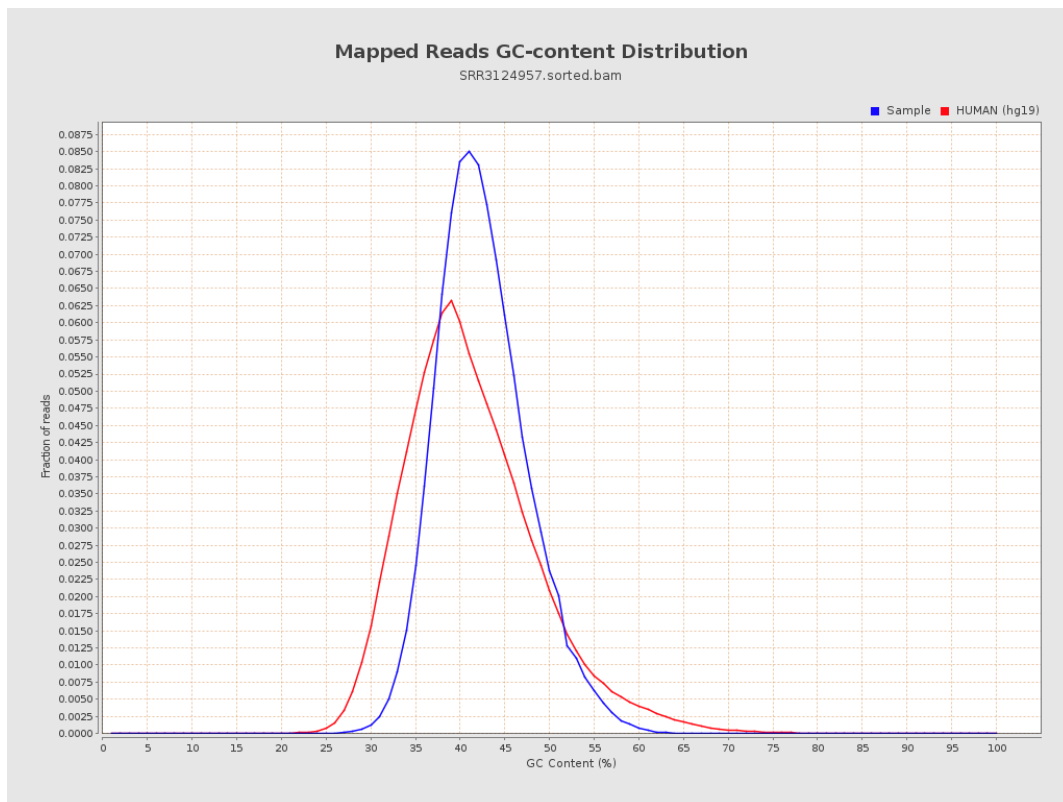
7. Results : Duplication Rate Histogram



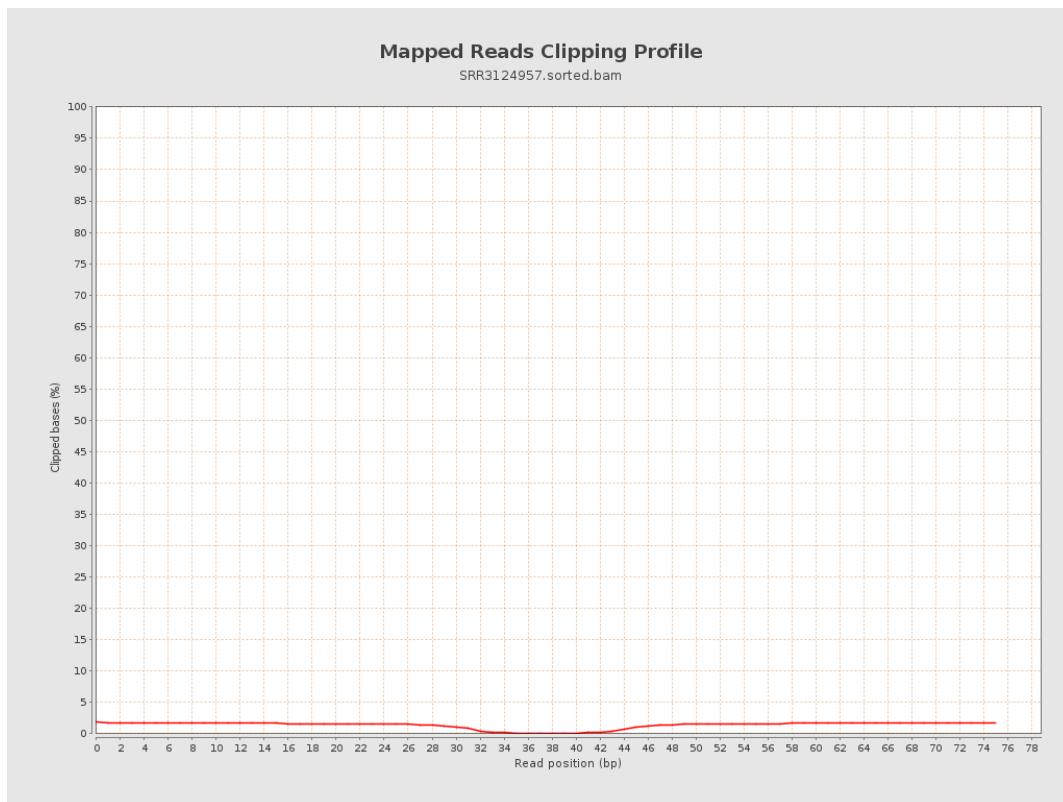
8. Results : Mapped