

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 03:58:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975198.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_SRR975198 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975198_1.fastq.gz SRR975198_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 03:58:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975198.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	34,199,330
Mapped reads	34,105,366 / 99.73%
Unmapped reads	93,964 / 0.27%
Mapped paired reads	34,105,366 / 99.73%
Mapped reads, first in pair	17,047,267 / 49.85%
Mapped reads, second in pair	17,058,099 / 49.88%
Mapped reads, both in pair	34,047,374 / 99.56%
Mapped reads, singletons	57,992 / 0.17%
Secondary alignments	0
Supplementary alignments	60,887 / 0.18%
Read min/max/mean length	30 / 101 / 101.07
Duplicated reads (estimated)	18,538,242 / 54.21%
Duplication rate	41%
Clipped reads	20,442,666 / 59.78%

2.2. ACGT Content

Number/percentage of A's	840,085,814 / 26.51%
Number/percentage of C's	704,459,741 / 22.23%
Number/percentage of T's	874,710,176 / 27.6%
Number/percentage of G's	749,995,900 / 23.66%
Number/percentage of N's	159,943 / 0.01%

GC Percentage	45.89%
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2.3. Coverage

Mean	1.0242
Standard Deviation	15.6069

2.4. Mapping Quality

Mean Mapping Quality	55.61
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2.5. Insert size

Mean	144,819.4
Standard Deviation	3,745,999.87
P25/Median/P75	189 / 233 / 284

2.6. Mismatches and indels

General error rate	0.73%
Mismatches	22,555,466
Insertions	284,937
Mapped reads with at least one insertion	0.83%
Deletions	826,186
Mapped reads with at least one deletion	2.39%
Homopolymer indels	50%

