

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/18 16:52:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618592.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_SRR618592 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618592_1.fastq.gz SRR618592_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Jan 18 16:52:25 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618592.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	57,902,748
Mapped reads	53,967,348 / 93.2%
Unmapped reads	3,935,400 / 6.8%
Mapped paired reads	53,967,348 / 93.2%
Mapped reads, first in pair	27,543,735 / 47.57%
Mapped reads, second in pair	26,423,613 / 45.63%
Mapped reads, both in pair	51,730,264 / 89.34%
Mapped reads, singletons	2,237,084 / 3.86%
Secondary alignments	0
Supplementary alignments	183,733 / 0.32%
Read min/max/mean length	30 / 100 / 100.13
Duplicated reads (estimated)	18,340,527 / 31.67%
Duplication rate	27.84%
Clipped reads	12,305,214 / 21.25%

2.2. ACGT Content

Number/percentage of A's	1,387,897,141 / 27.38%
Number/percentage of C's	1,108,879,133 / 21.88%
Number/percentage of T's	1,408,213,641 / 27.78%
Number/percentage of G's	1,162,406,921 / 22.93%
Number/percentage of N's	1,566,265 / 0.03%

GC Percentage	44.81%
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2.3. Coverage

Mean	1.6386
Standard Deviation	7.1994

2.4. Mapping Quality

Mean Mapping Quality	53.48
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2.5. Insert size

Mean	94,746.76
Standard Deviation	3,075,349.02
P25/Median/P75	191 / 220 / 257

2.6. Mismatches and indels

General error rate	1.42%
Mismatches	70,463,792
Insertions	941,748
Mapped reads with at least one insertion	1.72%
Deletions	2,555,283
Mapped reads with at least one deletion	4.62%
Homopolymer indels	52.6%

