

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/19 22:26:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618636.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_SRR618636 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618636_1.fastq.gz SRR618636_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Jan 19 22:26:21 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618636.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	17,930,890
Mapped reads	16,986,359 / 94.73%
Unmapped reads	944,531 / 5.27%
Mapped paired reads	16,986,359 / 94.73%
Mapped reads, first in pair	8,652,200 / 48.25%
Mapped reads, second in pair	8,334,159 / 46.48%
Mapped reads, both in pair	16,461,232 / 91.8%
Mapped reads, singletons	525,127 / 2.93%
Secondary alignments	0
Supplementary alignments	48,377 / 0.27%
Read min/max/mean length	30 / 100 / 100.11
Duplicated reads (estimated)	5,420,487 / 30.23%
Duplication rate	25.92%
Clipped reads	3,267,791 / 18.22%

2.2. ACGT Content

Number/percentage of A's	442,915,242 / 27.46%
Number/percentage of C's	351,588,619 / 21.79%
Number/percentage of T's	448,267,666 / 27.79%
Number/percentage of G's	370,406,773 / 22.96%
Number/percentage of N's	60,326 / 0%

GC Percentage	44.75%
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2.3. Coverage

Mean	0.5215
Standard Deviation	2.2933

2.4. Mapping Quality

Mean Mapping Quality	53.61
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2.5. Insert size

Mean	83,526.76
Standard Deviation	2,916,064.08
P25/Median/P75	181 / 204 / 233

2.6. Mismatches and indels

General error rate	1.2%
Mismatches	18,877,338
Insertions	294,339
Mapped reads with at least one insertion	1.7%
Deletions	820,639
Mapped reads with at least one deletion	4.71%
Homopolymer indels	53.31%

