

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/18 15:57:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618591.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_SRR618591 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618591_1.fastq.gz SRR618591_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Jan 18 15:57:49 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618591.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	60,596,386
Mapped reads	57,529,088 / 94.94%
Unmapped reads	3,067,298 / 5.06%
Mapped paired reads	57,529,088 / 94.94%
Mapped reads, first in pair	29,332,381 / 48.41%
Mapped reads, second in pair	28,196,707 / 46.53%
Mapped reads, both in pair	55,606,600 / 91.77%
Mapped reads, singletons	1,922,488 / 3.17%
Secondary alignments	0
Supplementary alignments	260,892 / 0.43%
Read min/max/mean length	30 / 100 / 100.17
Duplicated reads (estimated)	18,948,302 / 31.27%
Duplication rate	26.96%
Clipped reads	14,258,275 / 23.53%

2.2. ACGT Content

Number/percentage of A's	1,464,336,129 / 27.26%
Number/percentage of C's	1,166,237,970 / 21.71%
Number/percentage of T's	1,494,075,147 / 27.82%
Number/percentage of G's	1,244,067,365 / 23.16%
Number/percentage of N's	2,319,453 / 0.04%

GC Percentage	44.88%
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2.3. Coverage

Mean	1.7362
Standard Deviation	6.6265

2.4. Mapping Quality

Mean Mapping Quality	53.28
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2.5. Insert size

Mean	104,919.67
Standard Deviation	3,241,418.59
P25/Median/P75	159 / 189 / 230

2.6. Mismatches and indels

General error rate	1.29%
Mismatches	67,799,800
Insertions	974,680
Mapped reads with at least one insertion	1.67%
Deletions	2,620,287
Mapped reads with at least one deletion	4.44%
Homopolymer indels	52.34%