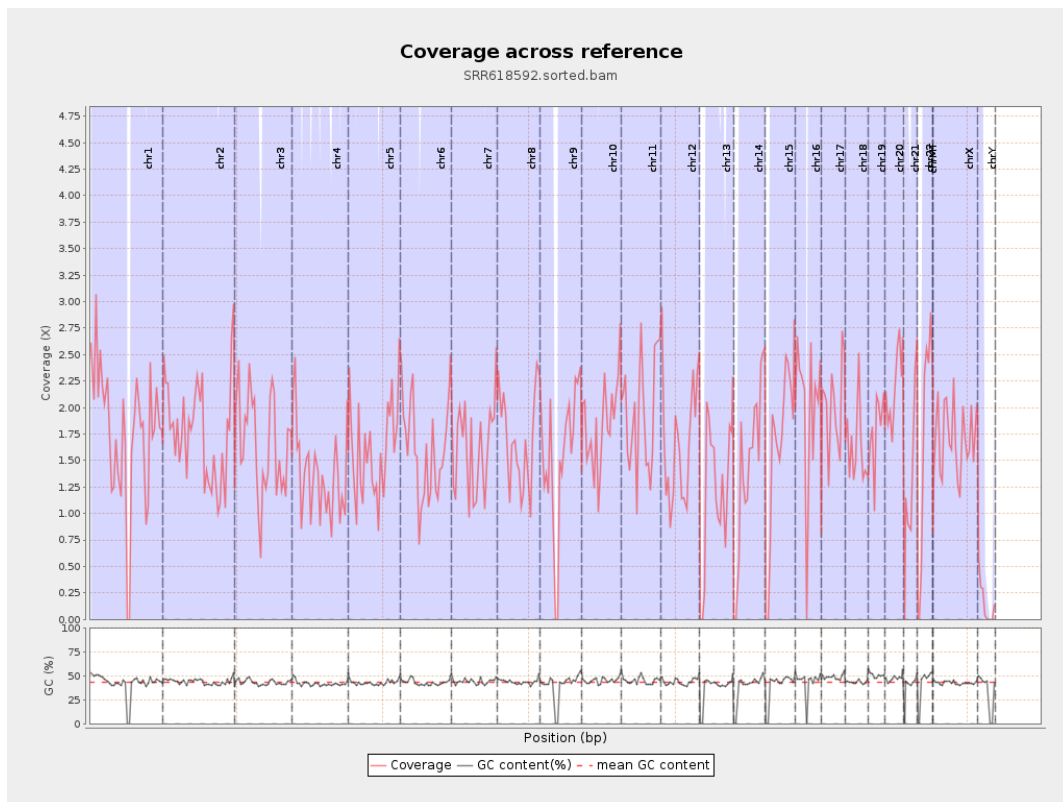
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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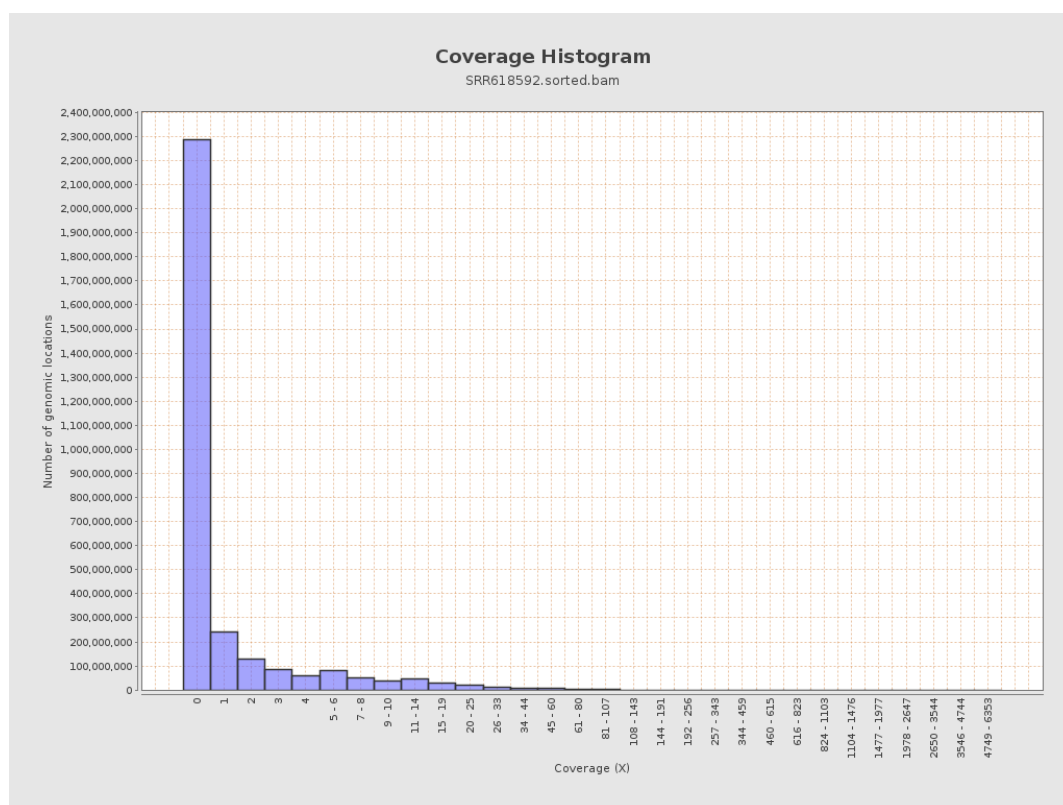
		bases	coverage	deviation
chr1	249250621	438413819	1.7589	7.9467
chr2	243199373	428484285	1.7619	8.2116
chr3	198022430	324538509	1.6389	5.6995
chr4	191154276	261830353	1.3697	6.1152
chr5	180915260	293268822	1.621	7.3665
chr6	171115067	271354980	1.5858	5.9661
chr7	159138663	258631991	1.6252	6.2142
chr8	146364022	246686654	1.6854	6.3833
chr9	141213431	215926475	1.5291	8.2275
chr10	135534747	248620850	1.8344	6.4164
chr11	135006516	261107537	1.934	7.4851
chr12	133851895	223452053	1.6694	6.9852
chr13	115169878	139395438	1.2103	4.9968
chr14	107349540	154823543	1.4422	5.989
chr15	102531392	166027830	1.6193	7.1797
chr16	90354753	178537567	1.976	12.5772
chr17	81195210	162932679	2.0067	8.1931
chr18	78077248	126417121	1.6191	8.0426
chr19	59128983	105405101	1.7826	7.4102
chr20	63025520	138037594	2.1902	7.3883
chr21	48129895	66305682	1.3776	9.6874
chr22	51304566	87190013	1.6995	7.1059
chrMT	16571	13265	0.8005	3.4745
chrX	155270560	265999173	1.7131	5.9168

