

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/19 16:05:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618626.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_SRR618626 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618626_1.fastq.gz SRR618626_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Jan 19 16:05:08 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618626.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	30,205,806
Mapped reads	28,592,736 / 94.66%
Unmapped reads	1,613,070 / 5.34%
Mapped paired reads	28,592,736 / 94.66%
Mapped reads, first in pair	14,561,525 / 48.21%
Mapped reads, second in pair	14,031,211 / 46.45%
Mapped reads, both in pair	27,719,656 / 91.77%
Mapped reads, singletons	873,080 / 2.89%
Secondary alignments	0
Supplementary alignments	177,798 / 0.59%
Read min/max/mean length	30 / 100 / 100.24
Duplicated reads (estimated)	5,613,806 / 18.59%
Duplication rate	16.87%
Clipped reads	7,612,346 / 25.2%

2.2. ACGT Content

Number/percentage of A's	717,716,630 / 27.01%
Number/percentage of C's	579,815,074 / 21.82%
Number/percentage of T's	729,100,507 / 27.44%
Number/percentage of G's	630,272,228 / 23.72%
Number/percentage of N's	65,937 / 0%

GC Percentage	45.54%
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2.3. Coverage

Mean	0.8589
Standard Deviation	3.6301

2.4. Mapping Quality

Mean Mapping Quality	53.31
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2.5. Insert size

Mean	120,174.34
Standard Deviation	3,432,012.37
P25/Median/P75	191 / 221 / 258

2.6. Mismatches and indels

General error rate	1.32%
Mismatches	34,346,491
Insertions	502,003
Mapped reads with at least one insertion	1.72%
Deletions	1,362,517
Mapped reads with at least one deletion	4.64%
Homopolymer indels	52.57%