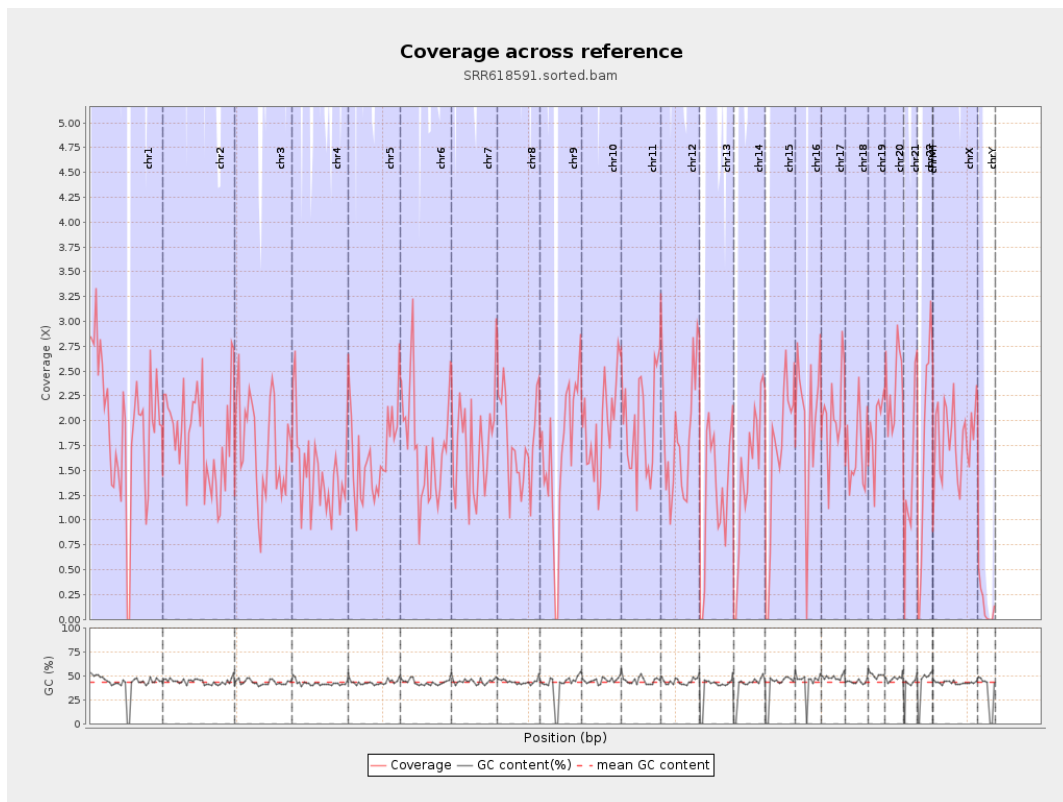
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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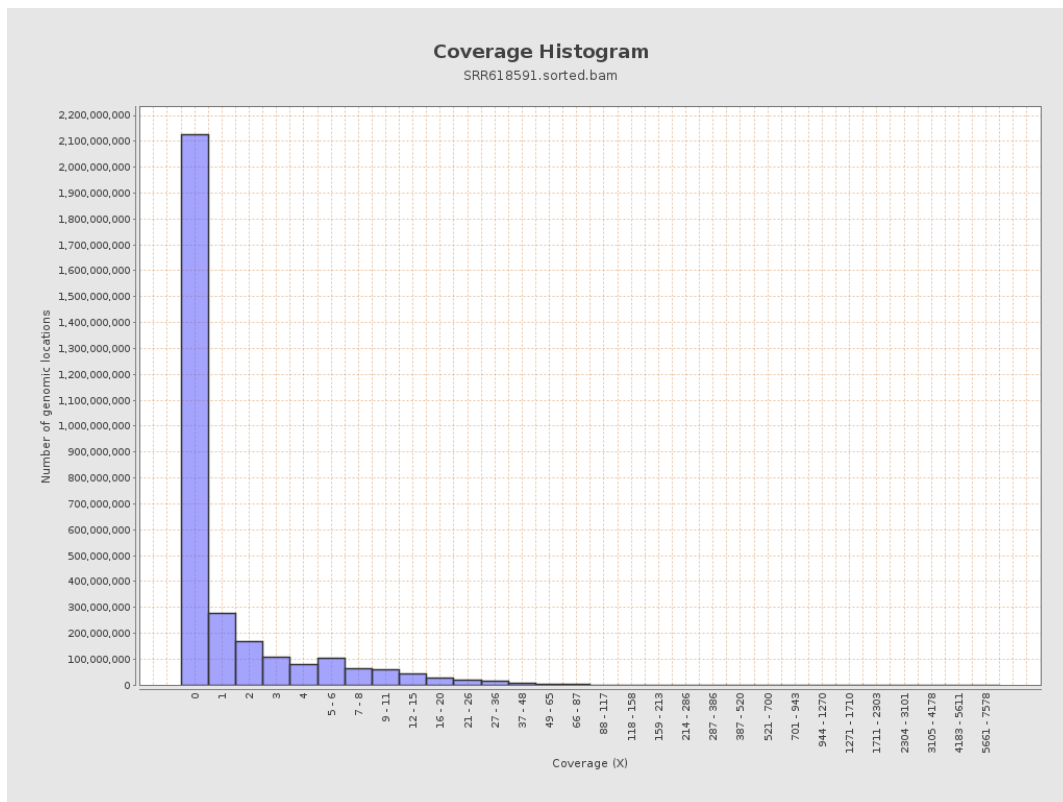
		bases	coverage	deviation
chr1	249250621	482651190	1.9364	8.1445
chr2	243199373	448239273	1.8431	7.8819
chr3	198022430	340832290	1.7212	5.4466
chr4	191154276	283401082	1.4826	5.432
chr5	180915260	301891259	1.6687	5.571
chr6	171115067	297388558	1.7379	5.7526
chr7	159138663	278700318	1.7513	5.5852
chr8	146364022	259687876	1.7743	5.6815
chr9	141213431	235000096	1.6641	7.1613
chr10	135534747	263255847	1.9423	5.7213
chr11	135006516	265673512	1.9679	7.77
chr12	133851895	249365174	1.863	6.1804
chr13	115169878	145355690	1.2621	4.32
chr14	107349540	157974519	1.4716	5.1038
chr15	102531392	169062325	1.6489	5.581
chr16	90354753	182625982	2.0212	12.9439
chr17	81195210	167937846	2.0683	6.766
chr18	78077248	129314248	1.6562	6.4485
chr19	59128983	114837326	1.9421	7.0143
chr20	63025520	148166602	2.3509	6.5432
chr21	48129895	71542862	1.4865	7.7291
chr22	51304566	89453424	1.7436	6.2234
chrMT	16571	14569	0.8792	2.3144
chrX	155270560	283974116	1.8289	5.3913