chrY	59373566	9053457	0.1525	4.5078
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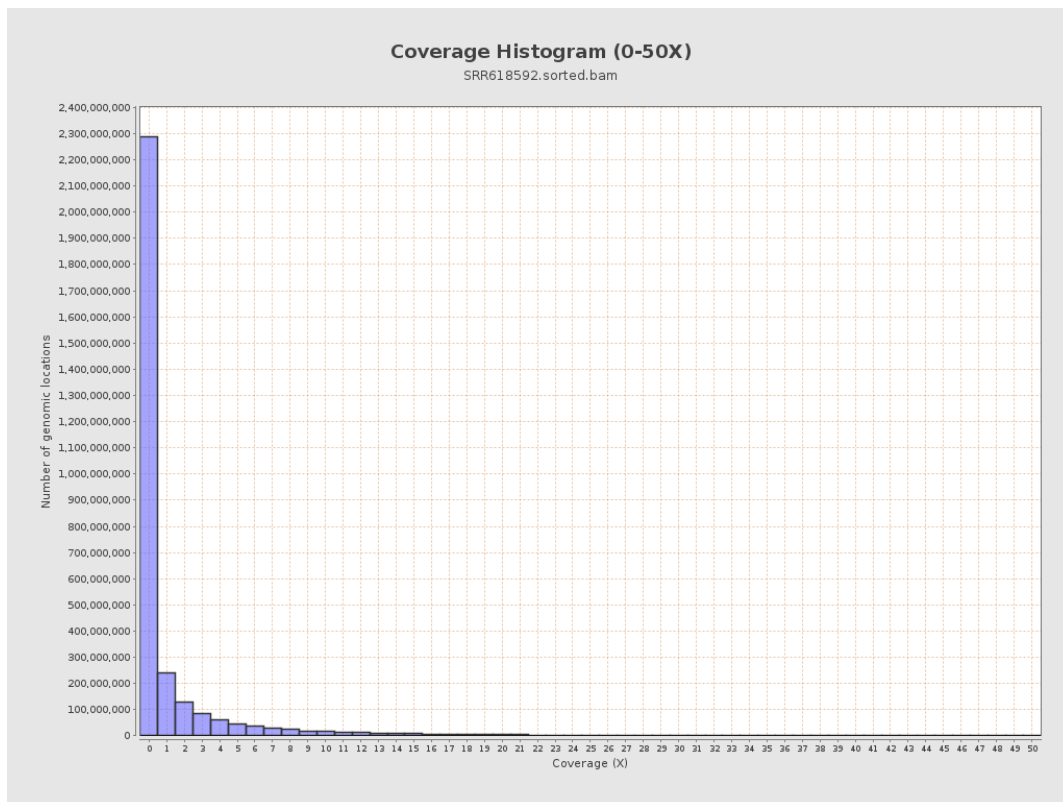
3. Results : Coverage across reference