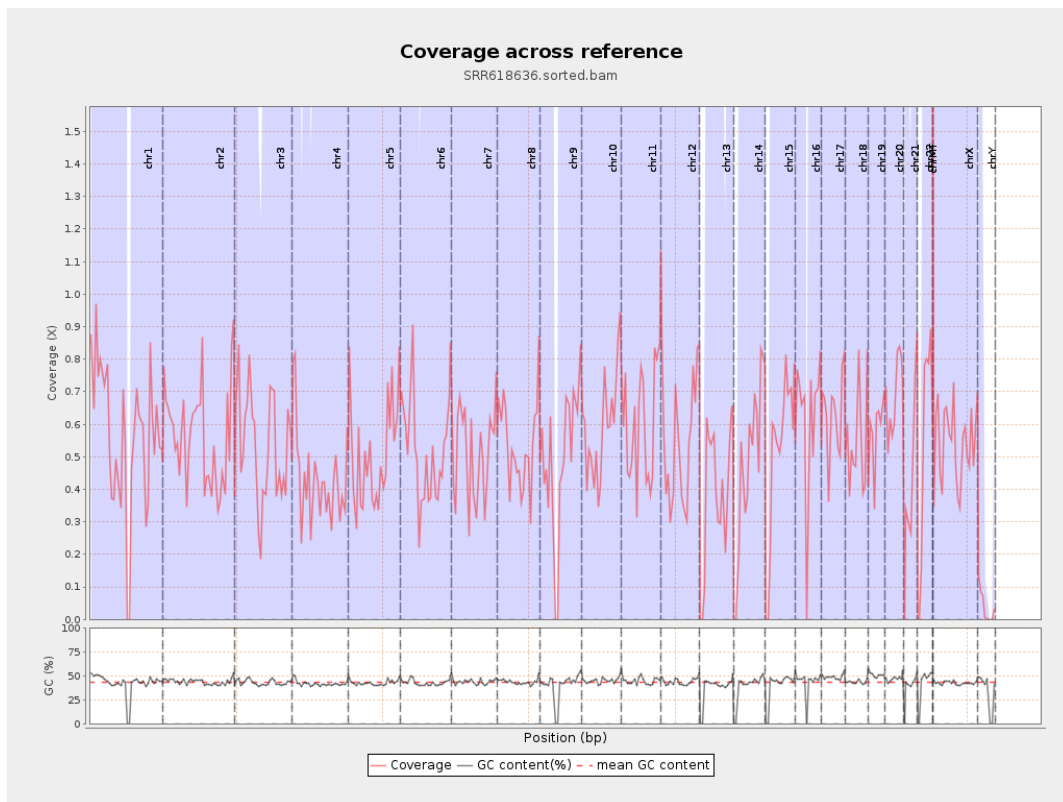
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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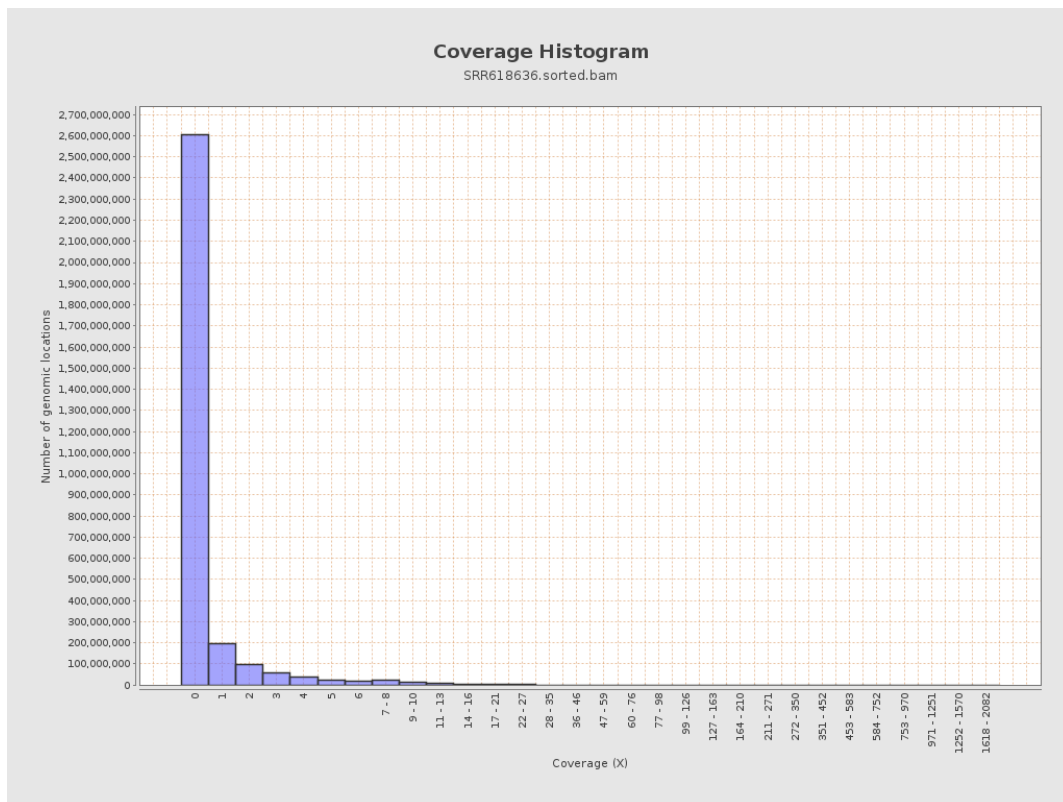
		bases	coverage	deviation
chr1	249250621	140149806	0.5623	2.5675
chr2	243199373	136040993	0.5594	2.7198
chr3	198022430	104850764	0.5295	2.1255
chr4	191154276	81843835	0.4282	1.8368
chr5	180915260	92664494	0.5122	2.0353
chr6	171115067	88380651	0.5165	2.0024
chr7	159138663	81458164	0.5119	2.0685
chr8	146364022	78064159	0.5334	2.2138
chr9	141213431	69443680	0.4918	2.4148
chr10	135534747	79682151	0.5879	2.1625
chr11	135006516	80645299	0.5973	2.5303
chr12	133851895	73226553	0.5471	2.2145
chr13	115169878	44471974	0.3861	1.6563
chr14	107349540	50848104	0.4737	2.017
chr15	102531392	52312392	0.5102	2.1051
chr16	90354753	54860169	0.6072	3.9344
chr17	81195210	50846102	0.6262	2.3087
chr18	78077248	41955344	0.5374	2.401
chr19	59128983	34200340	0.5784	2.3439
chr20	63025520	43233517	0.686	2.4869
chr21	48129895	21231775	0.4411	2.3043
chr22	51304566	27642079	0.5388	2.3123
chrMT	16571	28807	1.7384	6.6238
chrX	155270560	84066611	0.5414	2.0194