chrY	59373566	8317391	0.1401	4.802
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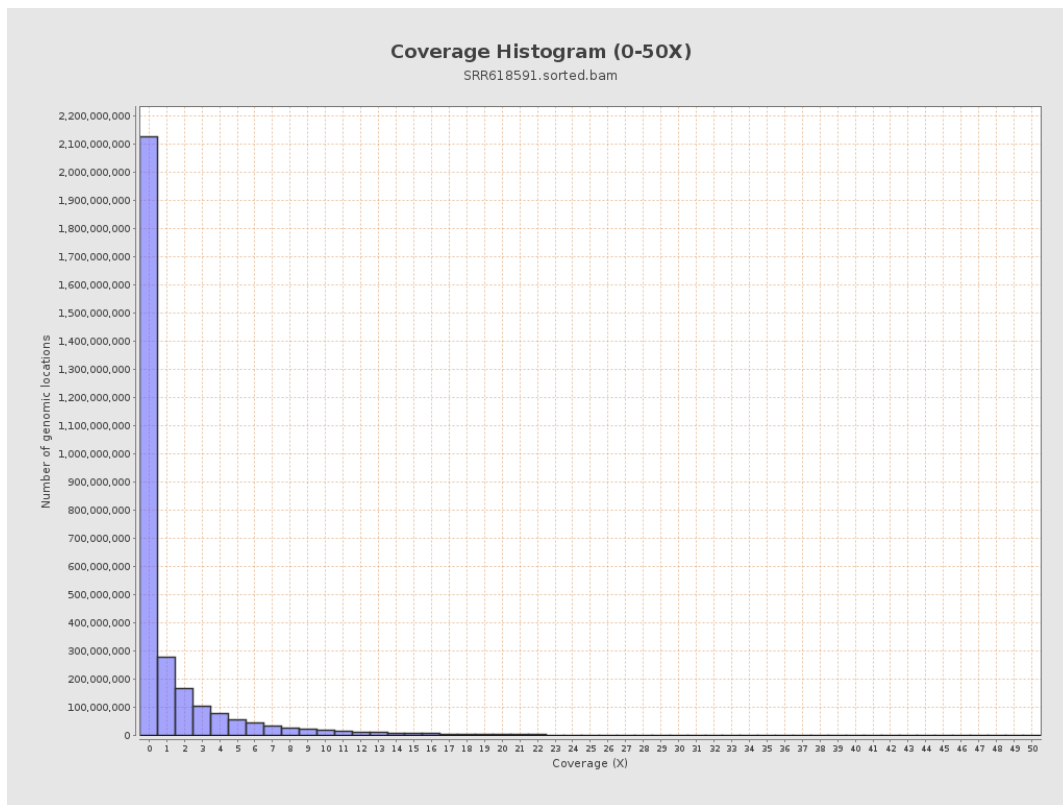
3. Results : Coverage across reference