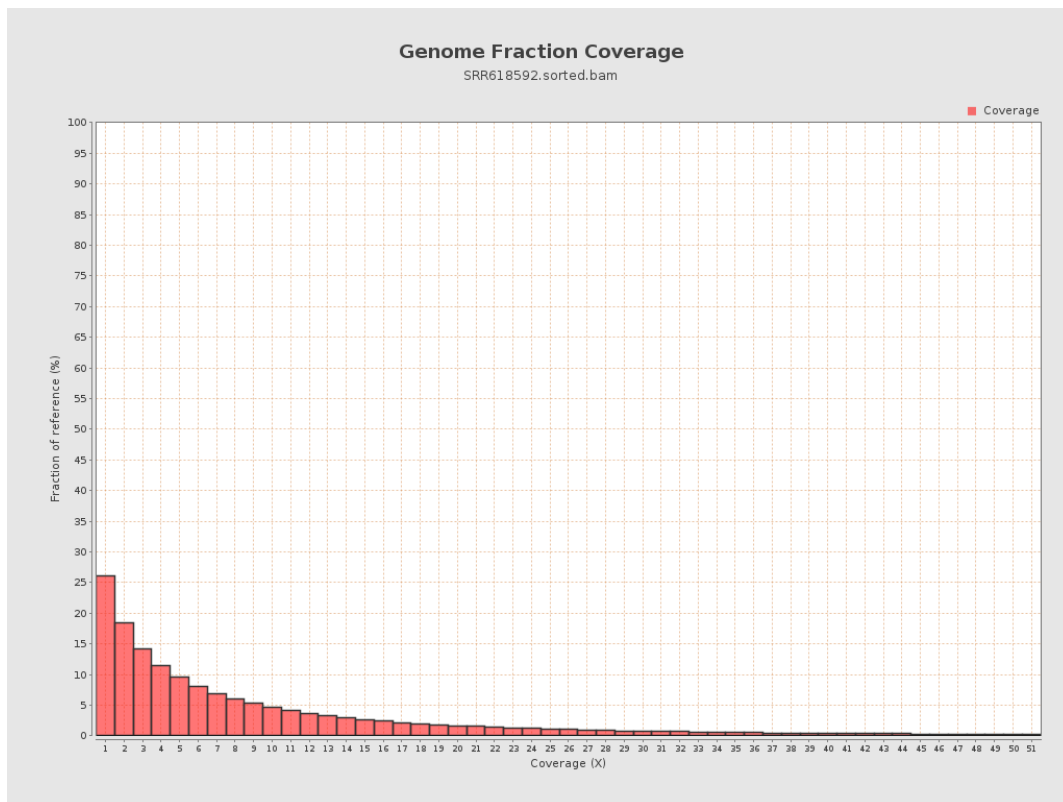
4. Results : Coverage Histogram



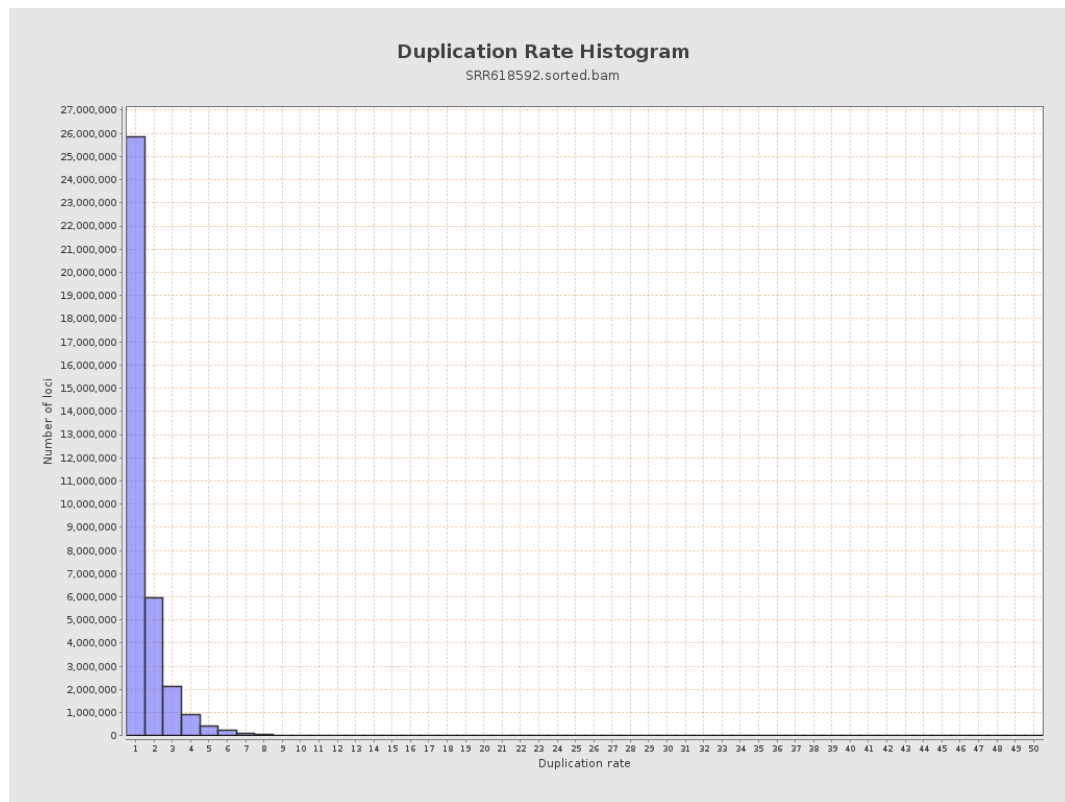
5. Results : Coverage Histogram (0-50X)