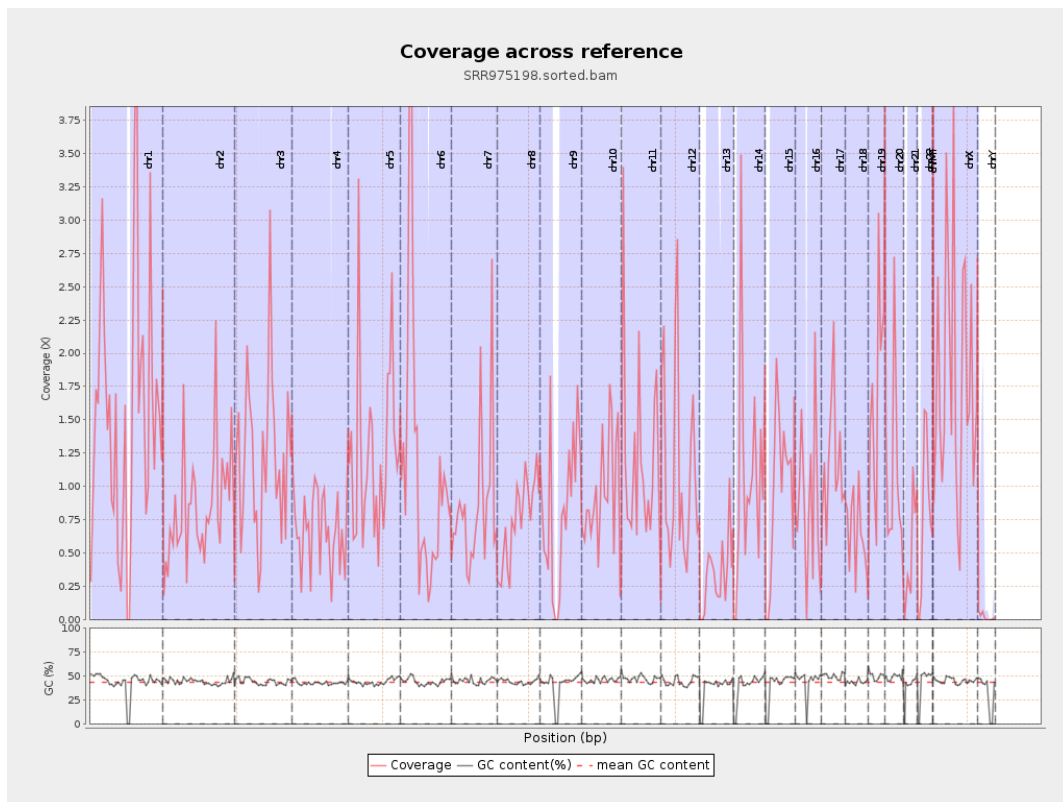
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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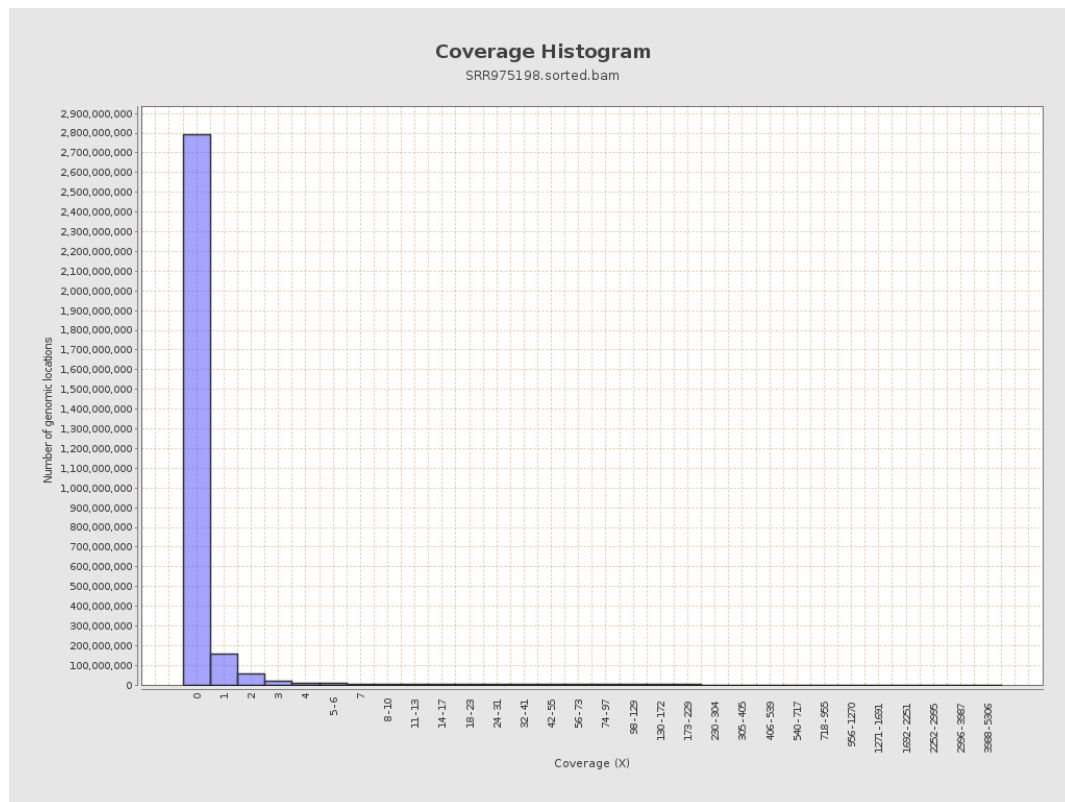
		bases	coverage	deviation
chr1	249250621	386742712	1.5516	20.5785
chr2	243199373	206021021	0.8471	12.1805
chr3	198022430	238972957	1.2068	15.6717
chr4	191154276	128996330	0.6748	10.5733
chr5	180915260	228757636	1.2644	17.7072
chr6	171115067	191182301	1.1173	18.3649
chr7	159138663	134643528	0.8461	14.1056
chr8	146364022	110059743	0.752	11.5506
chr9	141213431	112953340	0.7999	11.8227
chr10	135534747	129243894	0.9536	14.5233
chr11	135006516	159632267	1.1824	16.9674
chr12	133851895	154707874	1.1558	16.6261
chr13	115169878	38861958	0.3374	6.4622
chr14	107349540	113355444	1.0559	16.1215
chr15	102531392	97516621	0.9511	13.9383
chr16	90354753	76362155	0.8451	12.1151
chr17	81195210	96488979	1.1884	16.5803
chr18	78077248	51680483	0.6619	10.484
chr19	59128983	102816351	1.7388	21.9369
chr20	63025520	65360225	1.037	15.1539
chr21	48129895	24768877	0.5146	8.1742
chr22	51304566	39868346	0.7771	12.3165
chrMT	16571	126250	7.6187	11.5485
chrX	155270560	280342626	1.8055	25.554

