

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/17 23:20:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618575.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_SRR618575 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618575_1.fastq.gz SRR618575_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Jan 17 23:20:10 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618575.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	59,683,086
Mapped reads	57,711,914 / 96.7%
Unmapped reads	1,971,172 / 3.3%
Mapped paired reads	57,711,914 / 96.7%
Mapped reads, first in pair	29,110,037 / 48.77%
Mapped reads, second in pair	28,601,877 / 47.92%
Mapped reads, both in pair	56,725,008 / 95.04%
Mapped reads, singletons	986,906 / 1.65%
Secondary alignments	0
Supplementary alignments	73,726 / 0.12%
Read min/max/mean length	30 / 100 / 100.05
Duplicated reads (estimated)	12,085,375 / 20.25%
Duplication rate	18.65%
Clipped reads	9,619,796 / 16.12%

2.2. ACGT Content

Number/percentage of A's	1,480,973,164 / 26.78%
Number/percentage of C's	1,259,991,681 / 22.79%
Number/percentage of T's	1,485,530,240 / 26.86%
Number/percentage of G's	1,302,894,566 / 23.56%
Number/percentage of N's	229,021 / 0%

GC Percentage	46.35%
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2.3. Coverage

Mean	1.7874
Standard Deviation	7.7386

2.4. Mapping Quality

Mean Mapping Quality	54.02
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2.5. Insert size

Mean	23,352.58
Standard Deviation	1,501,967.42
P25/Median/P75	180 / 209 / 248

2.6. Mismatches and indels

General error rate	1.3%
Mismatches	70,154,562
Insertions	982,696
Mapped reads with at least one insertion	1.67%
Deletions	2,545,246
Mapped reads with at least one deletion	4.31%
Homopolymer indels	52.13%