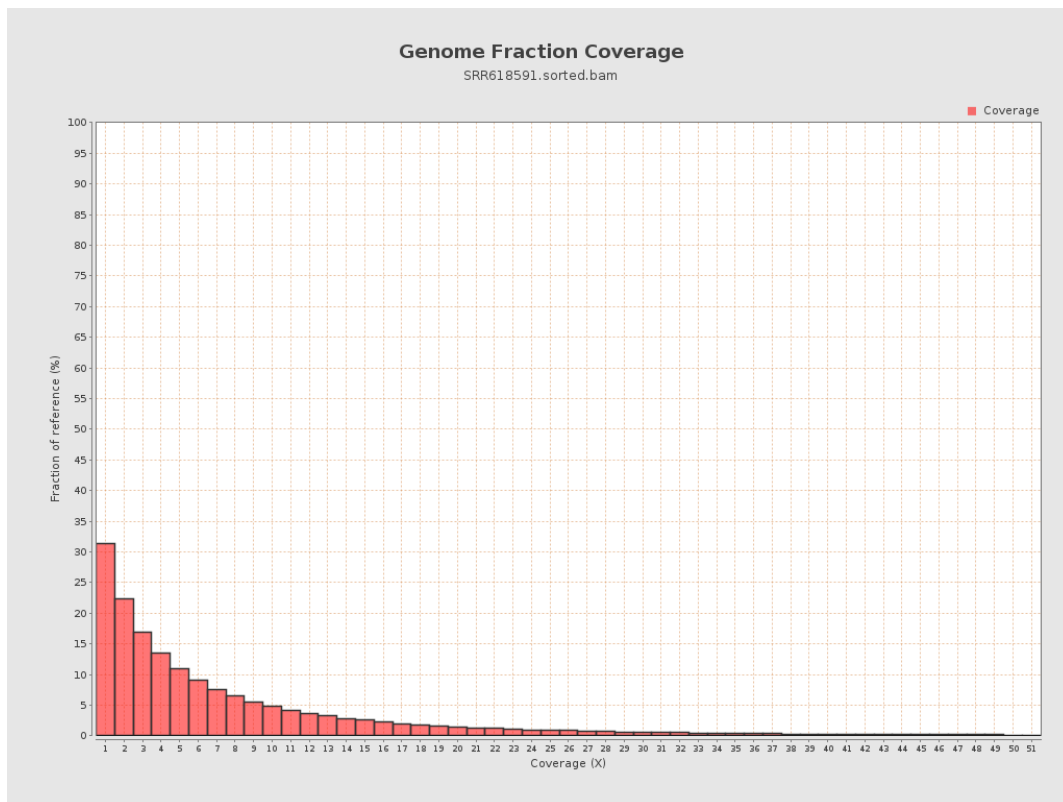
4. Results : Coverage Histogram



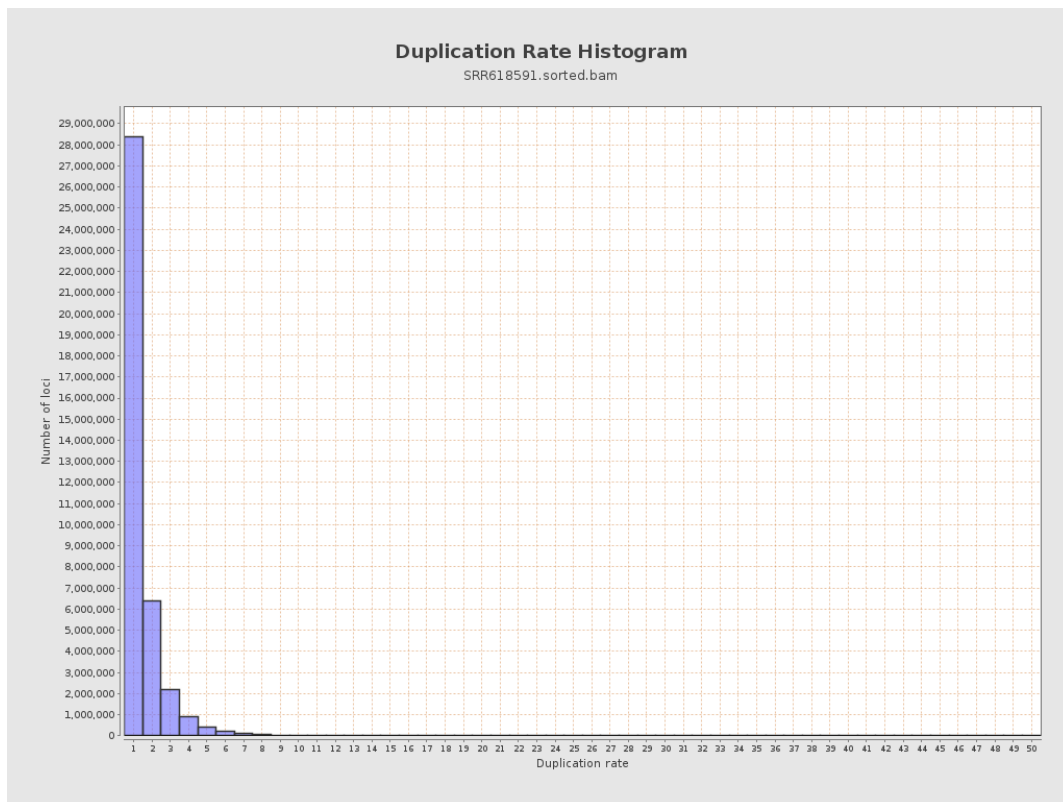
5. Results : Coverage Histogram (0-50X)