chrY	59373566	1111148	0.0187	0.8324
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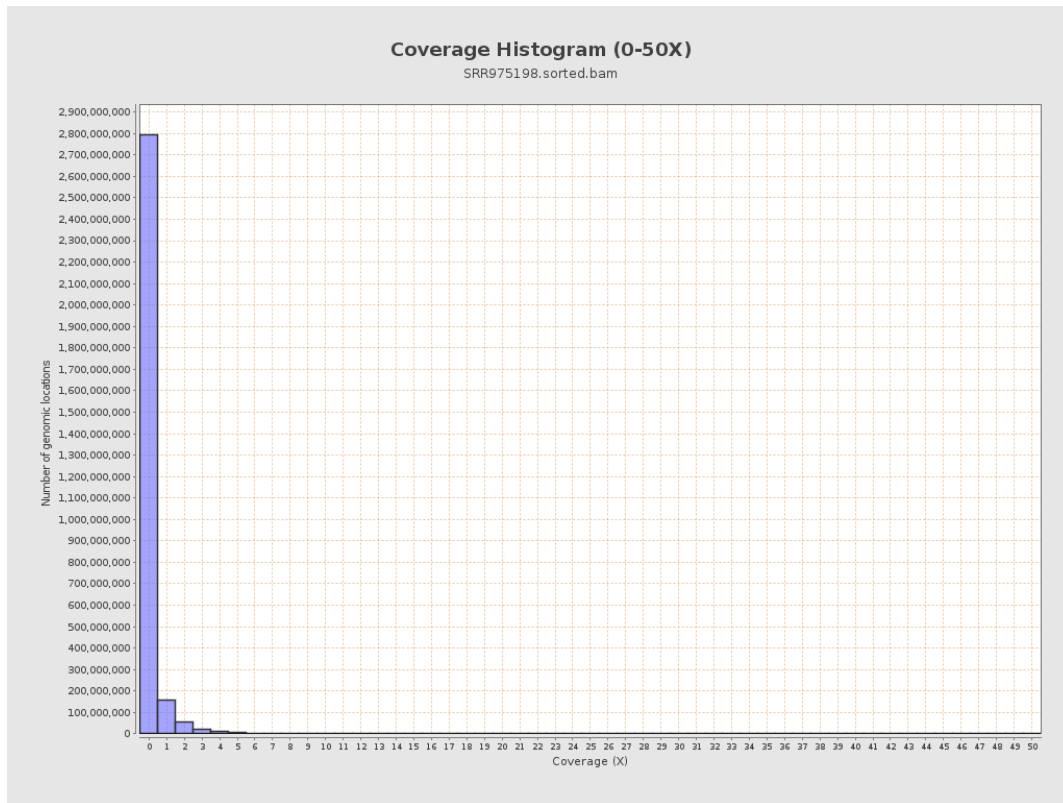
3. Results : Coverage across reference