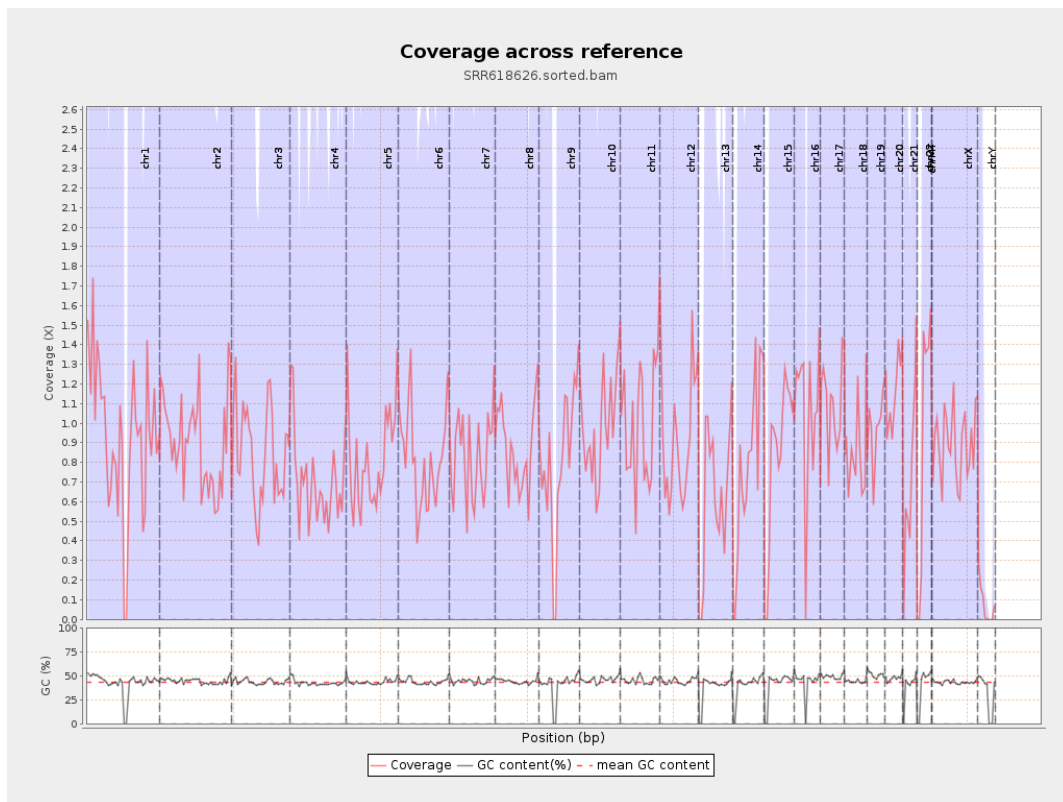
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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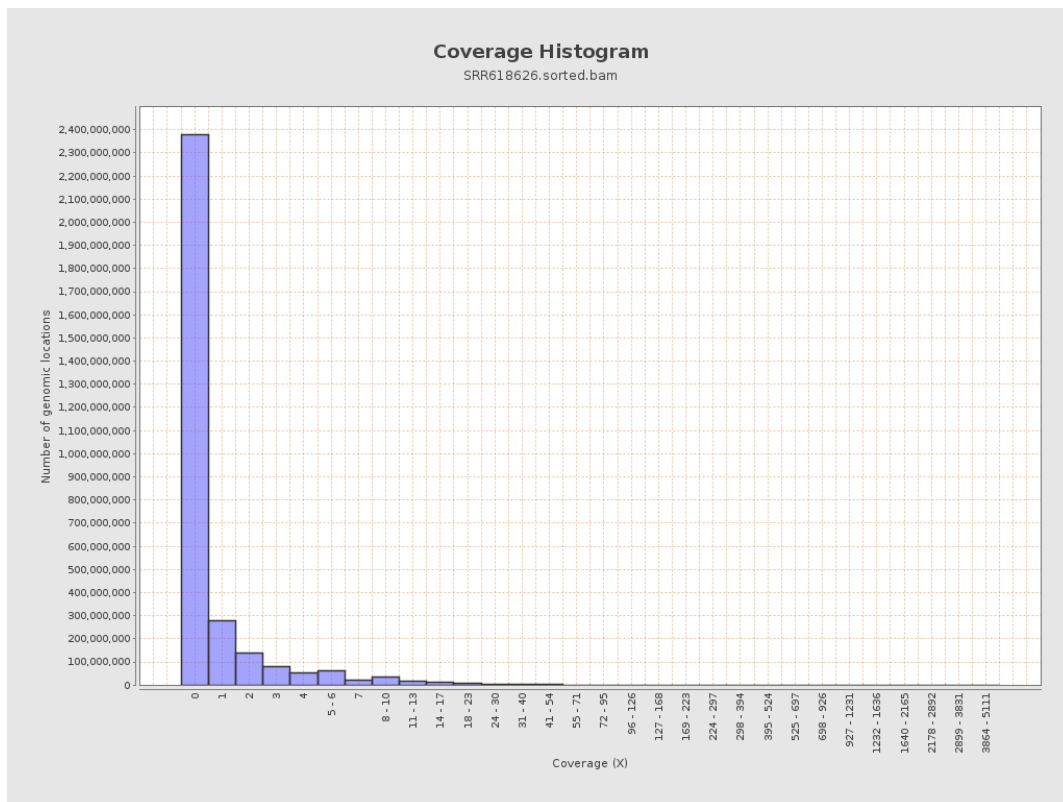
		bases	coverage	deviation
chr1	249250621	232559221	0.933	3.893
chr2	243199373	219800023	0.9038	4.7007
chr3	198022430	168097989	0.8489	2.7385
chr4	191154276	133158547	0.6966	2.8104
chr5	180915260	149468796	0.8262	2.6726
chr6	171115067	140969137	0.8238	2.7757
chr7	159138663	132752036	0.8342	2.7686
chr8	146364022	128481173	0.8778	2.9166
chr9	141213431	114829331	0.8132	3.4723
chr10	135534747	132913605	0.9807	3.3118
chr11	135006516	134841264	0.9988	3.5187
chr12	133851895	122221613	0.9131	3.2494
chr13	115169878	72380727	0.6285	2.3995
chr14	107349540	84268891	0.785	2.9866
chr15	102531392	85112738	0.8301	3.2032
chr16	90354753	94535728	1.0463	9.1835
chr17	81195210	89447448	1.1016	3.6902
chr18	78077248	66648250	0.8536	3.188
chr19	59128983	57593560	0.974	3.7099
chr20	63025520	73091861	1.1597	3.6608
chr21	48129895	35246892	0.7323	4.3272
chr22	51304566	48900622	0.9531	3.6489
chrMT	16571	17195	1.0377	3.4459
chrX	155270560	137195789	0.8836	2.8022