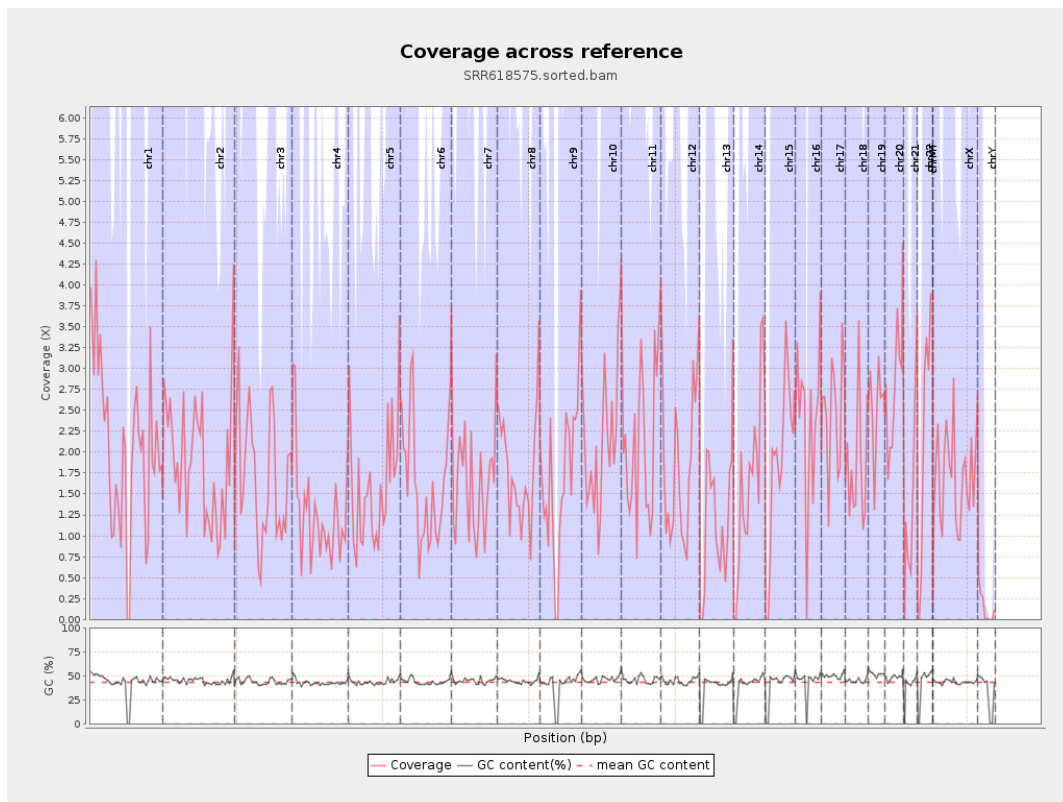
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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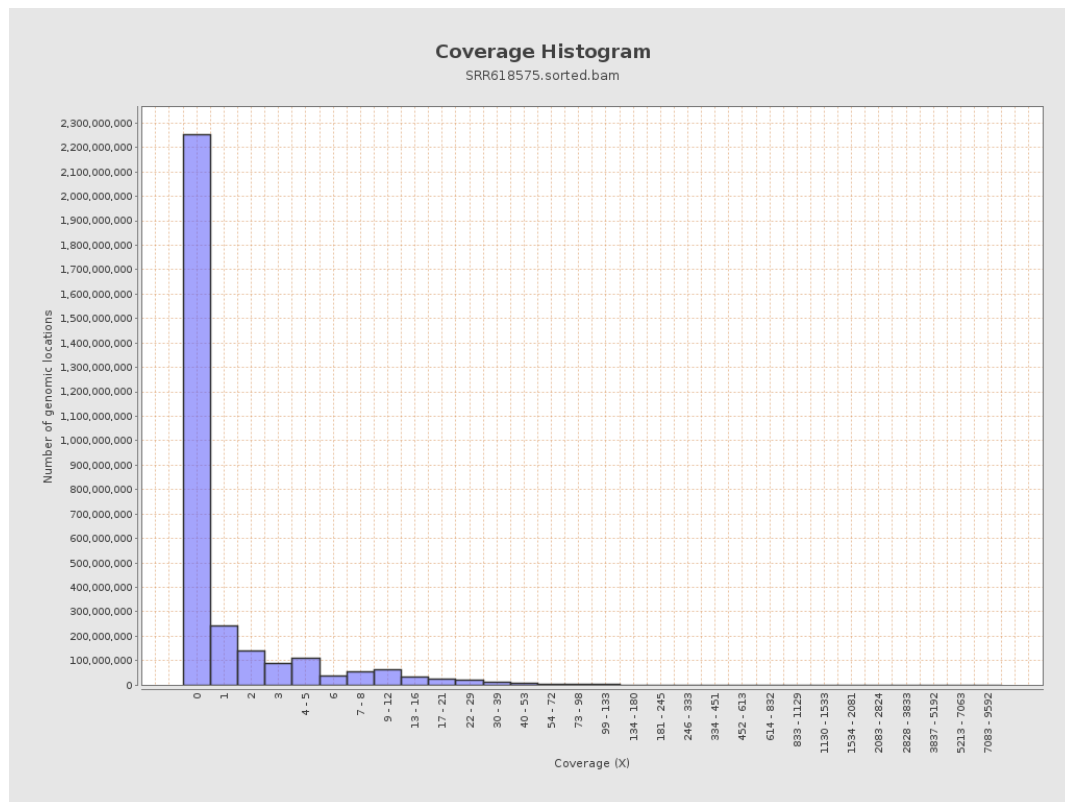
		bases	coverage	deviation
chr1	249250621	509360003	2.0436	8.3666
chr2	243199373	457500376	1.8812	9.2517
chr3	198022430	333871996	1.686	5.999
chr4	191154276	241025162	1.2609	5.5434
chr5	180915260	292483670	1.6167	5.7745
chr6	171115067	276563259	1.6162	5.9889
chr7	159138663	265353381	1.6674	6.0353
chr8	146364022	260768518	1.7816	6.3092
chr9	141213431	239120230	1.6933	7.2768
chr10	135534747	283576487	2.0923	7.342
chr11	135006516	288702800	2.1384	7.9122
chr12	133851895	248164106	1.854	6.9348
chr13	115169878	131265523	1.1398	4.7822
chr14	107349540	176025403	1.6397	6.4925
chr15	102531392	193504523	1.8873	7.1842
chr16	90354753	213521638	2.3631	18.0929
chr17	81195210	200847154	2.4736	8.8625
chr18	78077248	140487504	1.7993	7.2786
chr19	59128983	148470777	2.511	9.5626
chr20	63025520	171871850	2.727	9.2476
chr21	48129895	70876223	1.4726	10.0758
chr22	51304566	114246407	2.2268	8.8853
chrMT	16571	2558	0.1544	0.7128
chrX	155270560	267464633	1.7226	6.0457