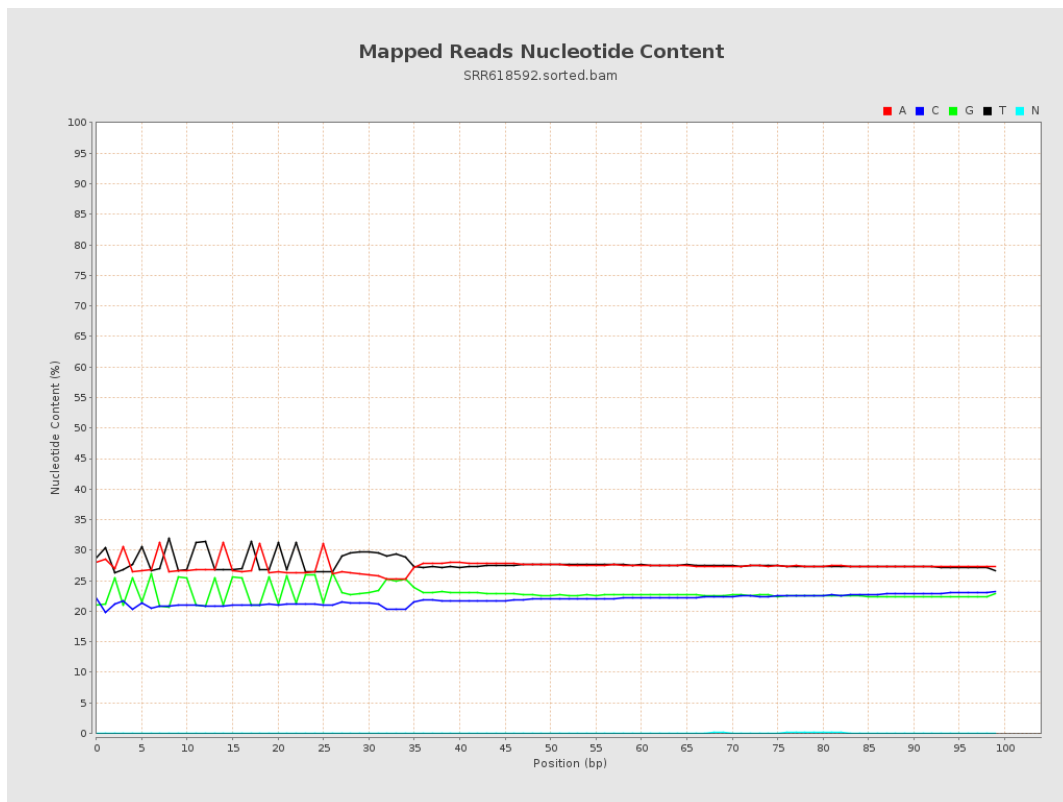
6. Results : Genome Fraction Coverage



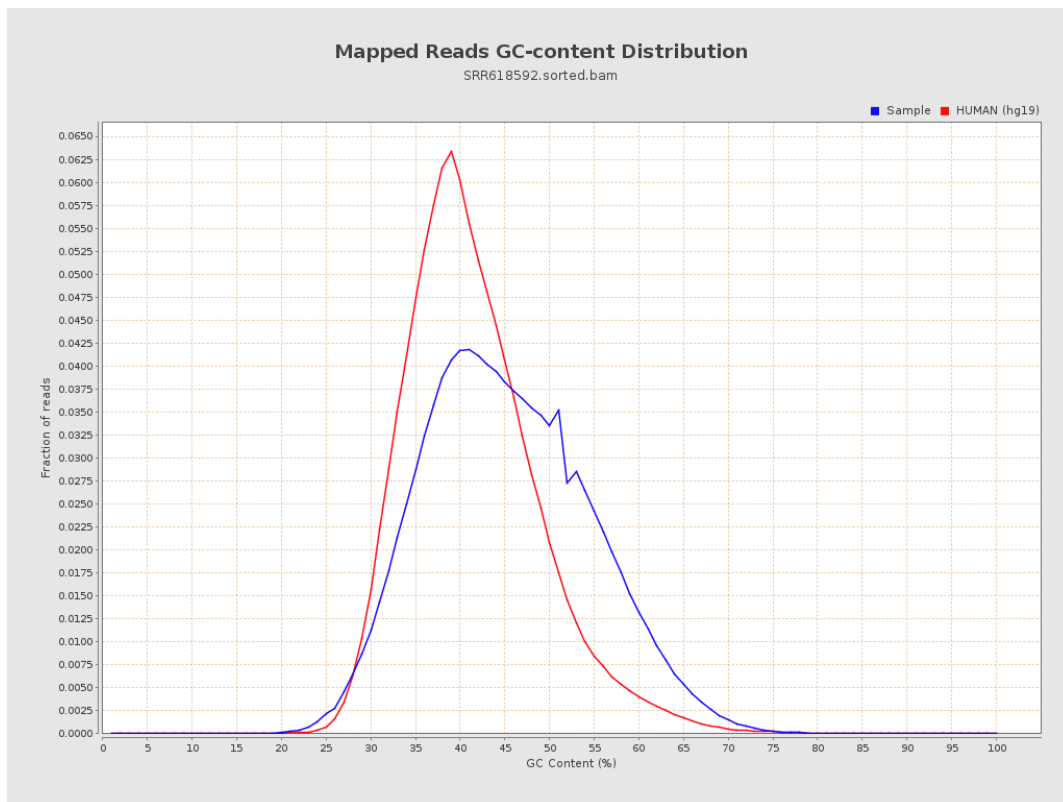