Reads Nucleotide Content



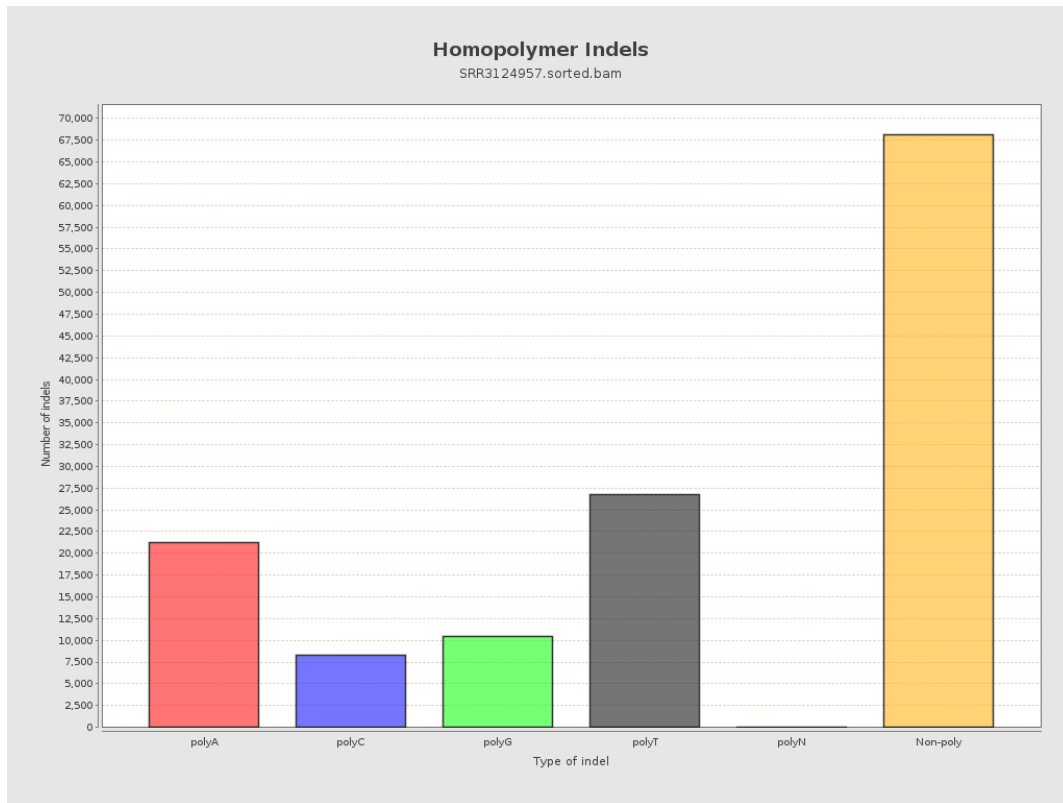
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



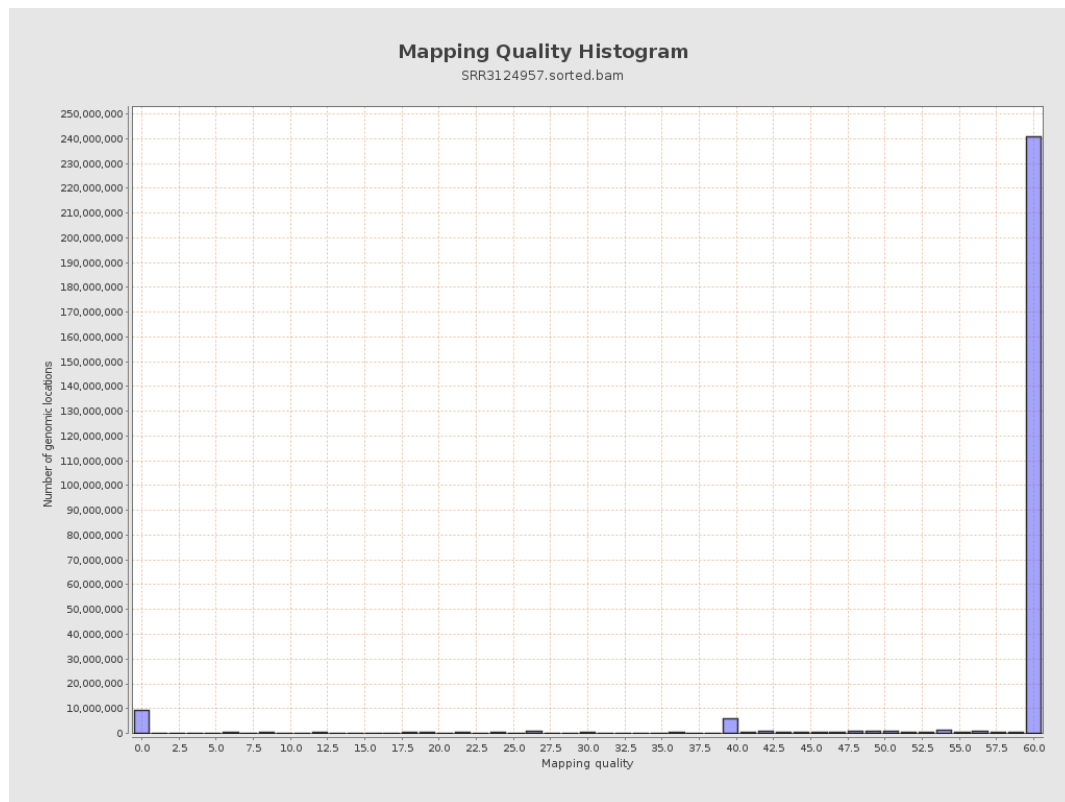