chrY	59373566	2215553	0.0373	1.2704
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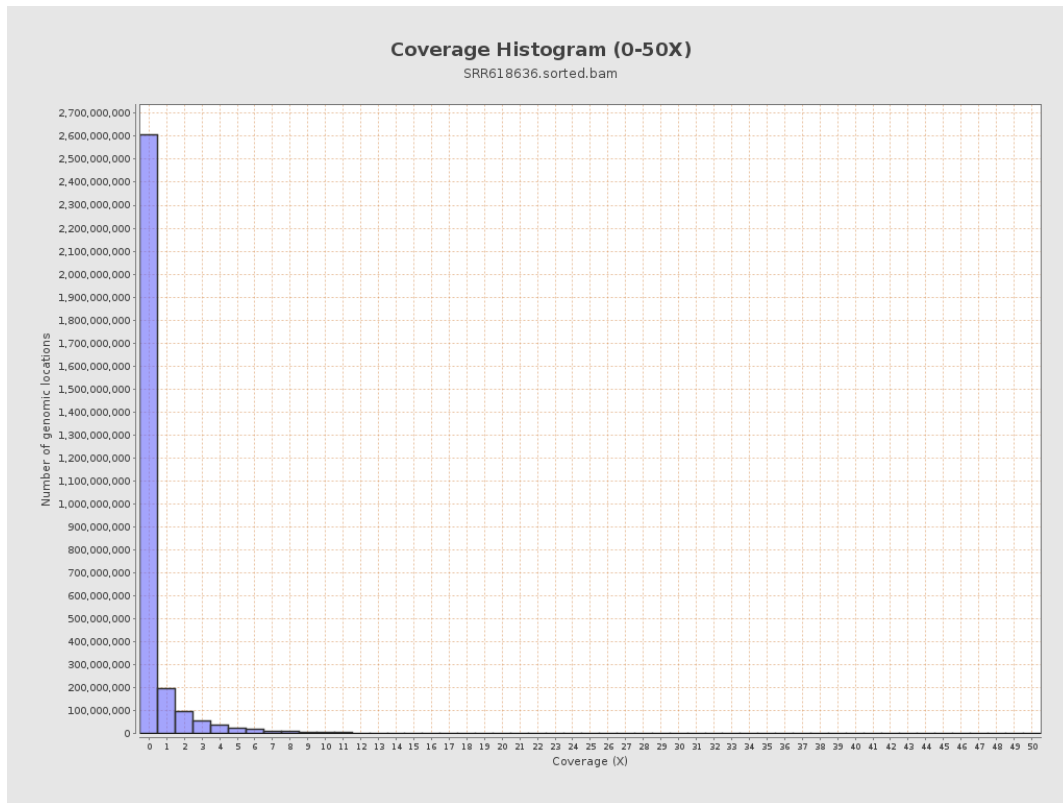
3. Results : Coverage across reference