7. Results : Duplication Rate Histogram



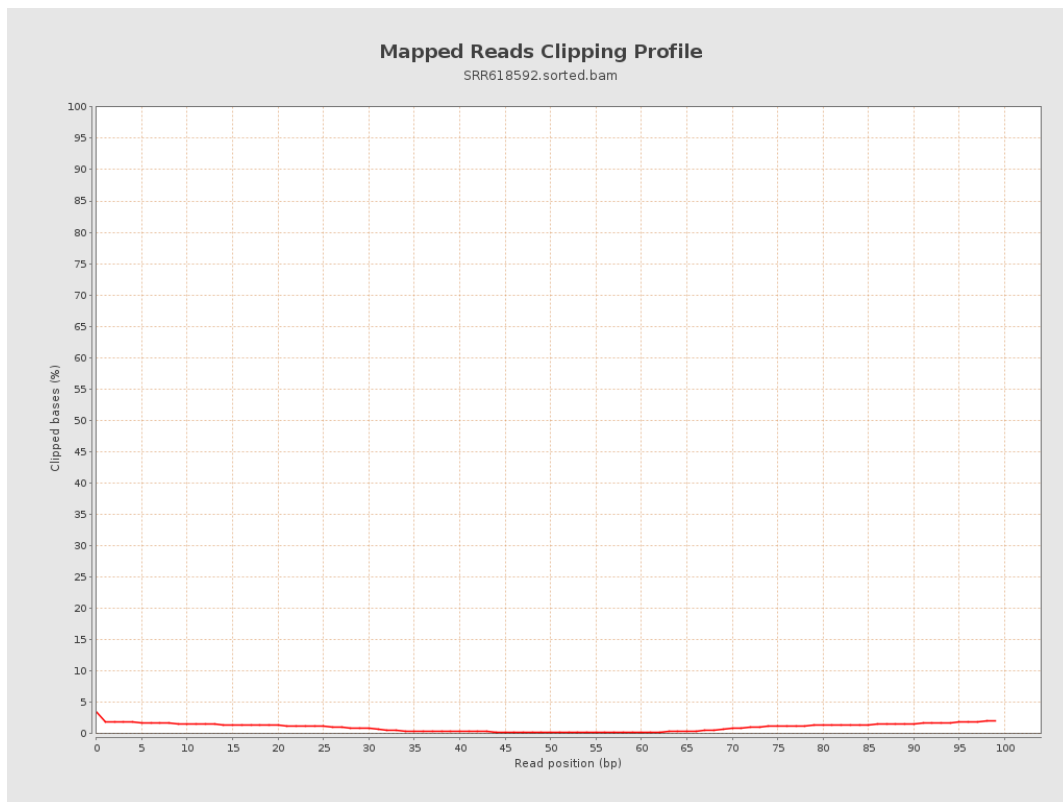
8. Results : Mapped Reads Nucleotide Content