chrY	59373566	4324944	0.0728	3.1072
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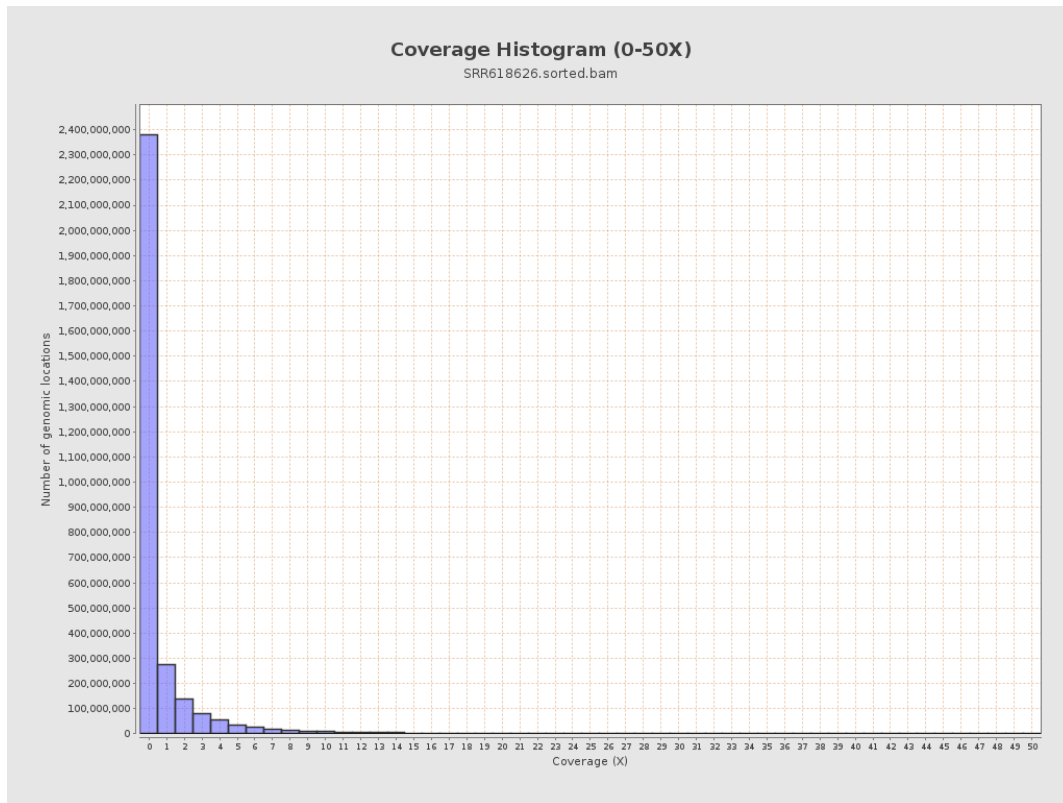
3. Results : Coverage across reference