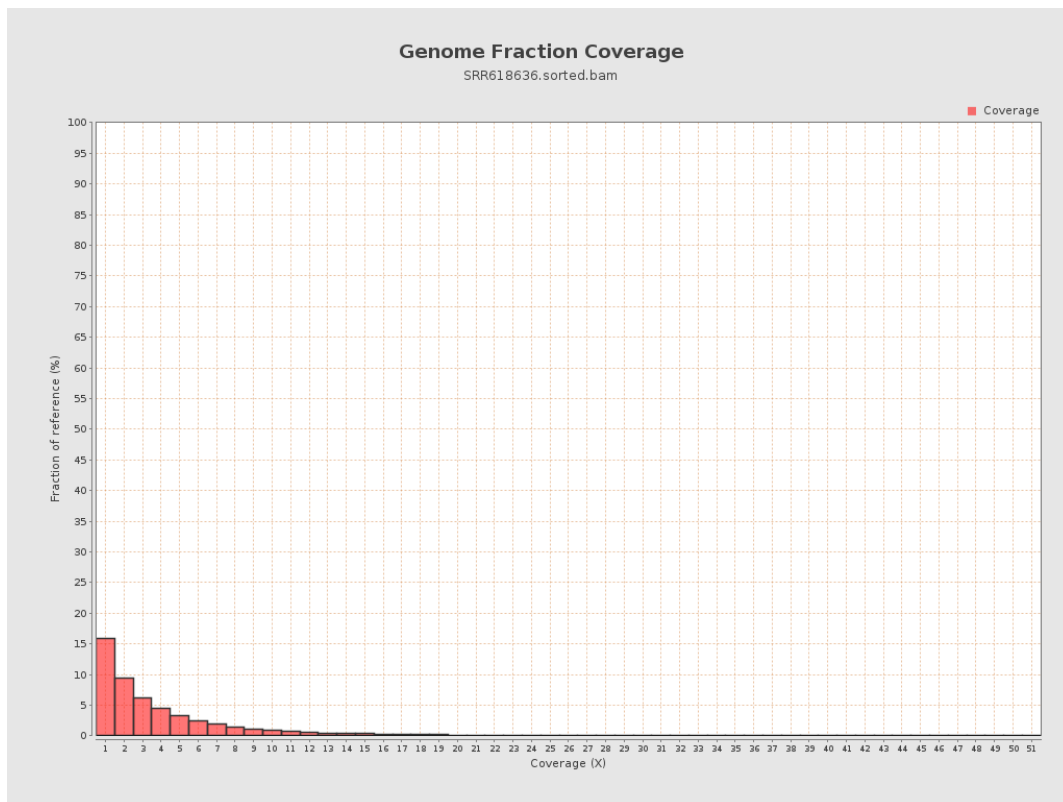
4. Results : Coverage Histogram



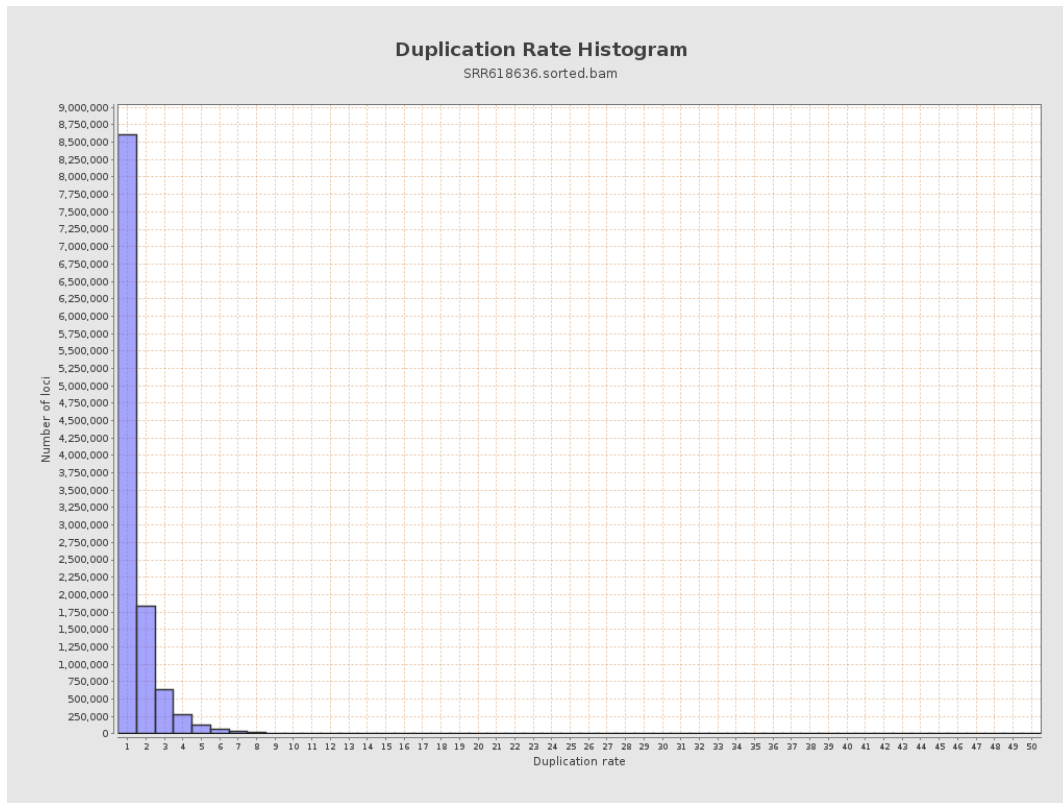
5. Results : Coverage Histogram (0-50X)