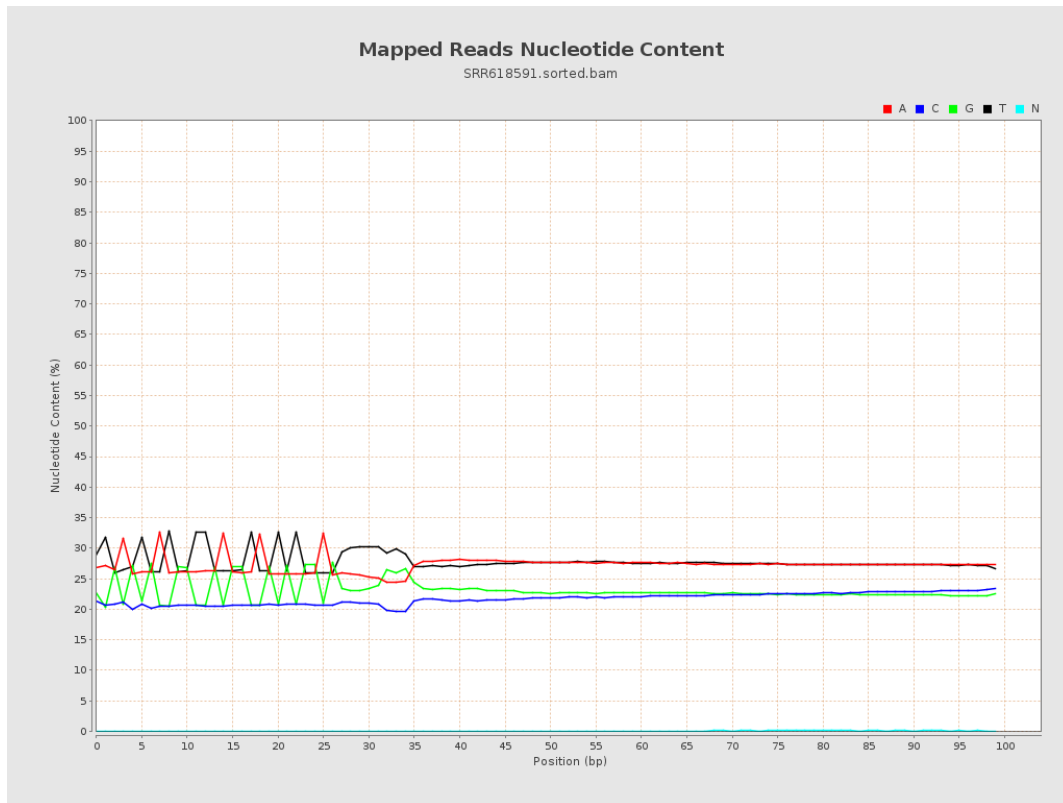
6. Results : Genome Fraction Coverage



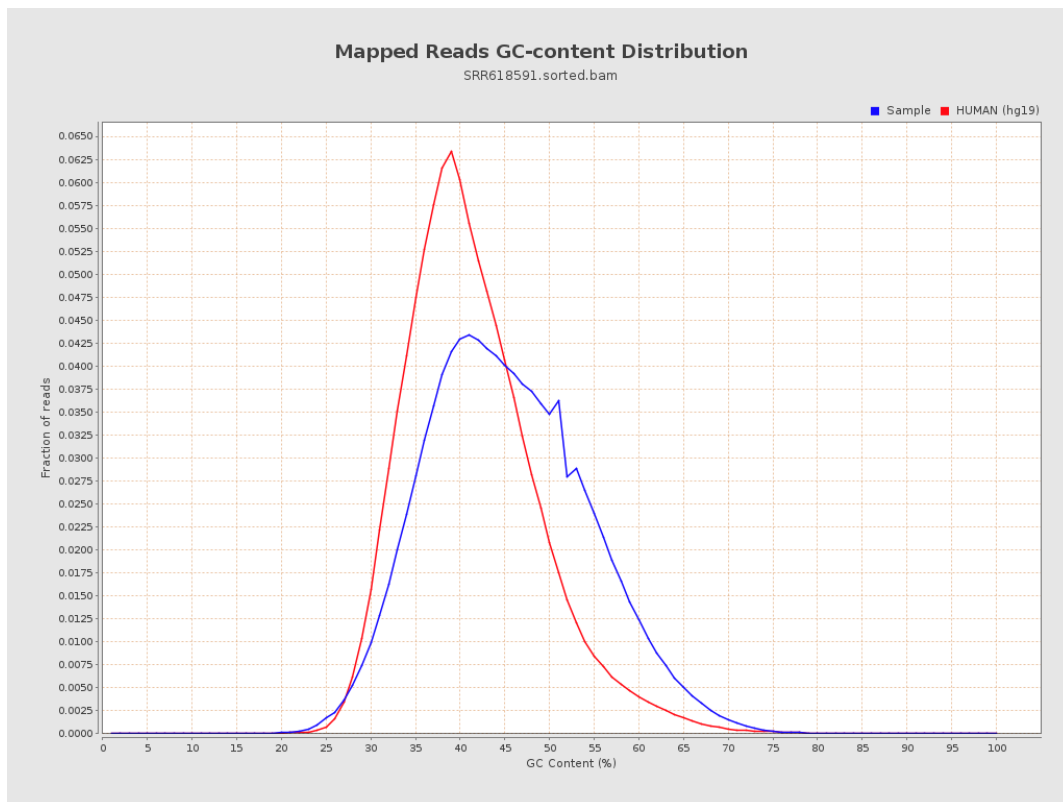