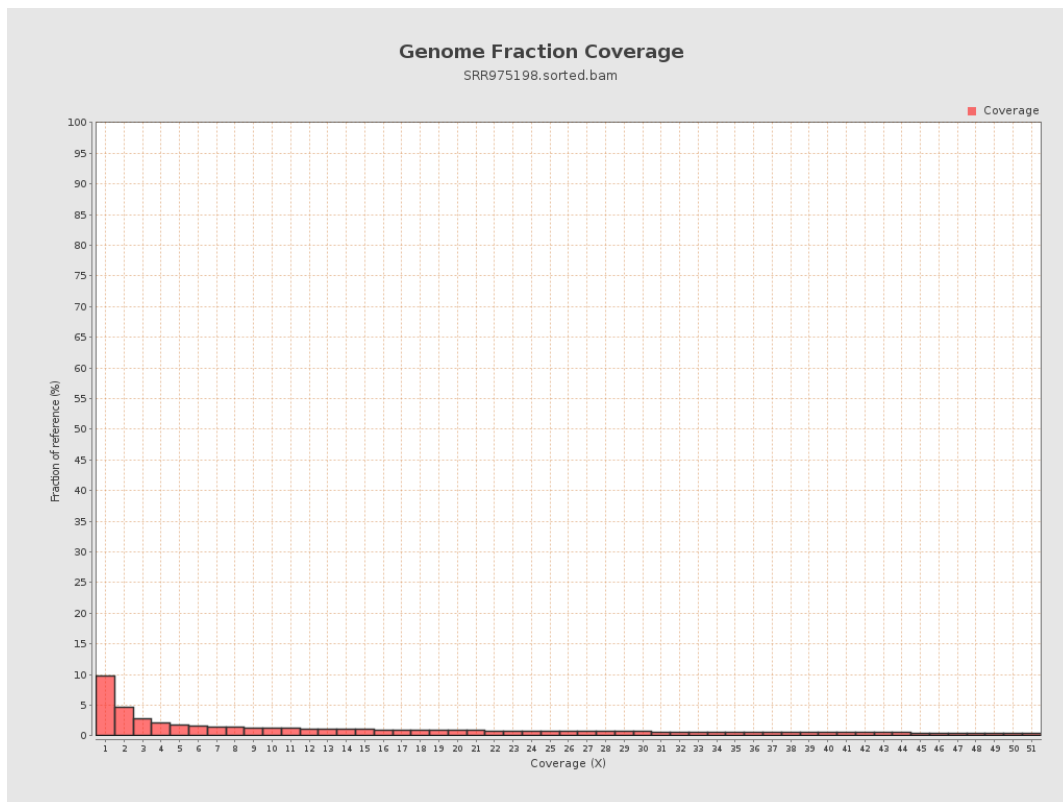
4. Results : Coverage Histogram



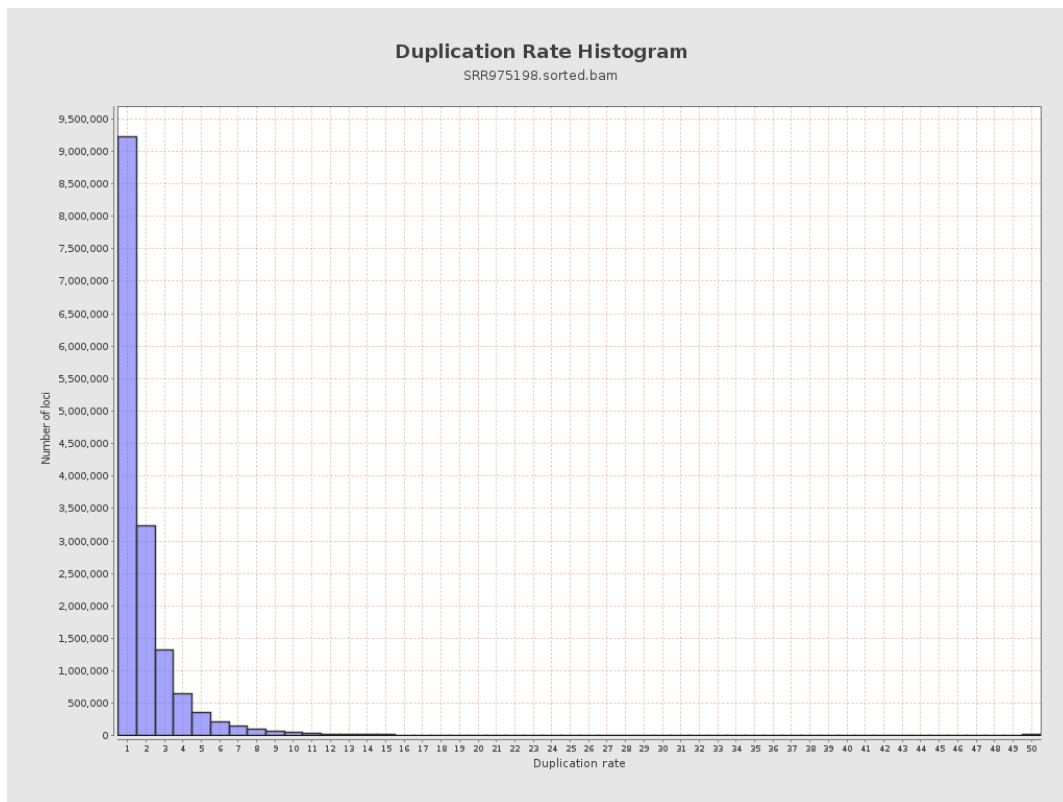
5. Results : Coverage Histogram (0-50X)