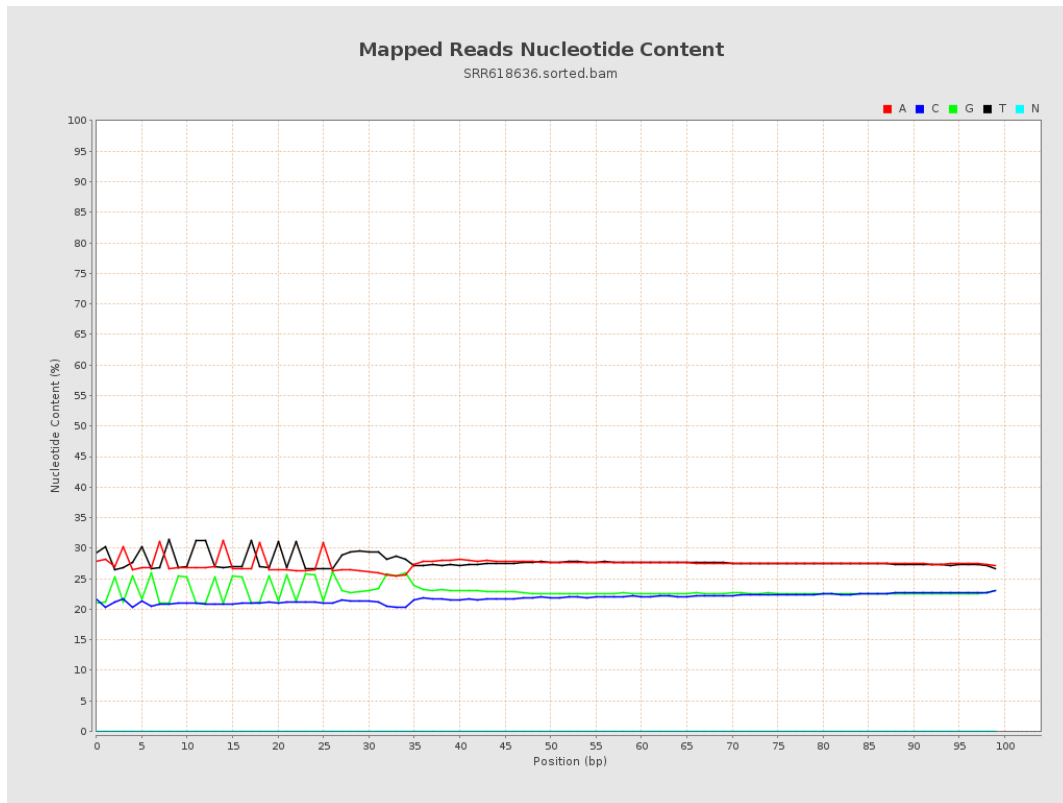
6. Results : Genome Fraction Coverage



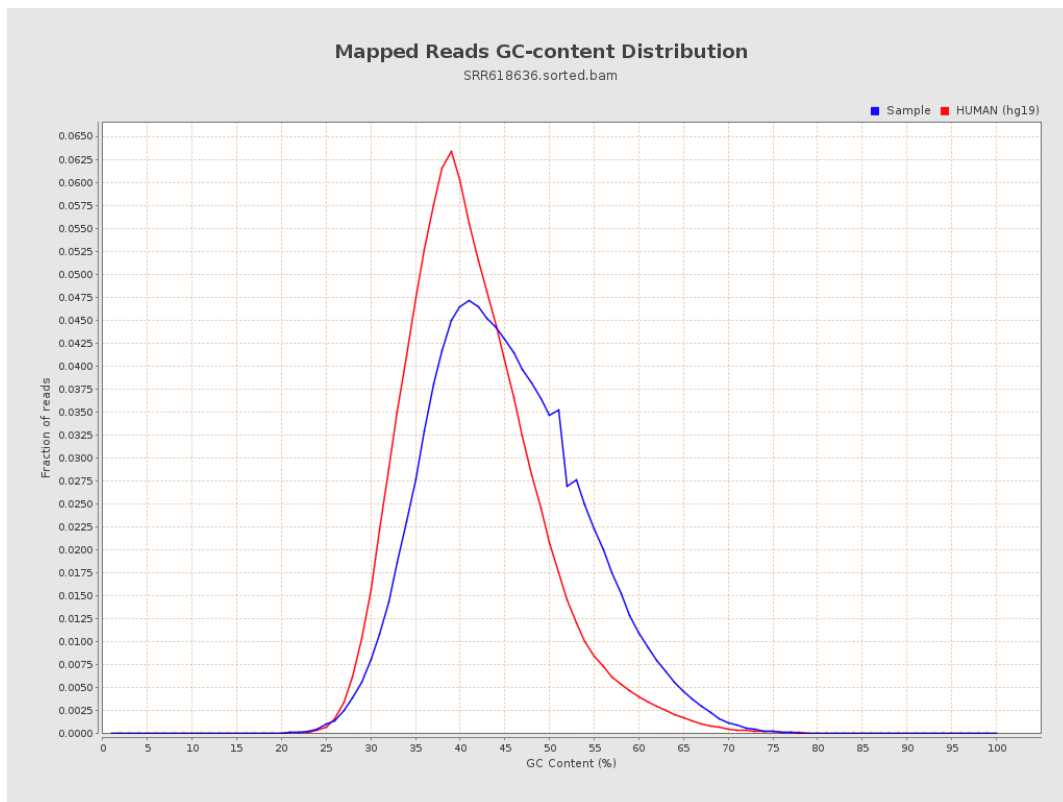
7. Results : Duplication Rate Histogram