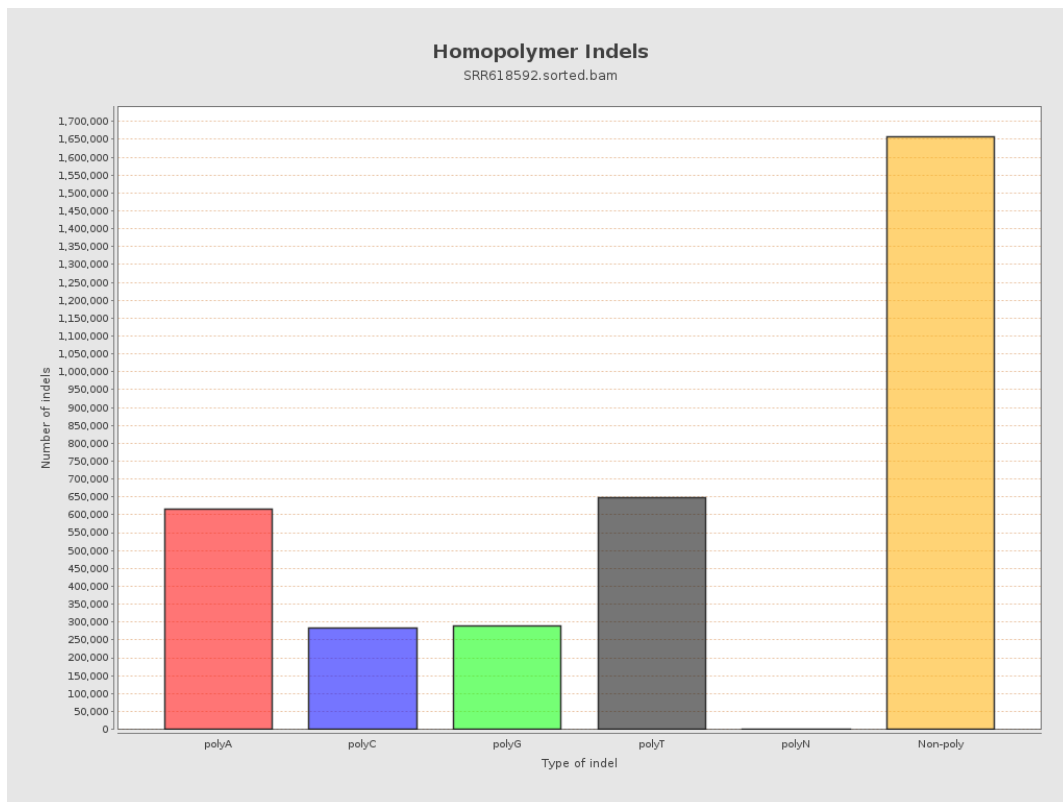
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