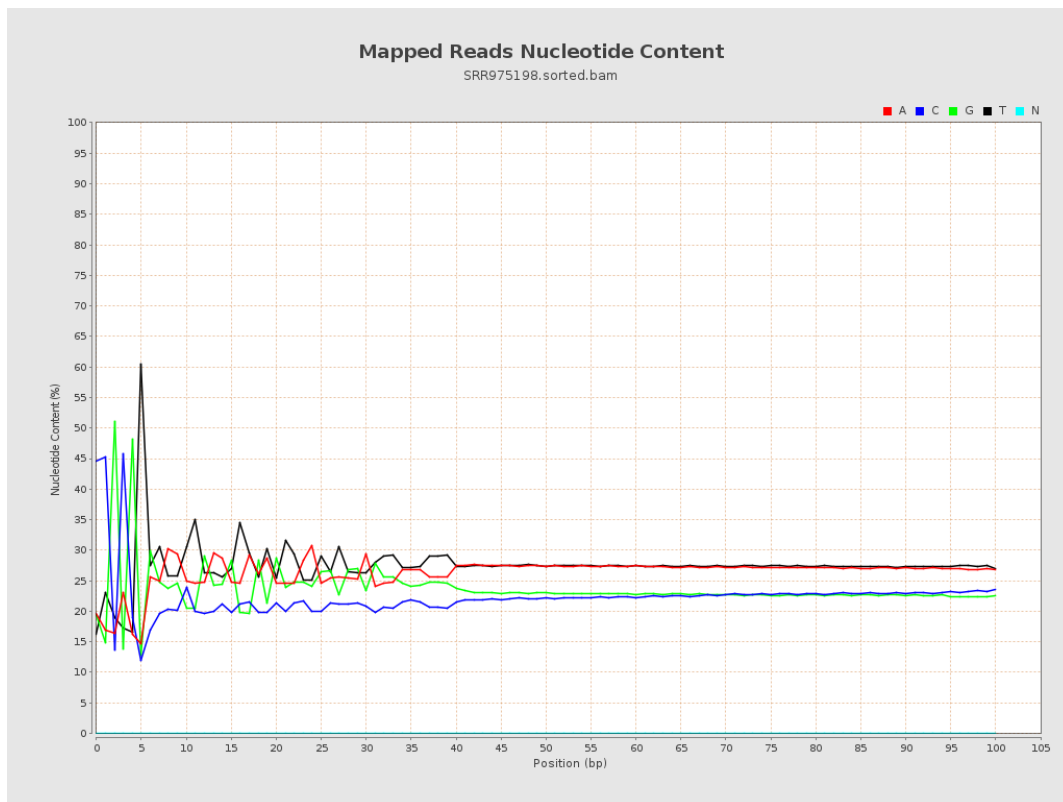
6. Results : Genome Fraction Coverage



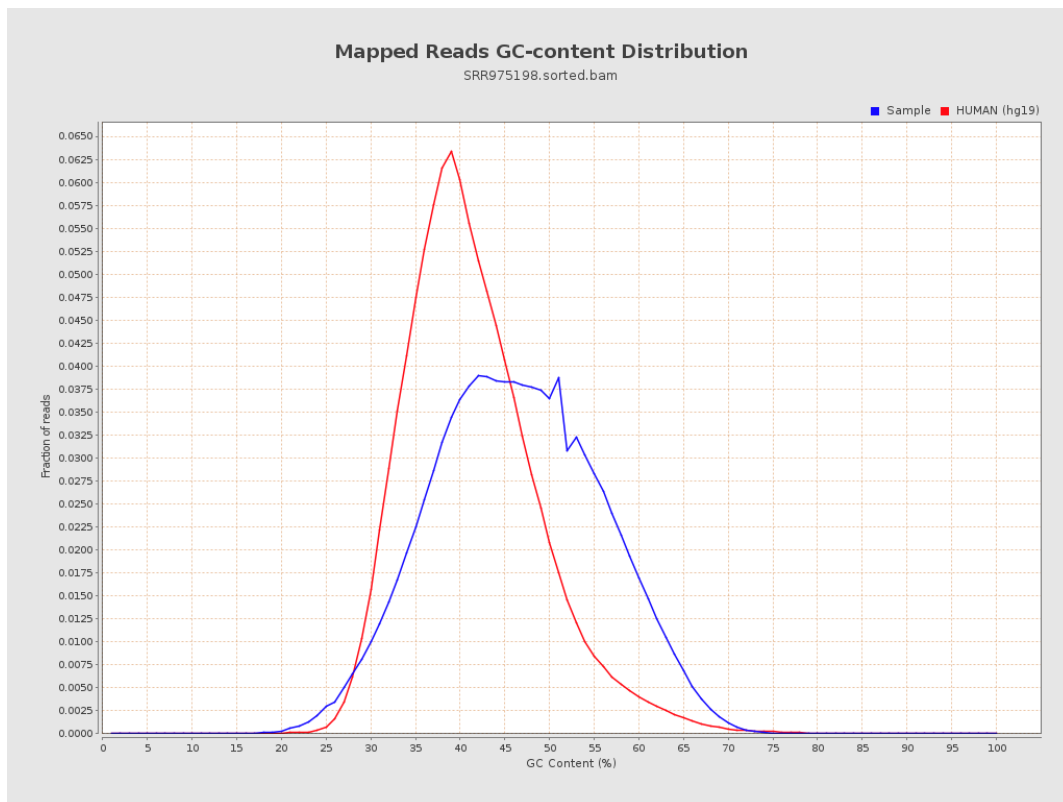