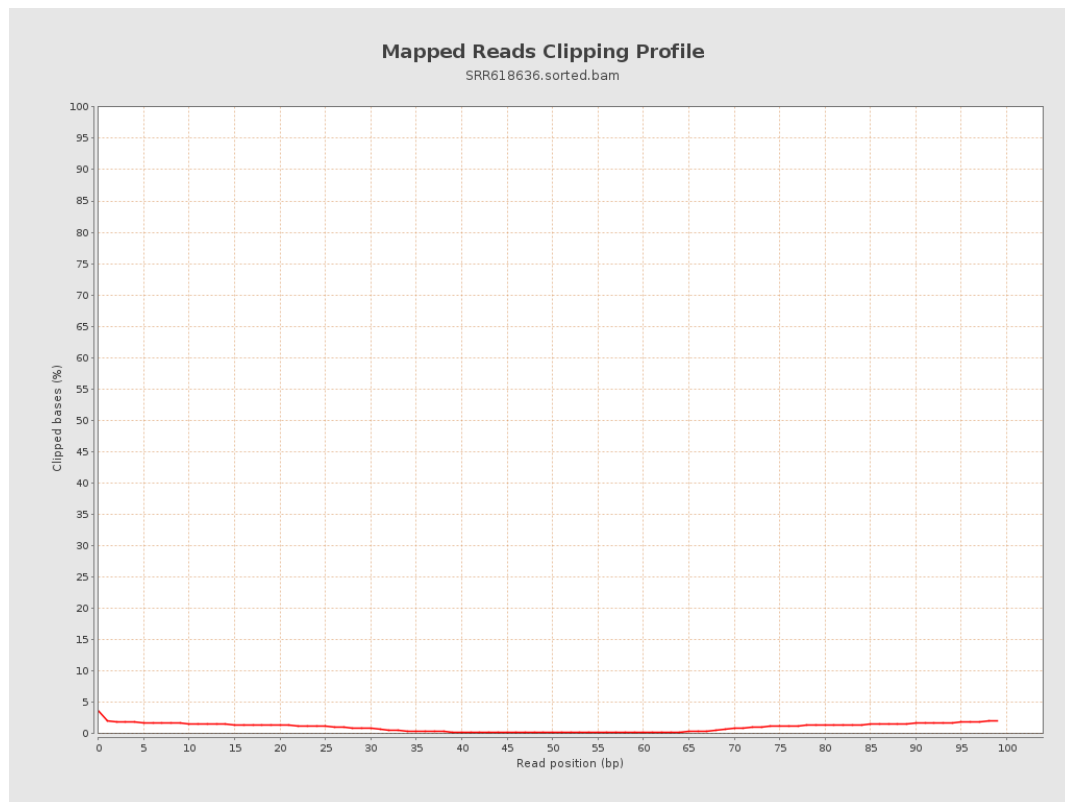
8. Results : Mapped Reads Nucleotide Content



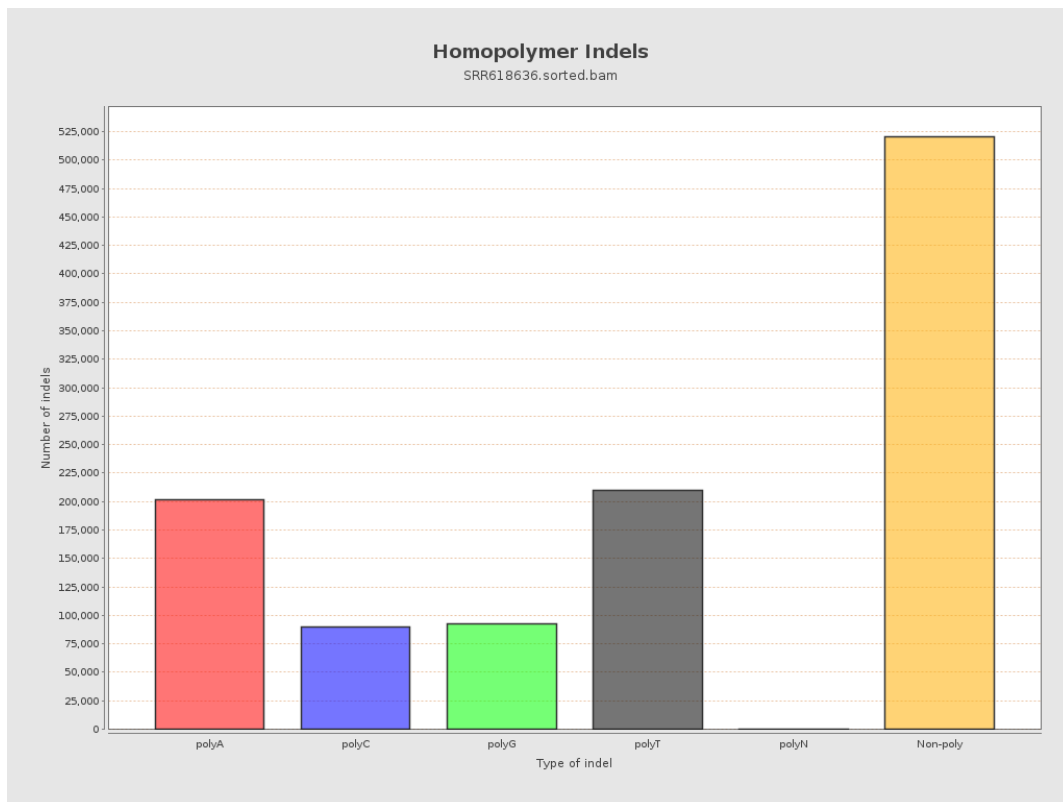
9. Results : Mapped Reads GC-content Distribution