7. Results : Duplication Rate Histogram



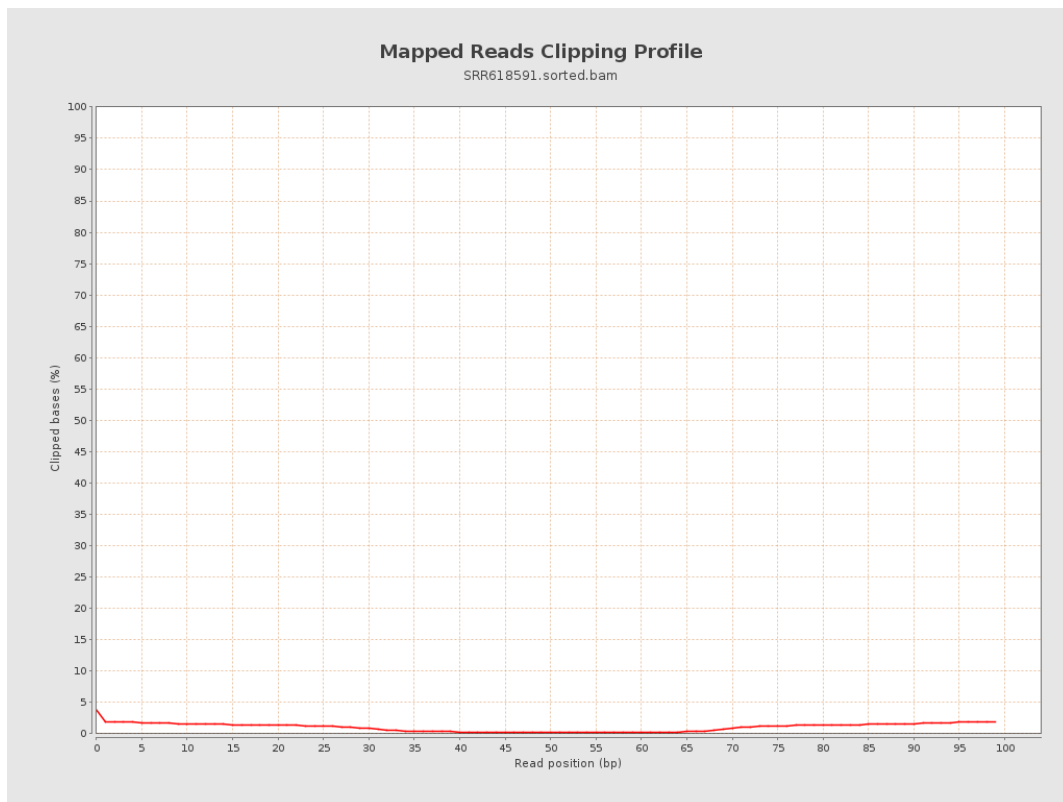
8. Results : Mapped Reads Nucleotide Content