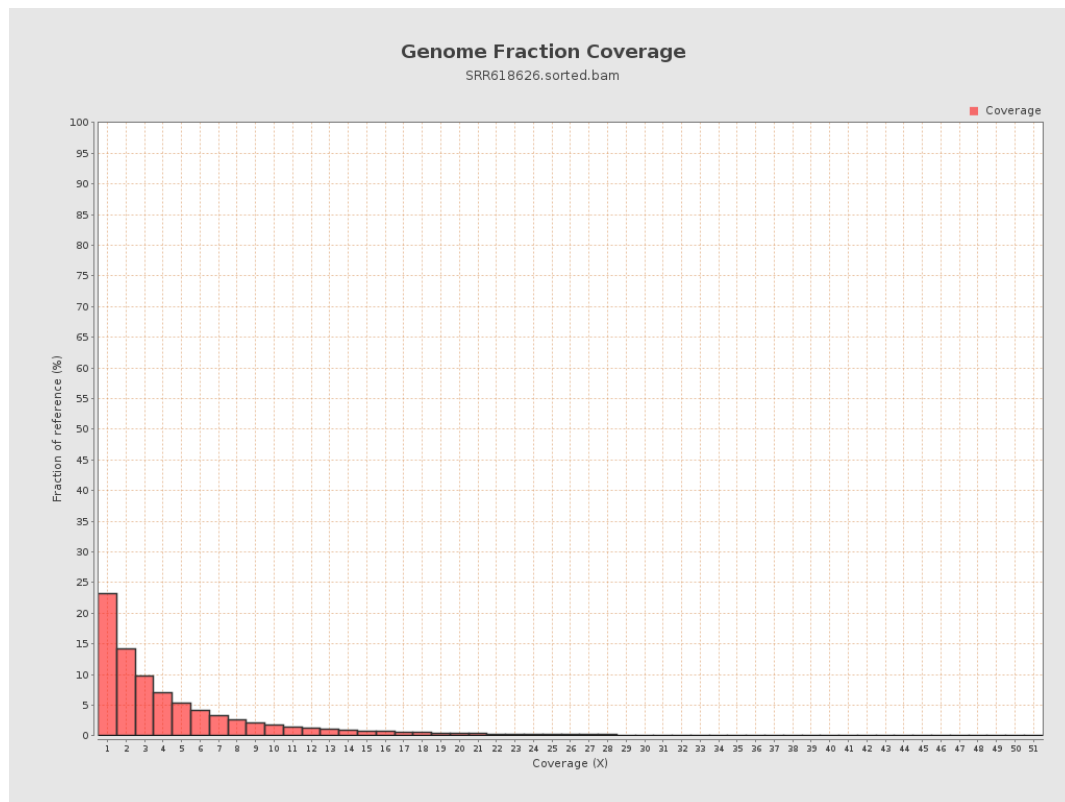
4. Results : Coverage Histogram



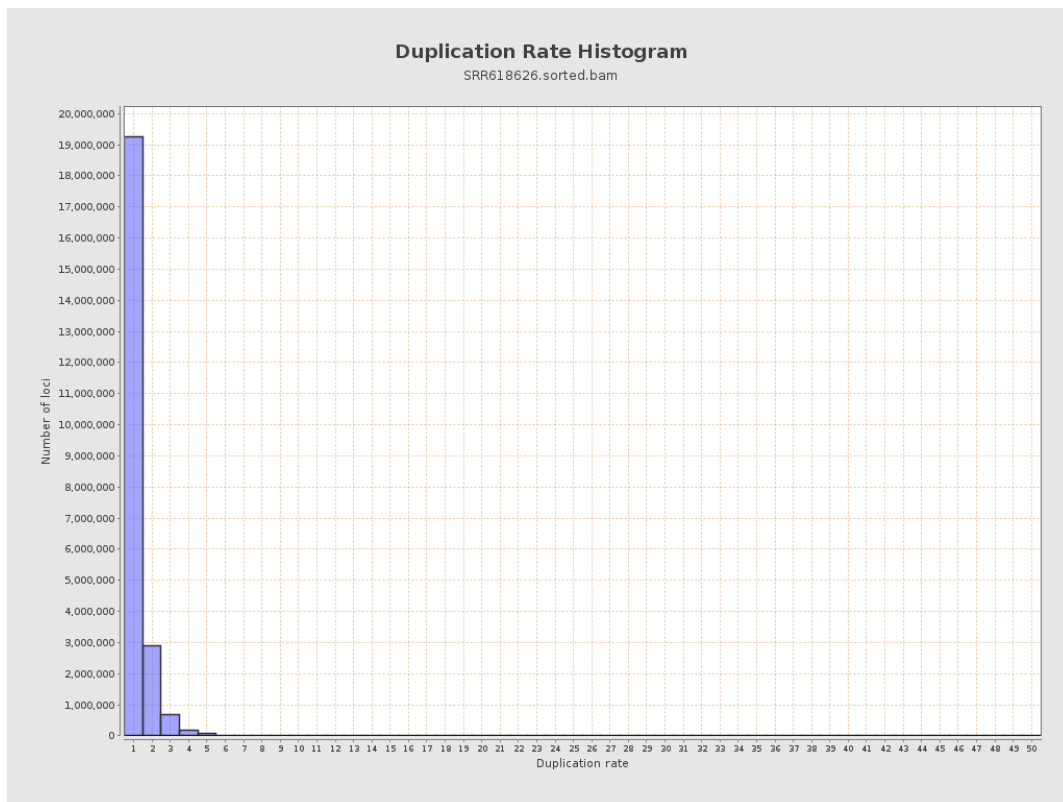
5. Results : Coverage Histogram (0-50X)