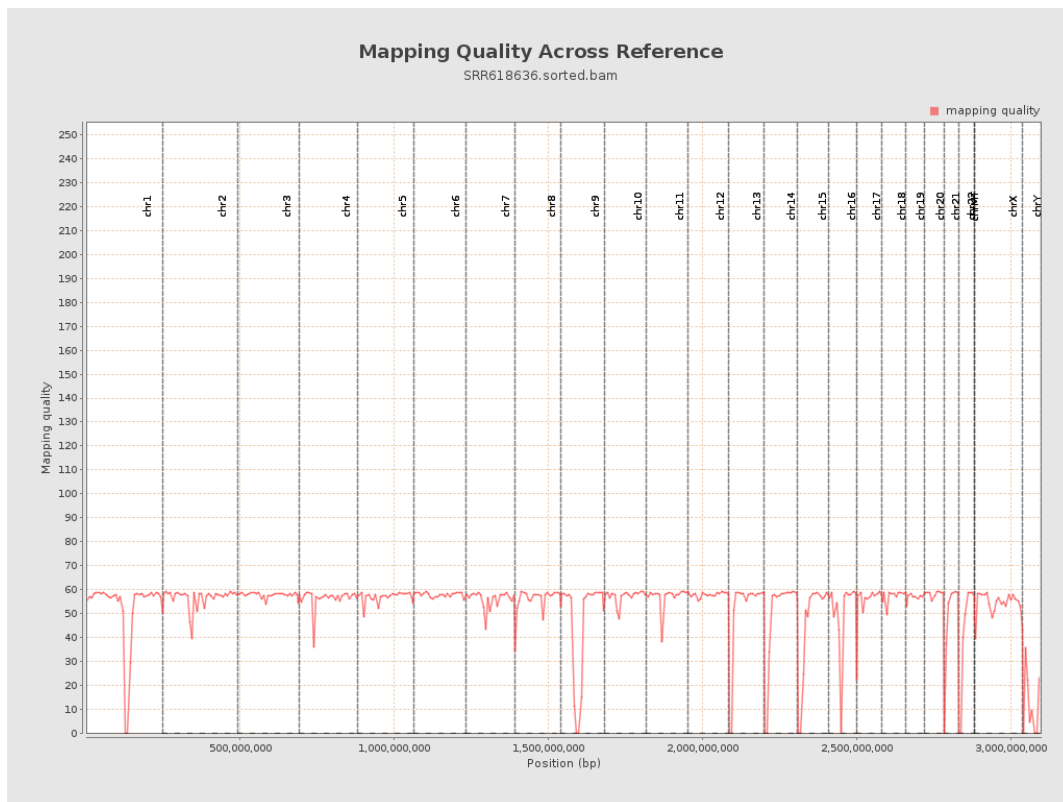
10. Results : Mapped Reads Clipping Profile