7. Results : Duplication Rate Histogram



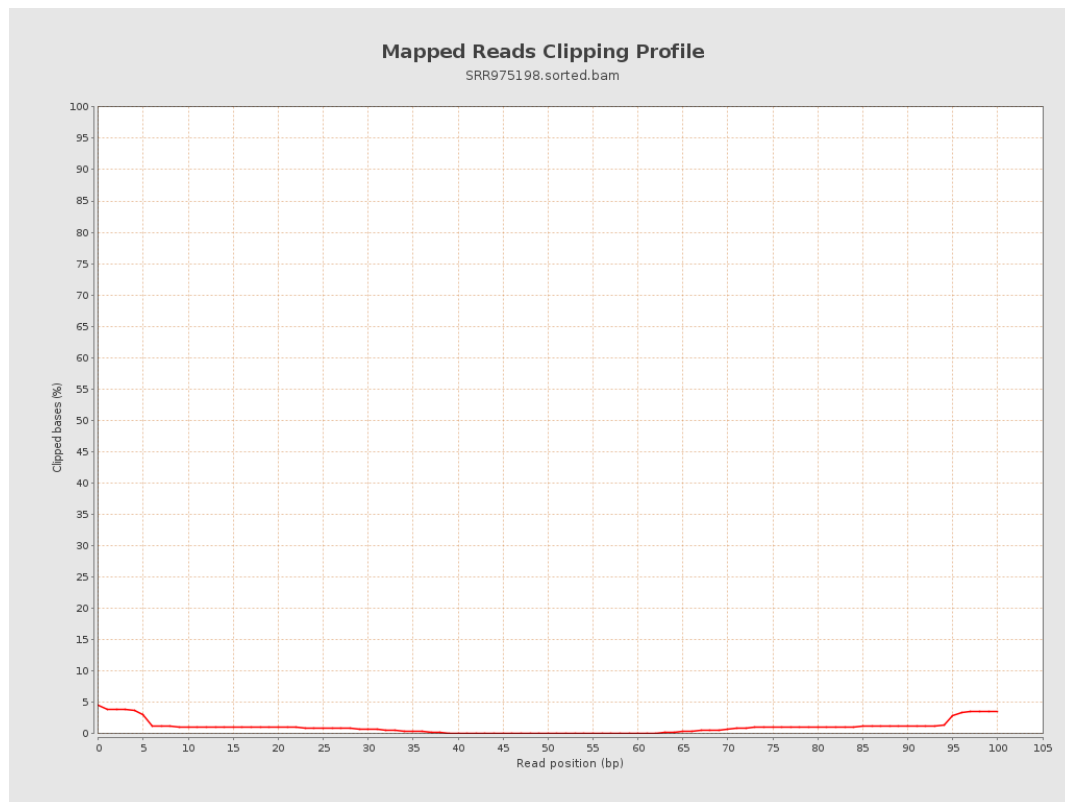
8. Results : Mapped Reads Nucleotide Content