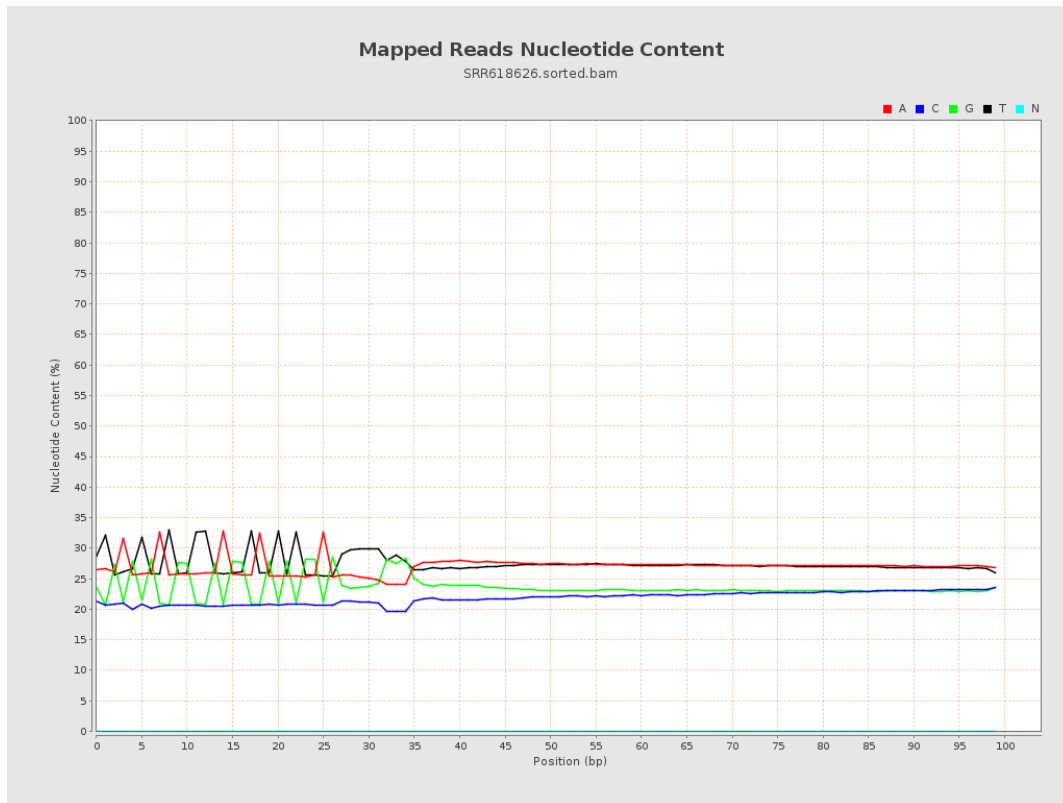
6. Results : Genome Fraction Coverage



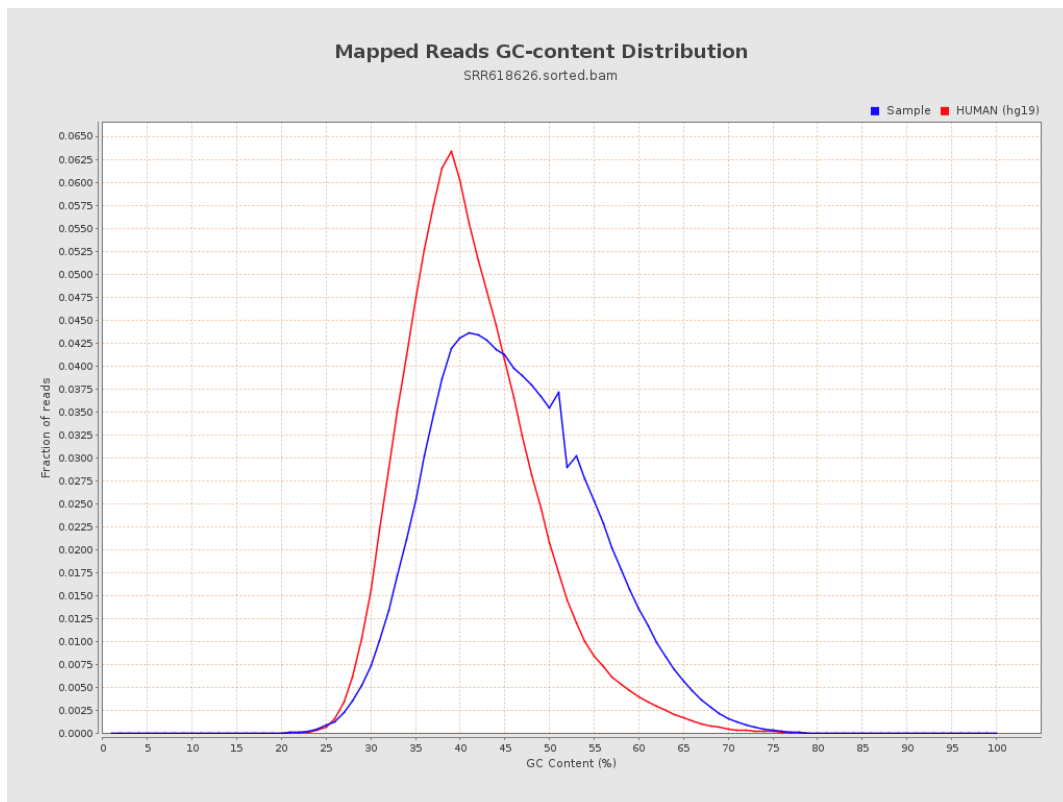