11. Results : Homopolymer Indels



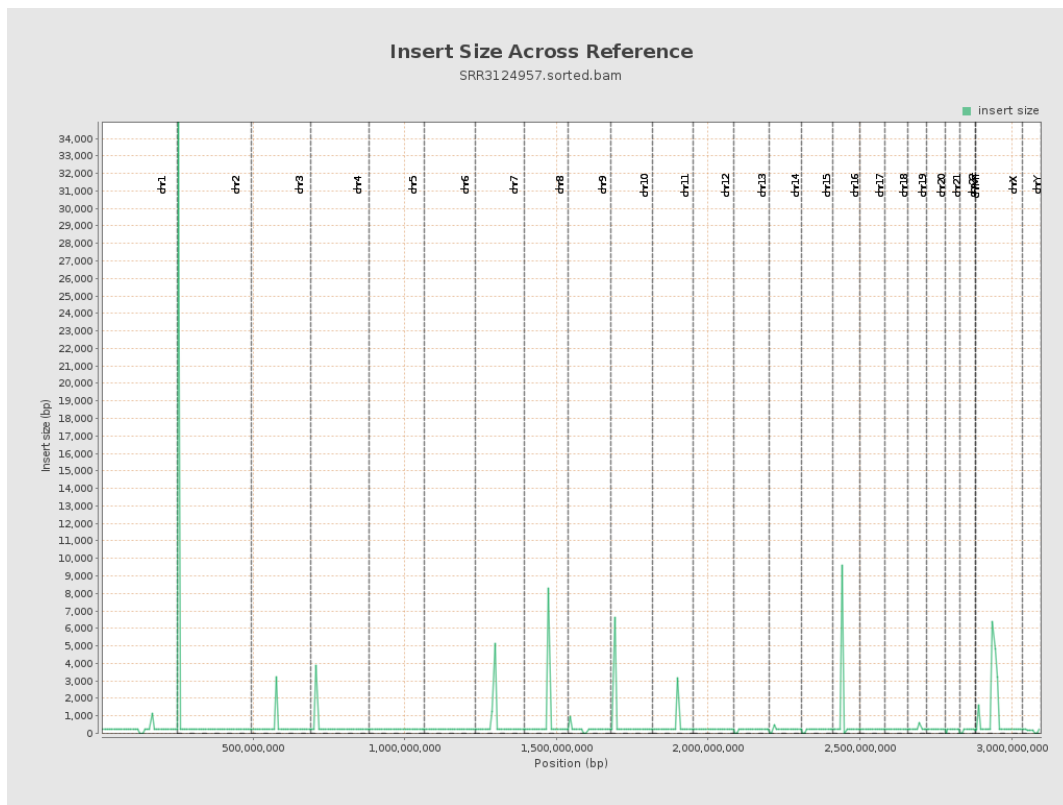
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