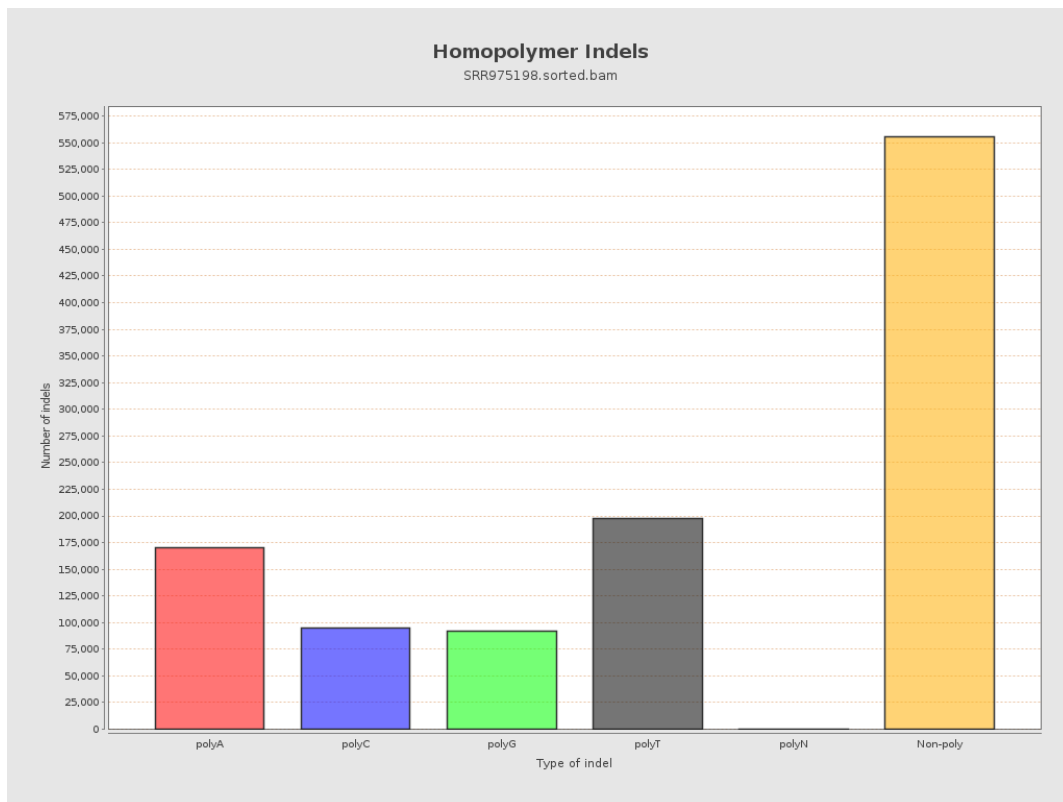
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