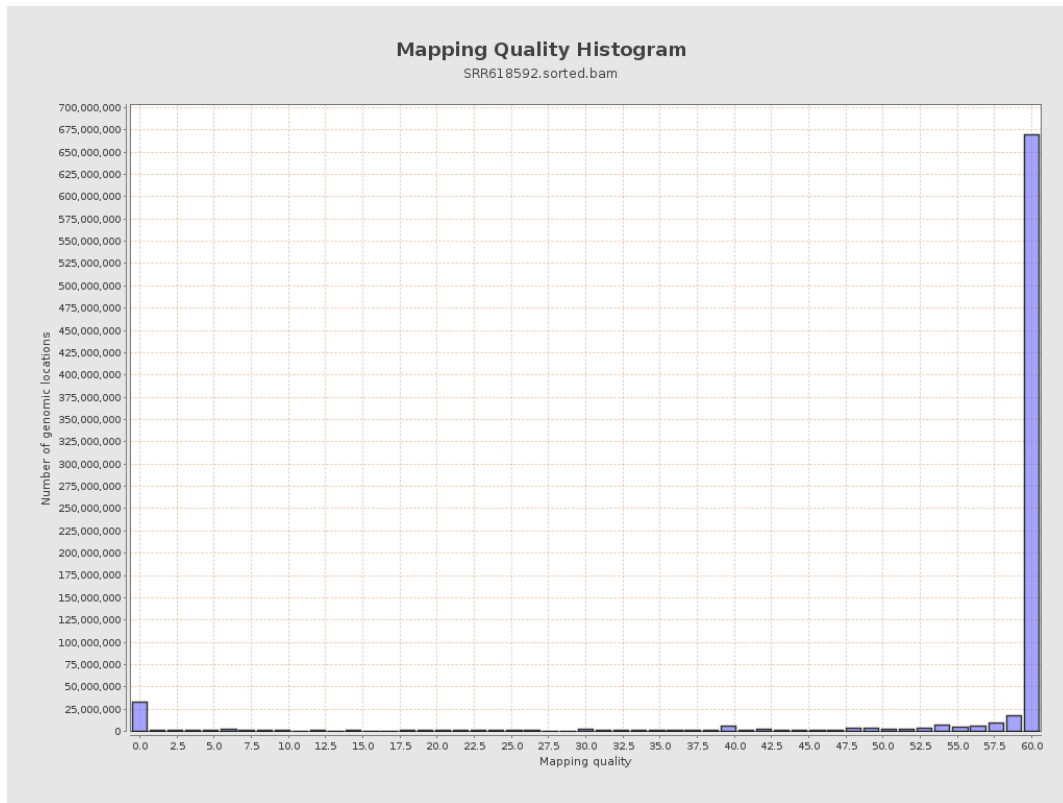
11. Results : Homopolymer Indels



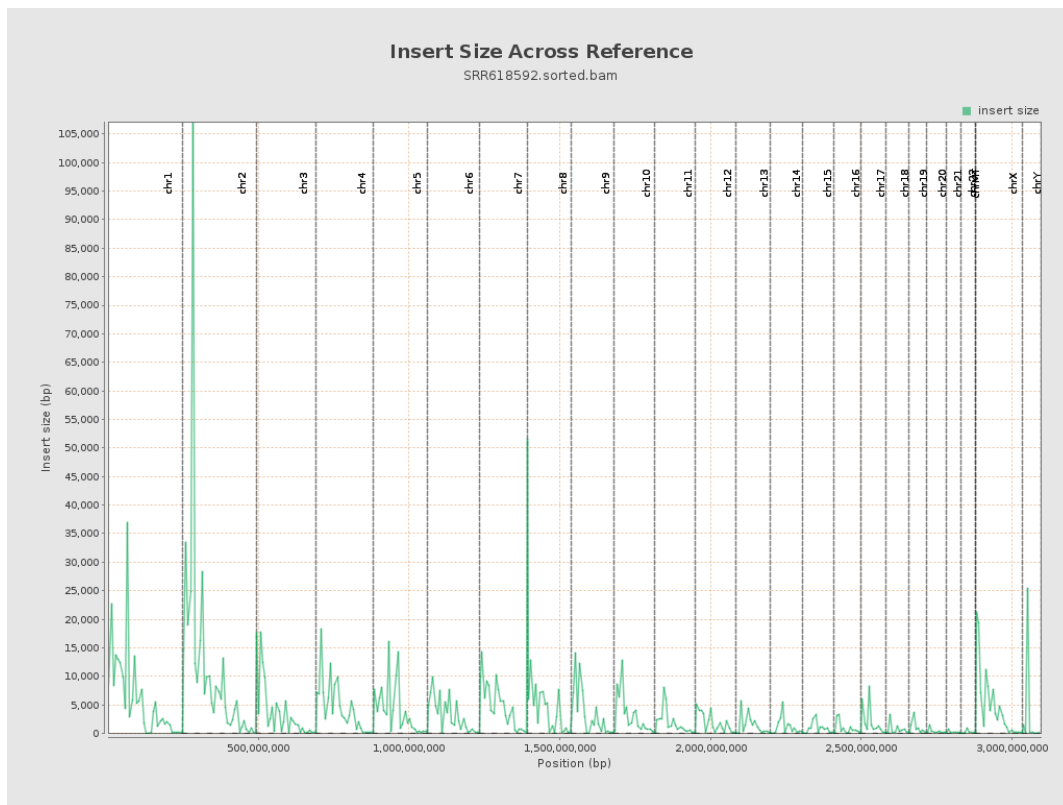
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