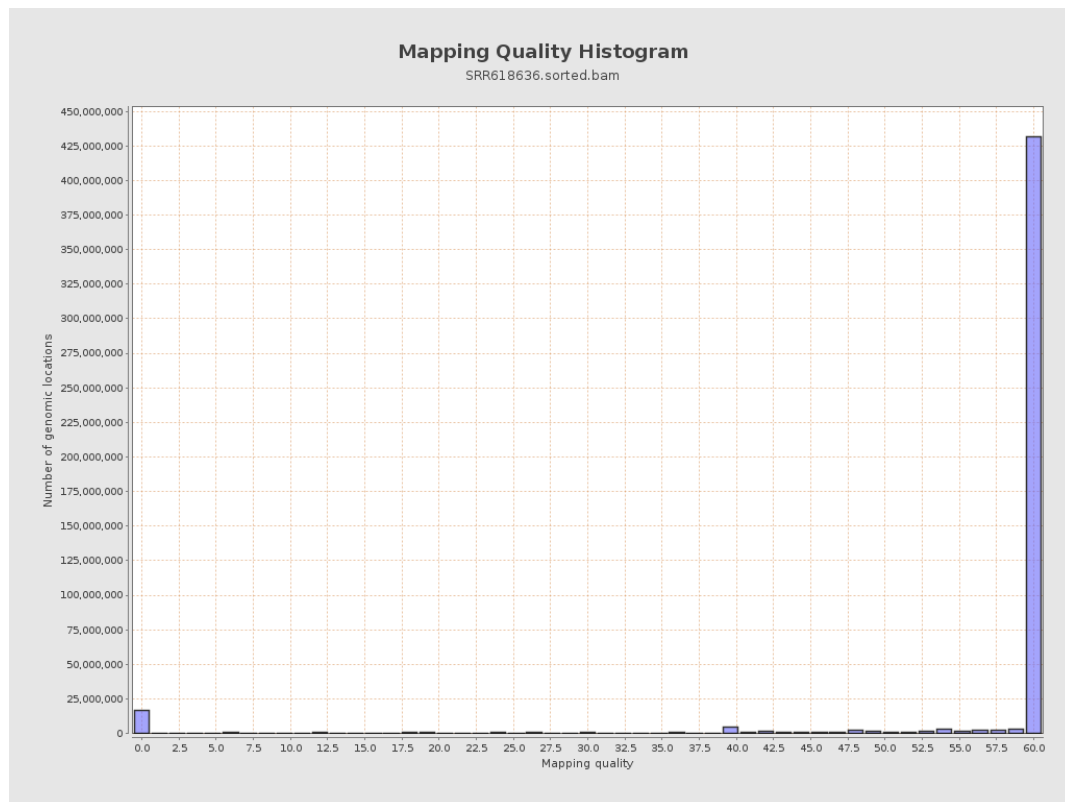
11. Results : Homopolymer Indels



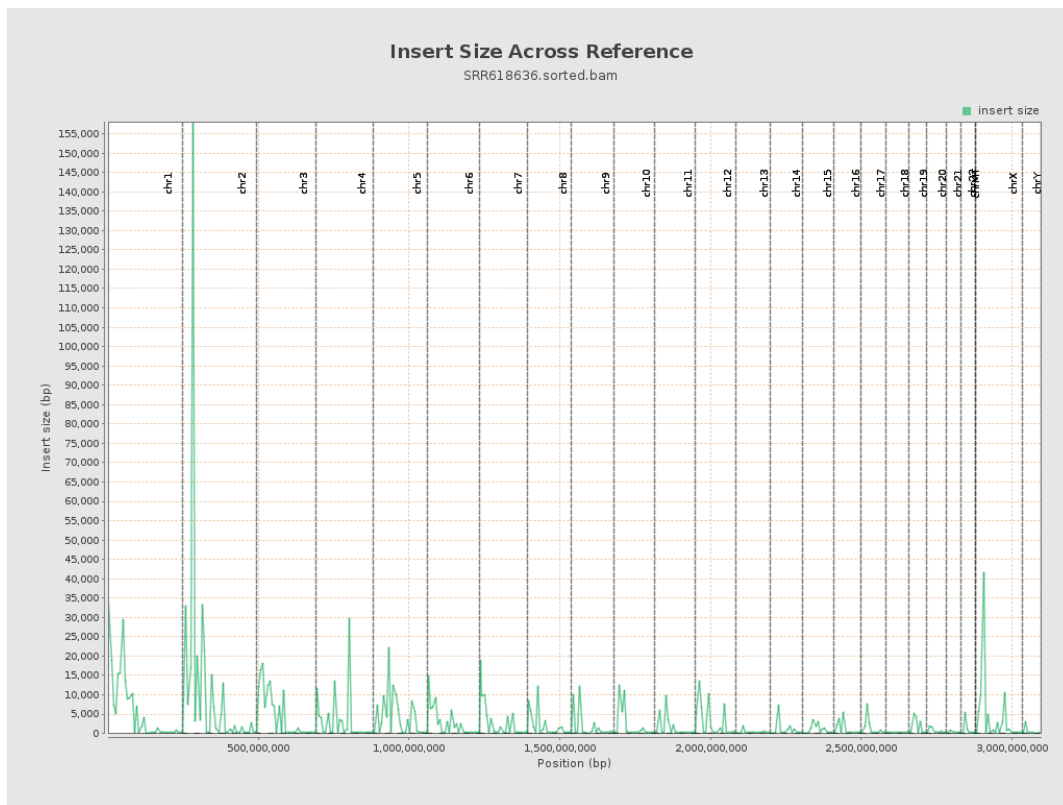
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