7. Results : Duplication Rate Histogram



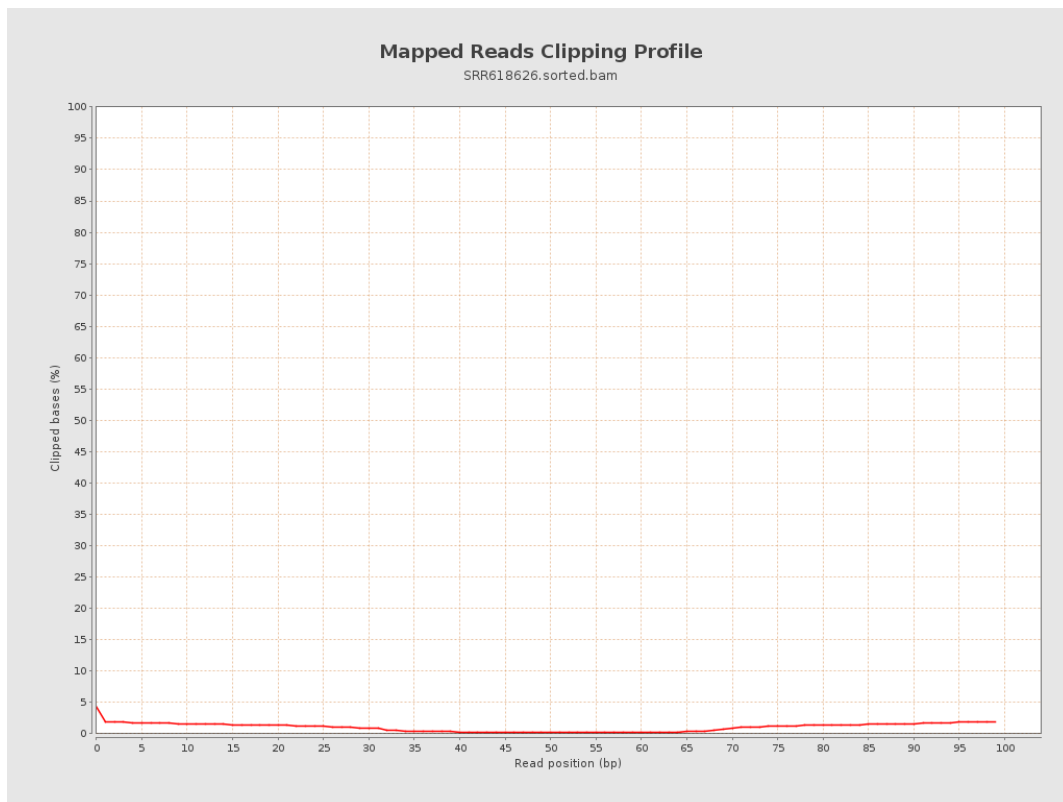
8. Results : Mapped Reads Nucleotide Content