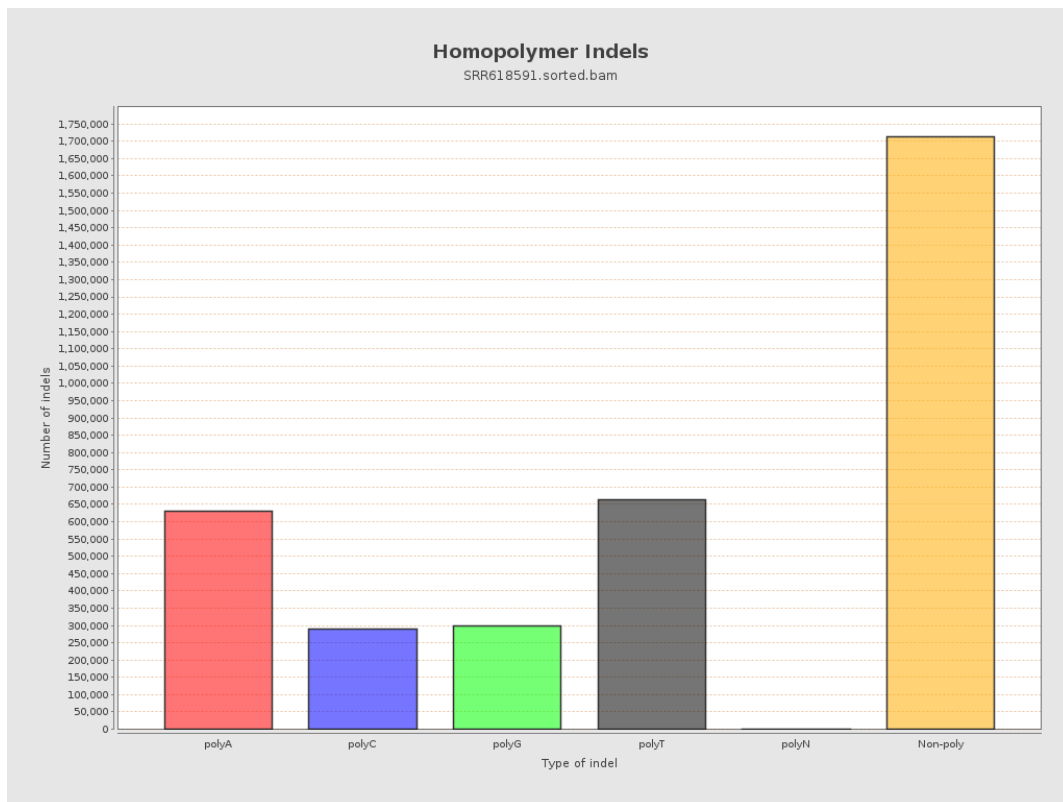
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