chrY	59373566	8072326	0.136	6.0964
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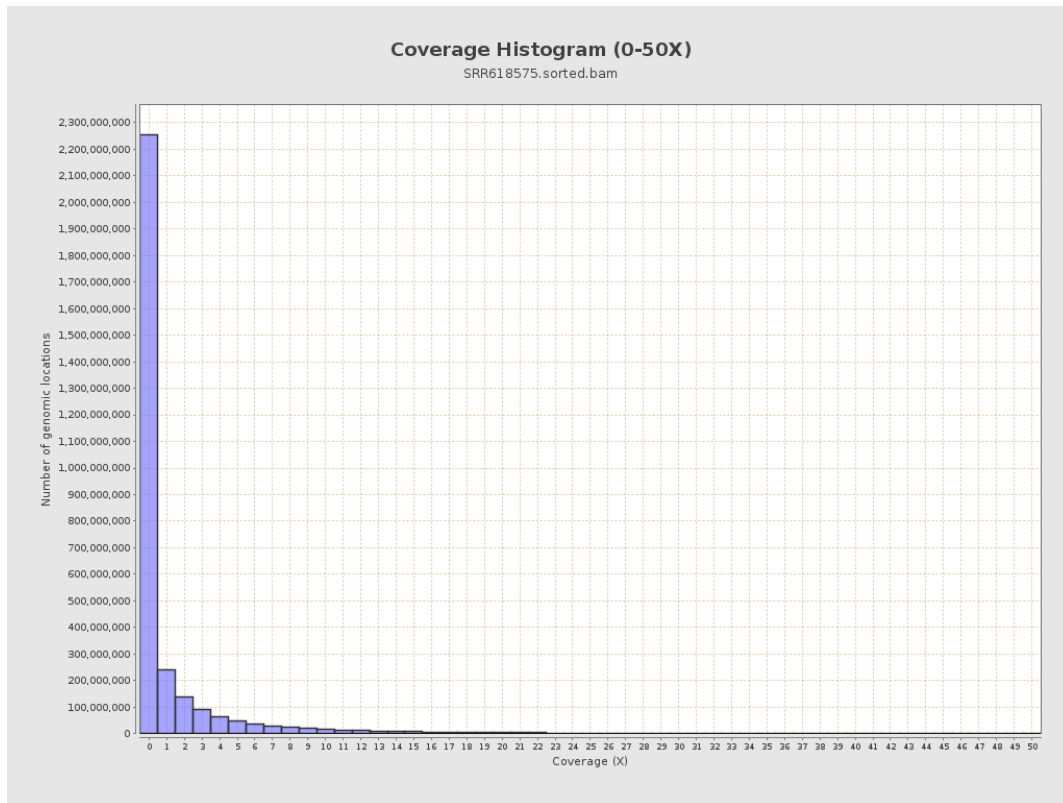
3. Results : Coverage across reference