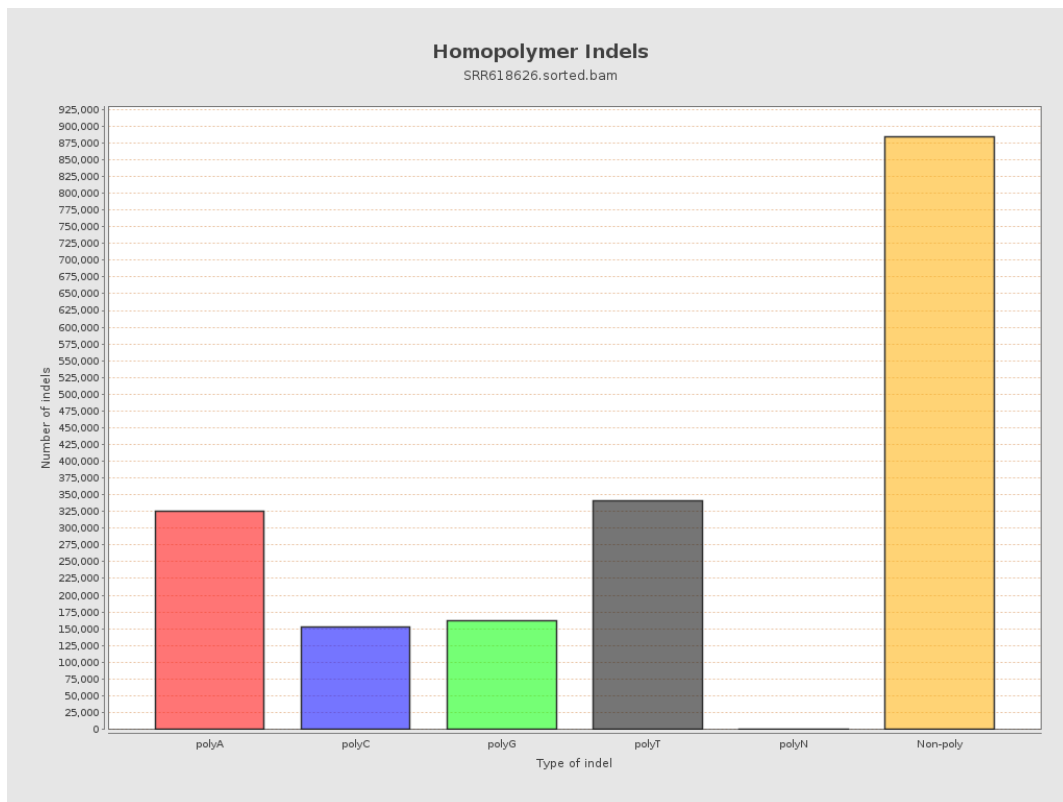
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