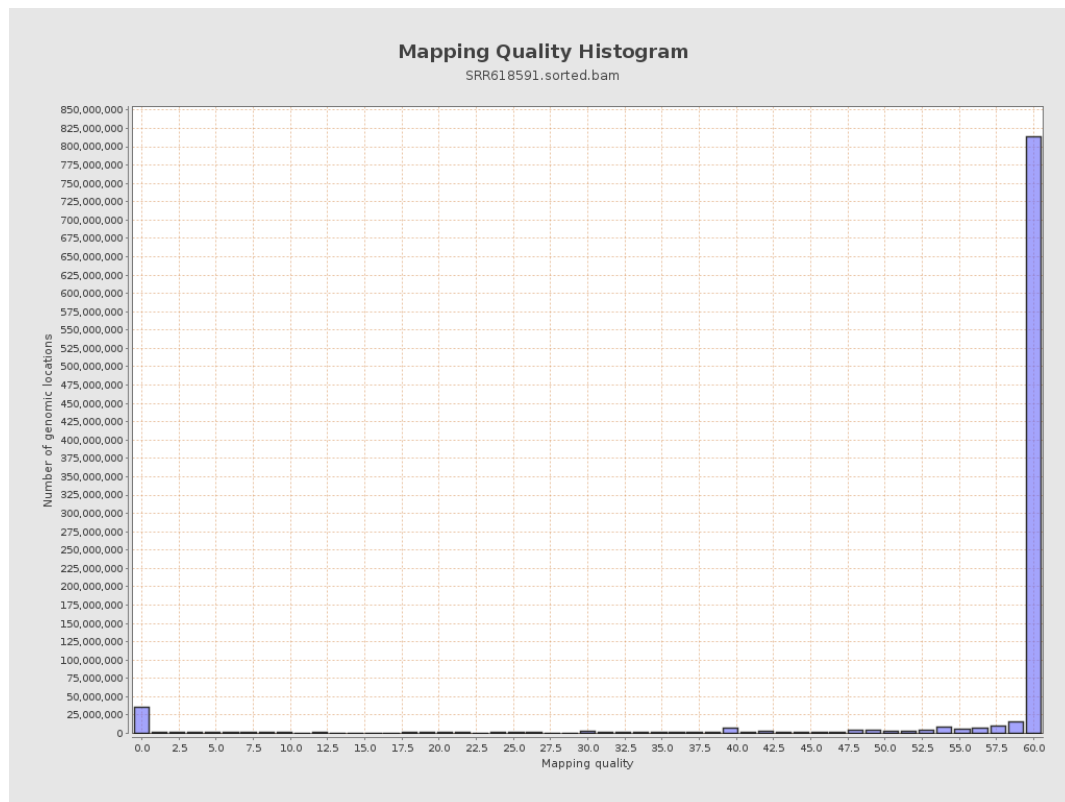
11. Results : Homopolymer Indels



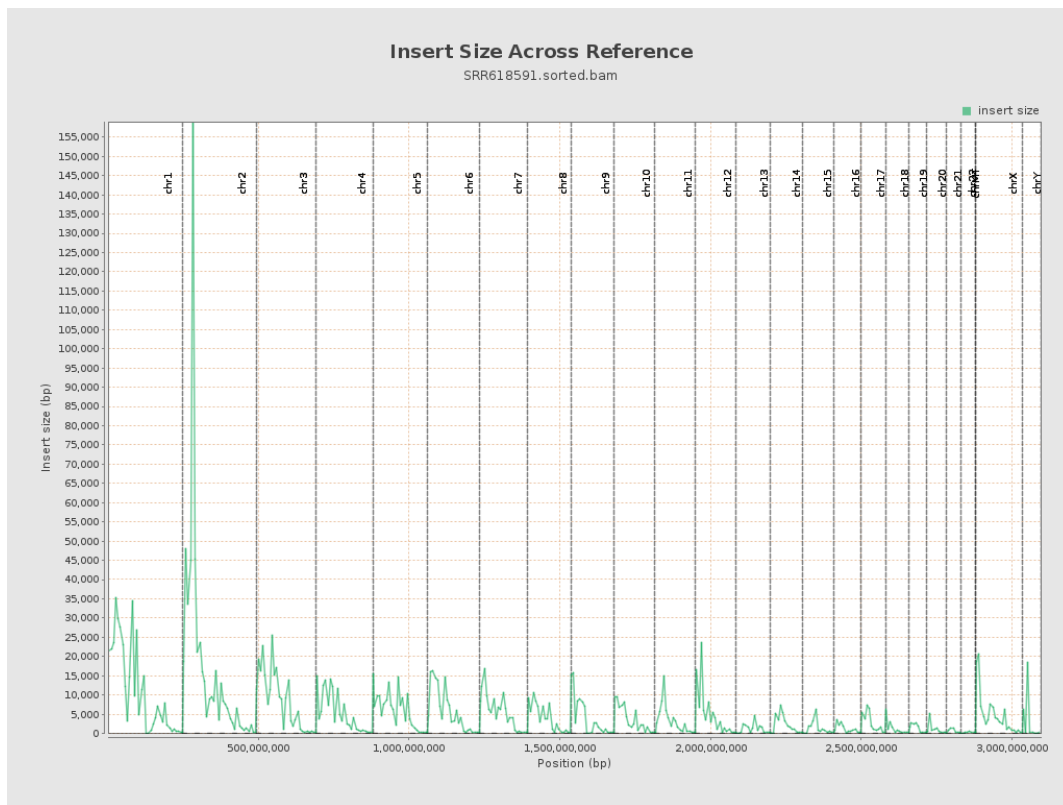
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