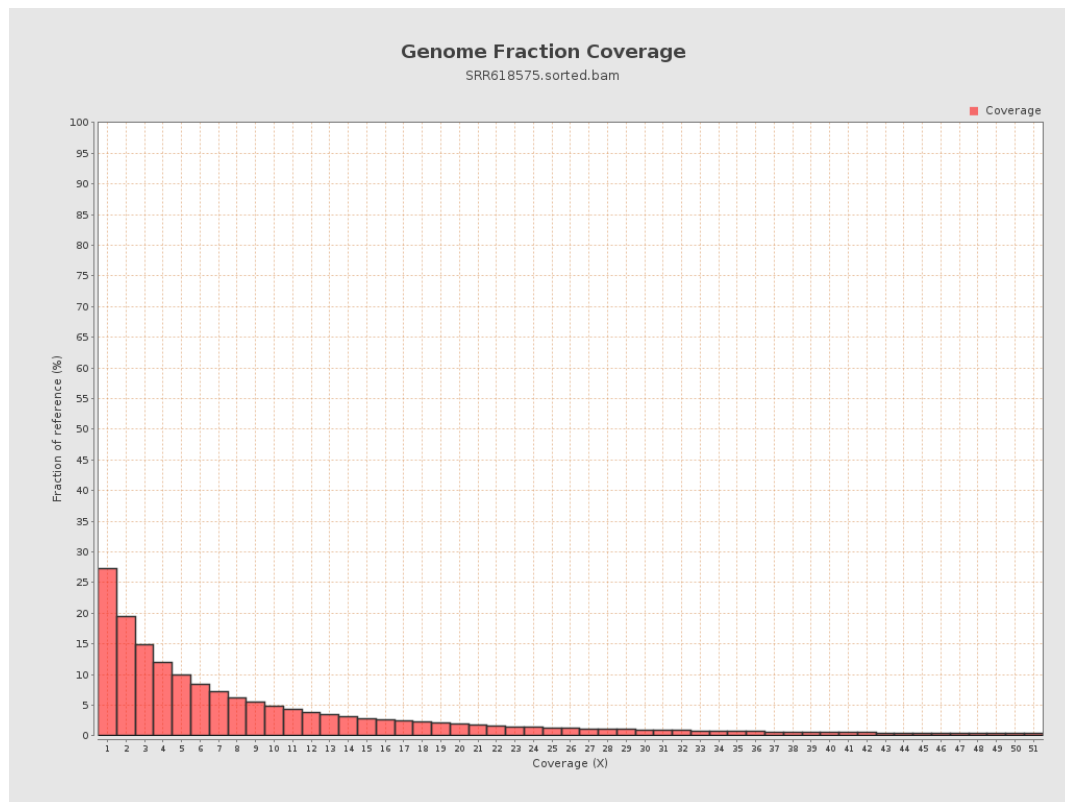
4. Results : Coverage Histogram



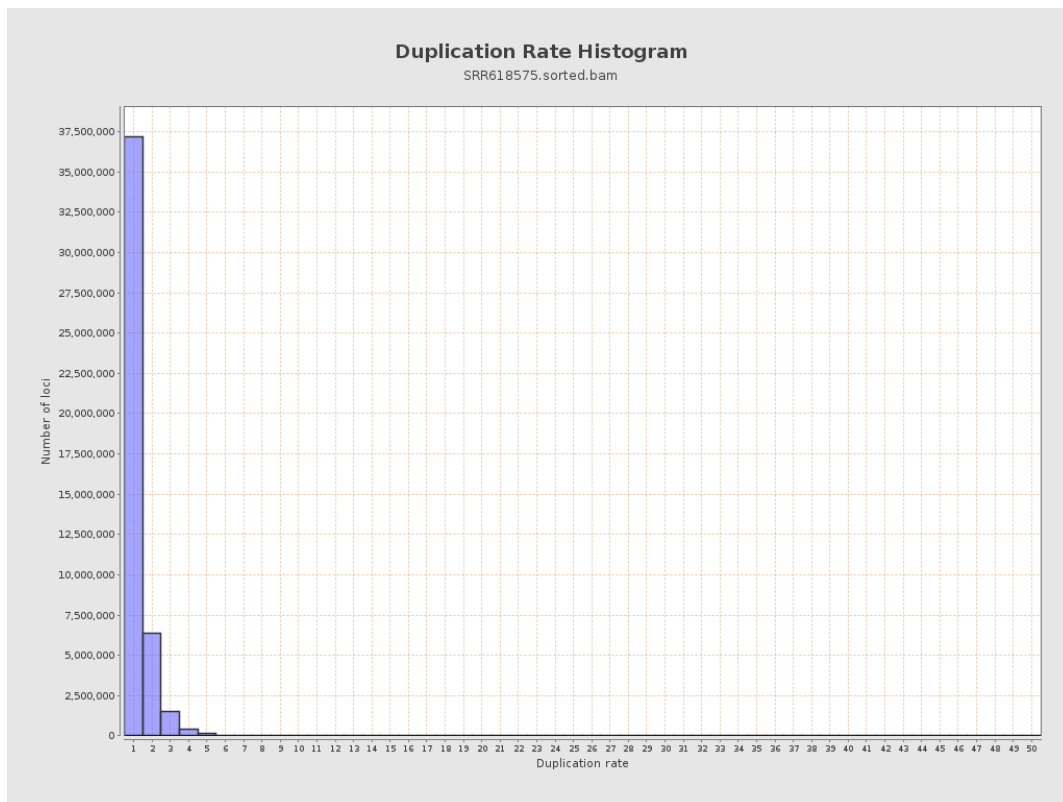
5. Results : Coverage Histogram (0-50X)