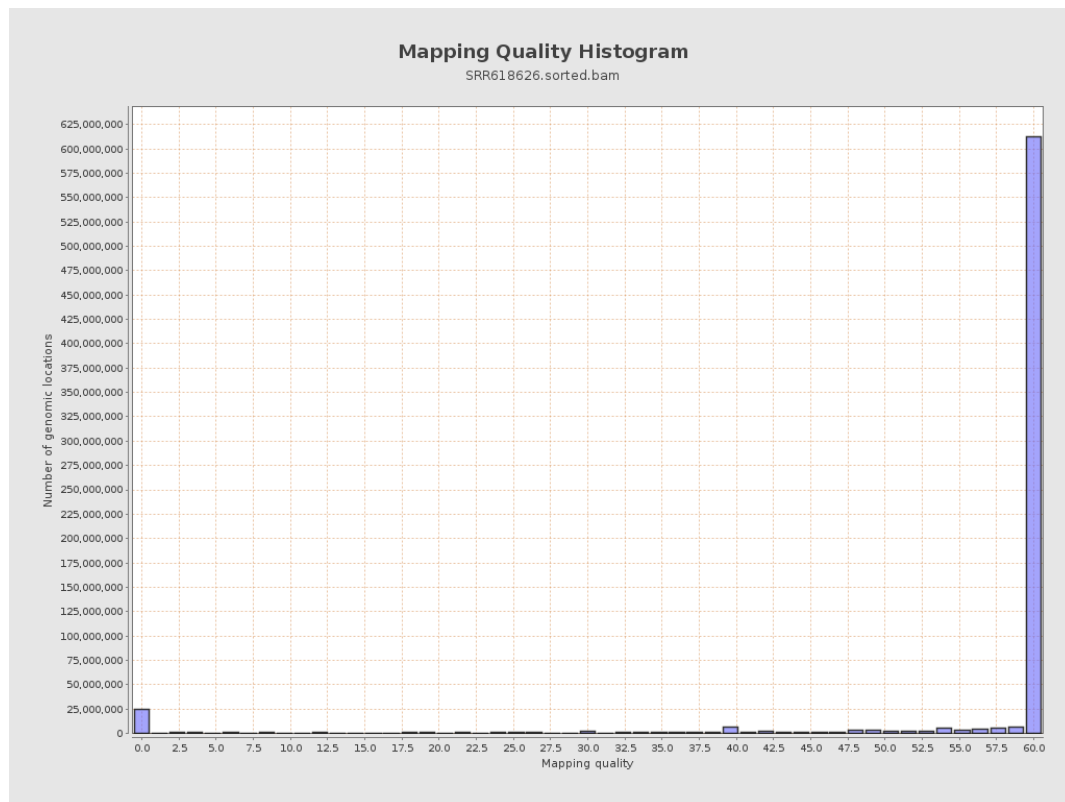
11. Results : Homopolymer Indels



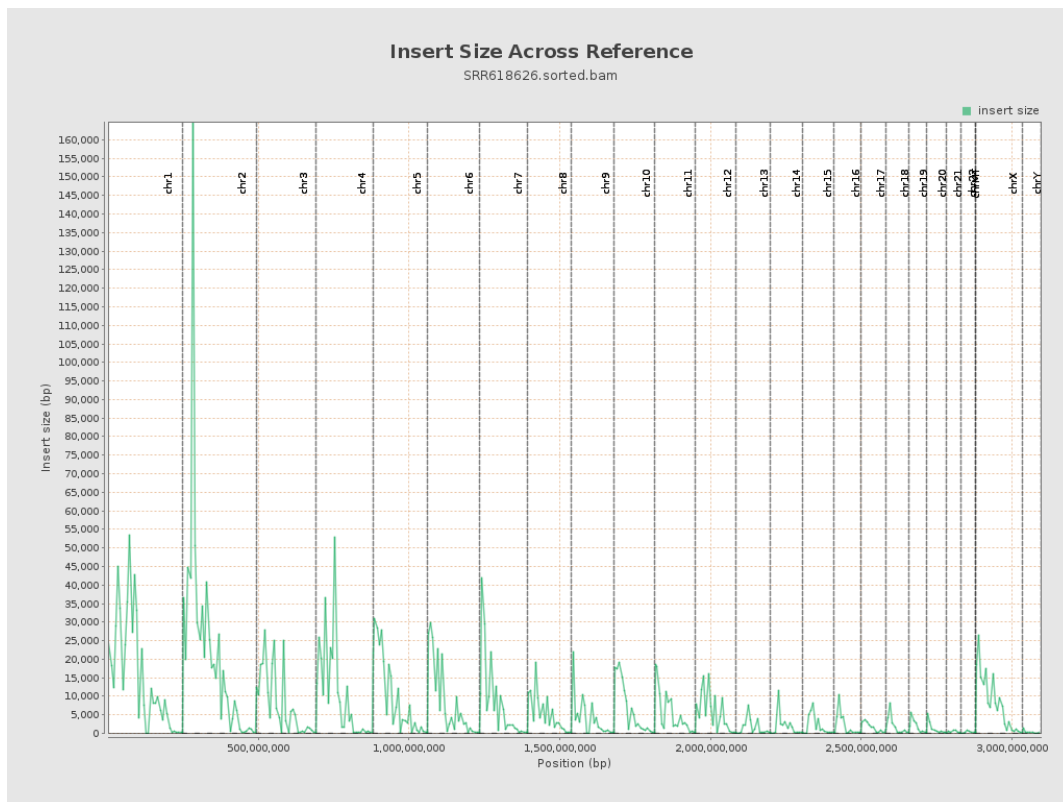
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