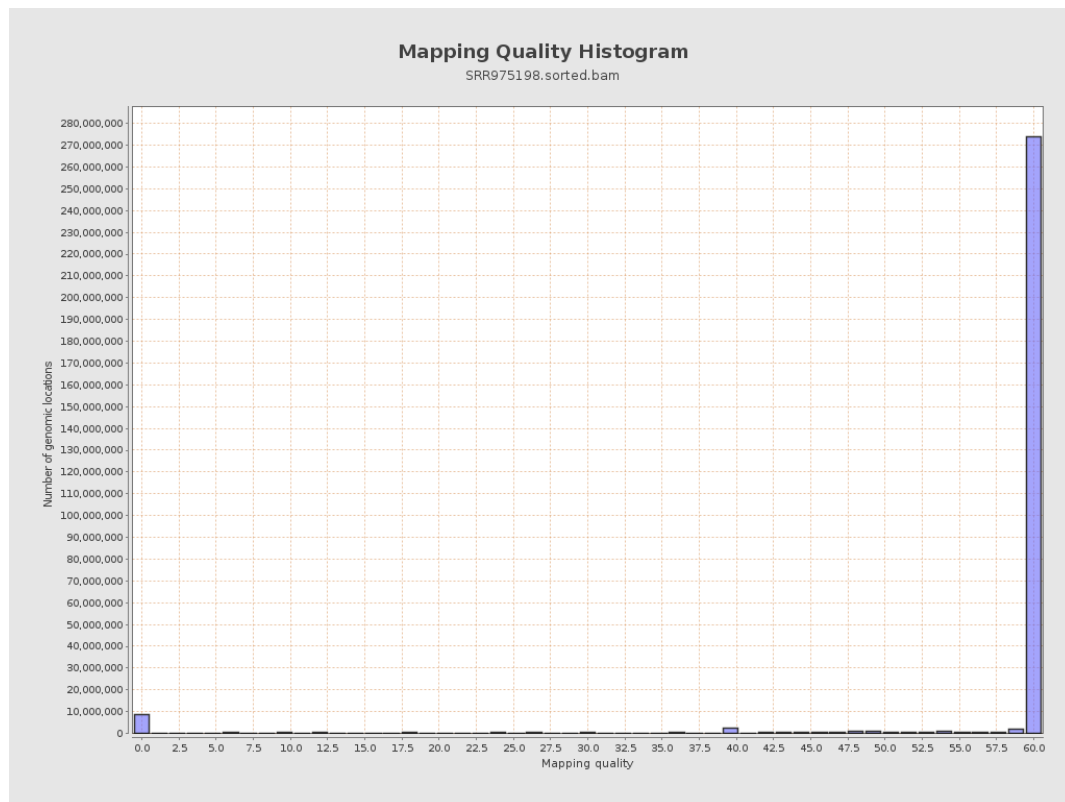
11. Results : Homopolymer Indels



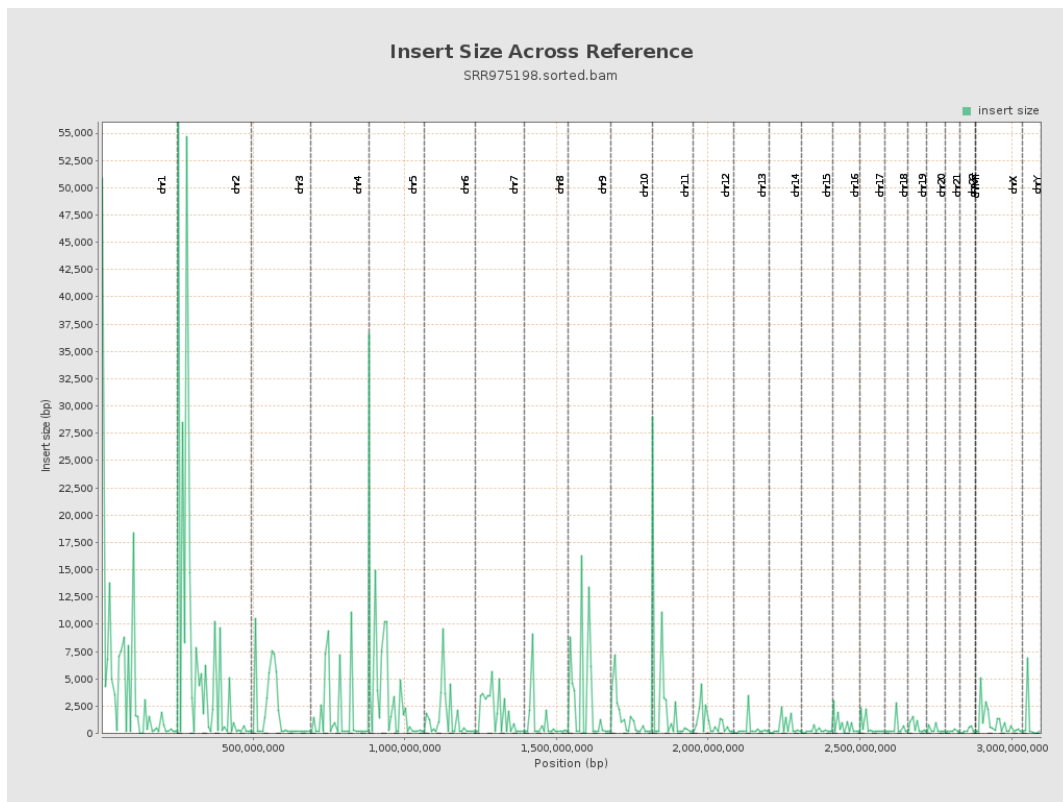
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