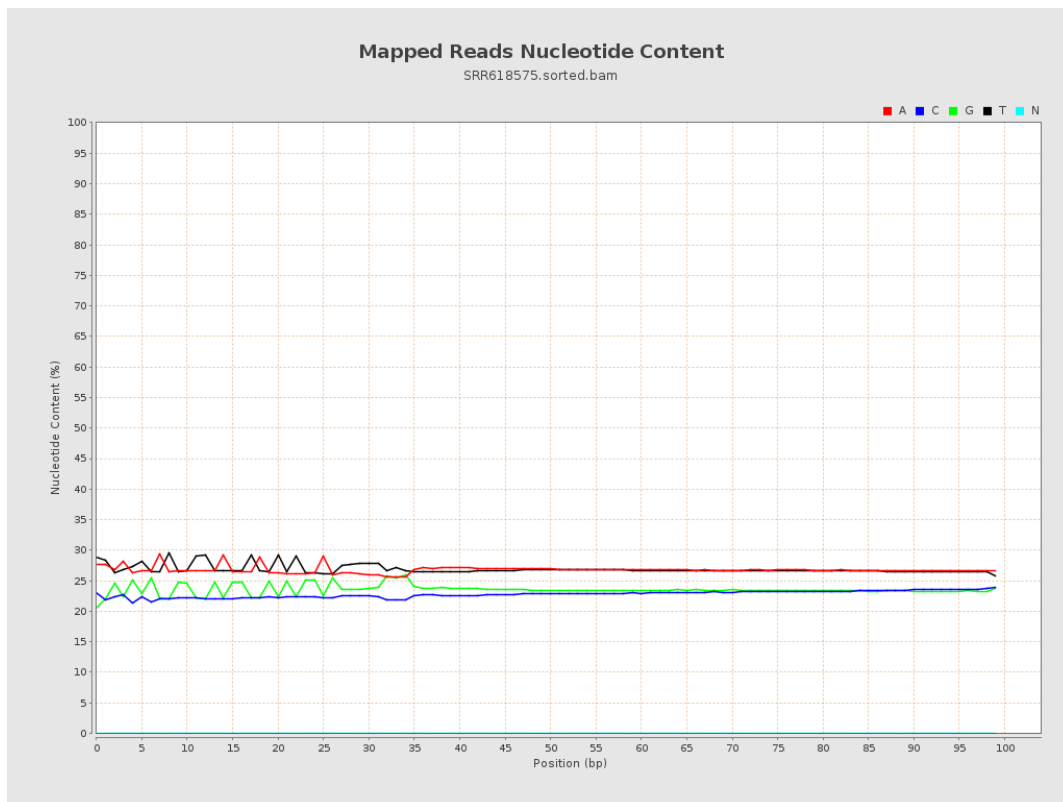
6. Results : Genome Fraction Coverage



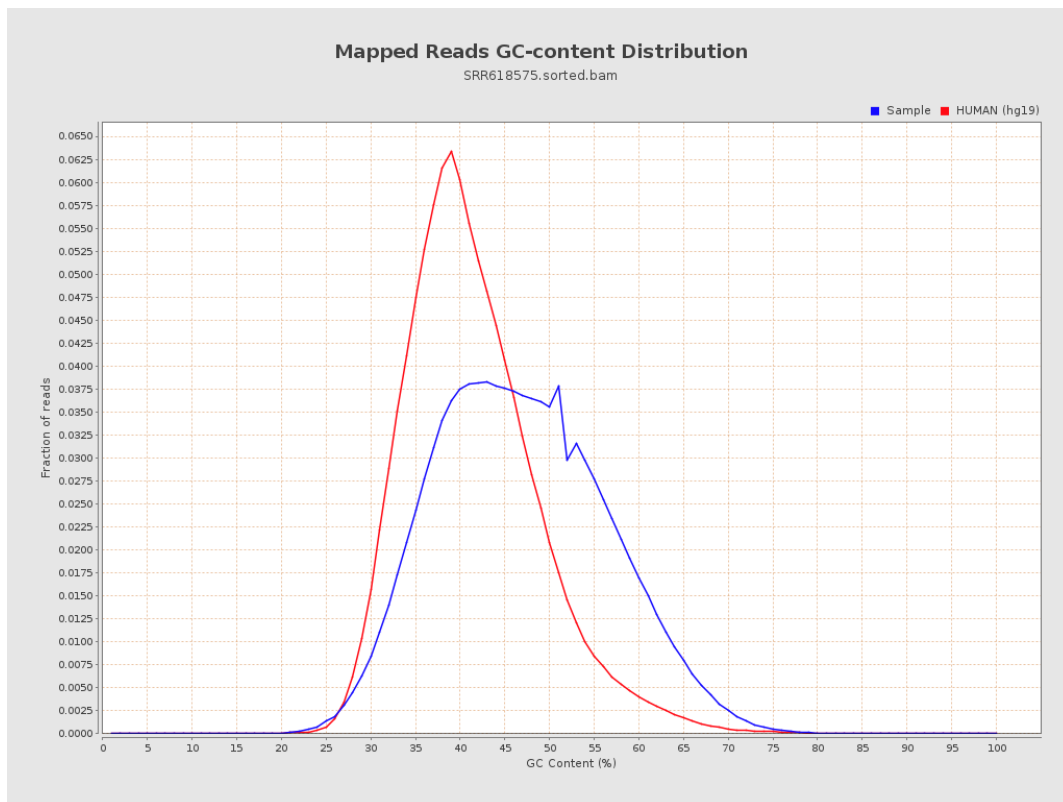
7. Results : Duplication Rate Histogram



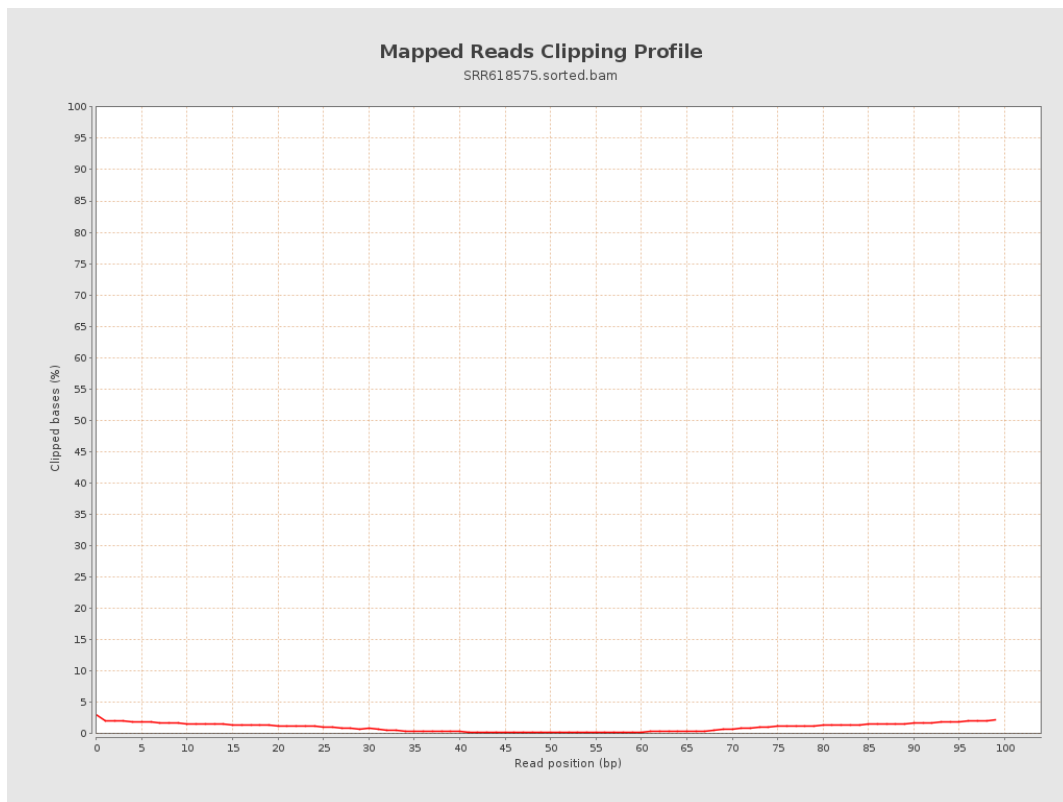
8. Results : Mapped Reads Nucleotide Content



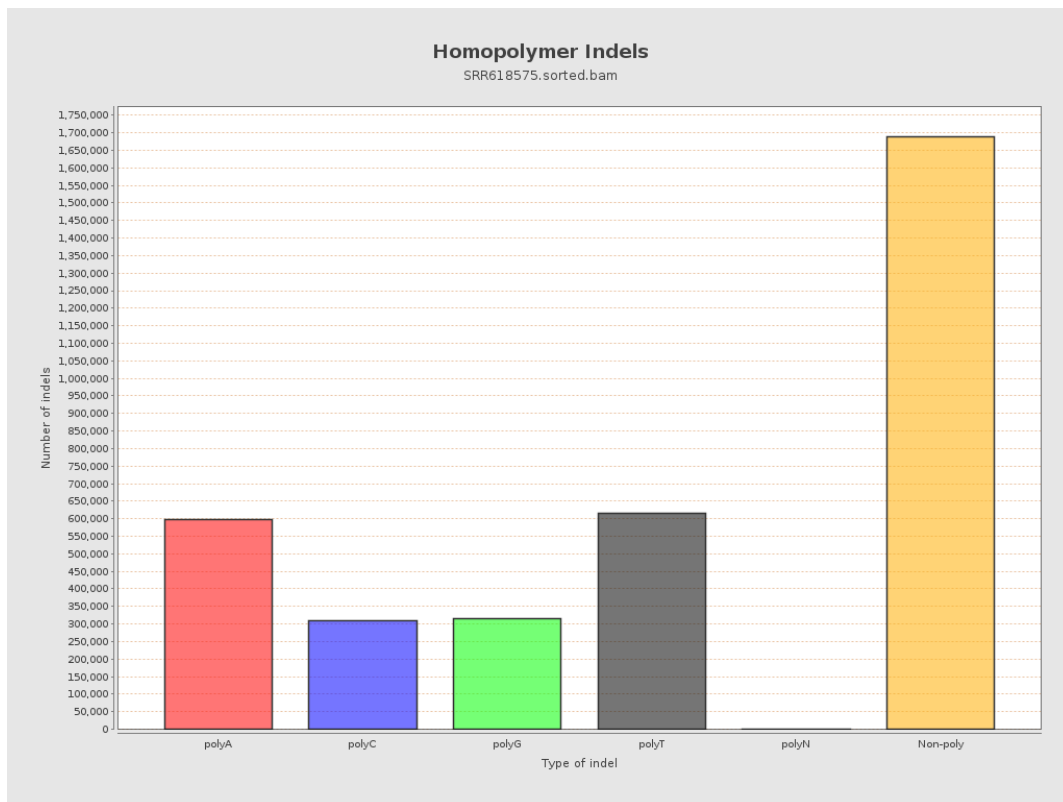
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



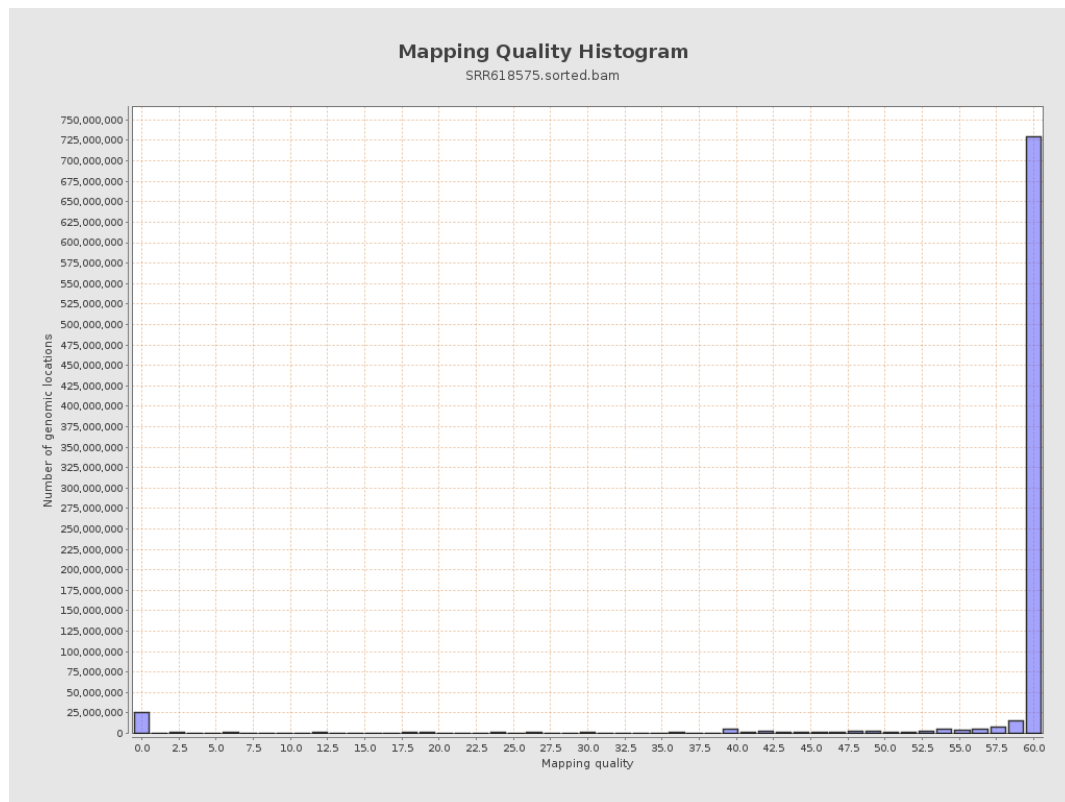
11. Results : Homopolymer Indels



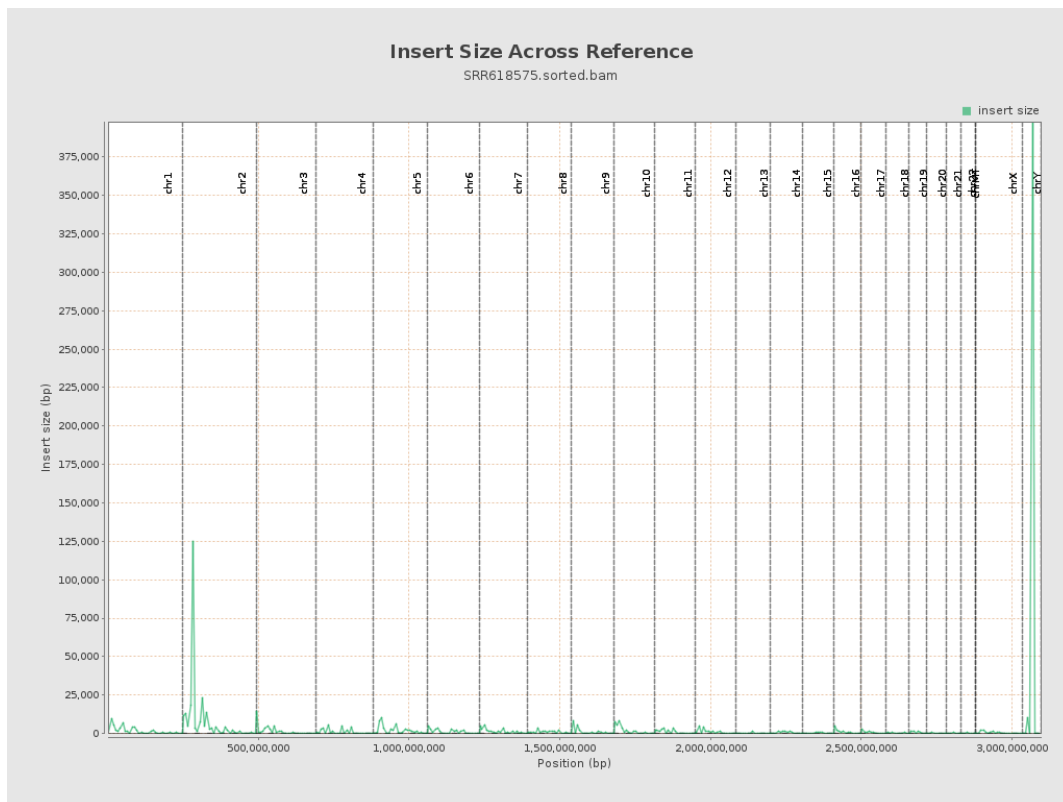
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

