

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/18 15:00:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618590.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_SRR618590 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618590_1.fastq.gz SRR618590_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Jan 18 15:00:22 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618590.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	51,015,138
Mapped reads	49,398,807 / 96.83%
Unmapped reads	1,616,331 / 3.17%
Mapped paired reads	49,398,807 / 96.83%
Mapped reads, first in pair	24,936,899 / 48.88%
Mapped reads, second in pair	24,461,908 / 47.95%
Mapped reads, both in pair	48,672,934 / 95.41%
Mapped reads, singletons	725,873 / 1.42%
Secondary alignments	0
Supplementary alignments	185,901 / 0.36%
Read min/max/mean length	30 / 100 / 100.15
Duplicated reads (estimated)	13,943,796 / 27.33%
Duplication rate	24.07%
Clipped reads	8,548,455 / 16.76%

2.2. ACGT Content

Number/percentage of A's	1,290,912,591 / 27.27%
Number/percentage of C's	1,049,564,518 / 22.17%
Number/percentage of T's	1,291,636,706 / 27.28%
Number/percentage of G's	1,102,110,121 / 23.28%
Number/percentage of N's	233,694 / 0%

GC Percentage	45.45%
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2.3. Coverage

Mean	1.5305
Standard Deviation	7.1125

2.4. Mapping Quality

Mean Mapping Quality	52.82
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2.5. Insert size

Mean	69,689.87
Standard Deviation	2,607,027.64
P25/Median/P75	173 / 201 / 240

2.6. Mismatches and indels

General error rate	1.32%
Mismatches	60,715,983
Insertions	914,483
Mapped reads with at least one insertion	1.81%
Deletions	2,517,712
Mapped reads with at least one deletion	4.96%
Homopolymer indels	51.42%

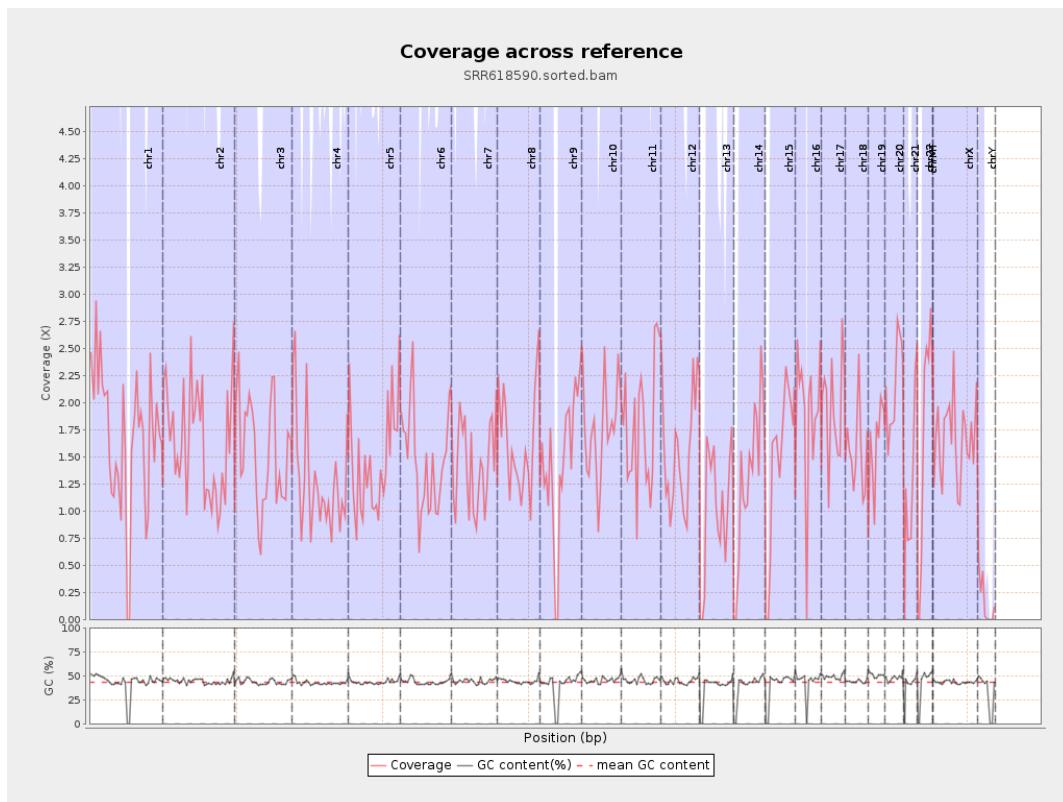
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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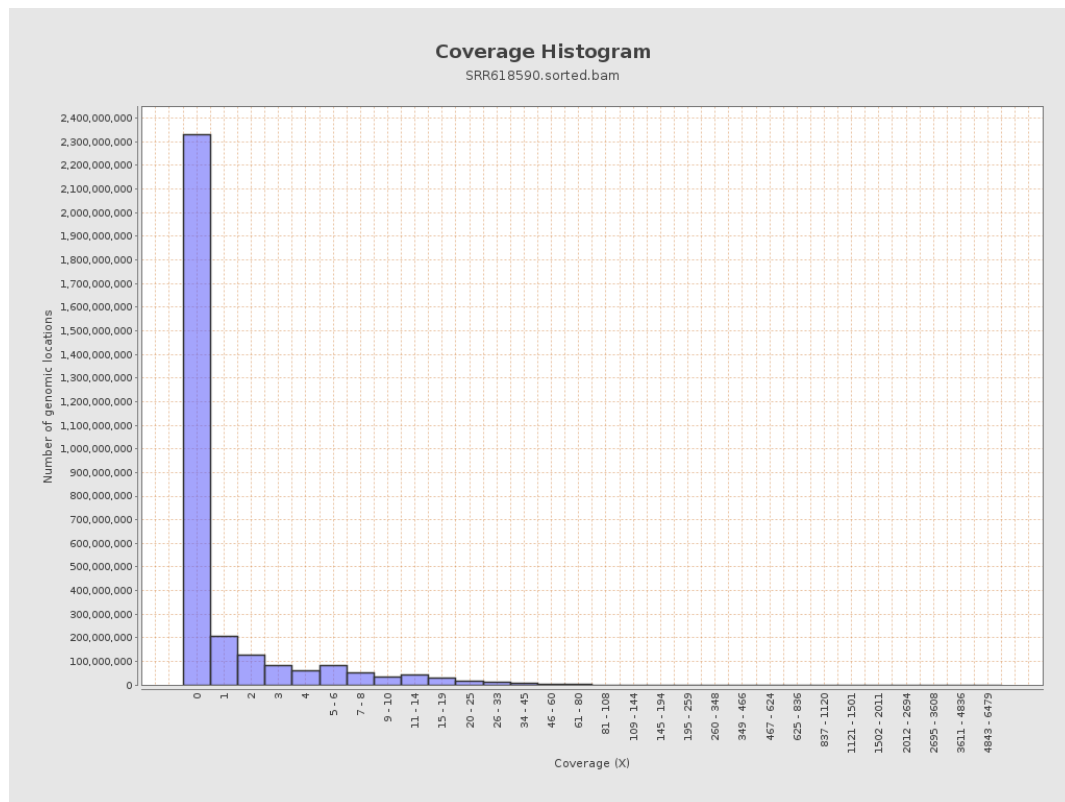
		bases	coverage	deviation
chr1	249250621	416355275	1.6704	7.6848
chr2	243199373	397647757	1.6351	9.699
chr3	198022430	301817447	1.5242	4.9478
chr4	191154276	245023397	1.2818	7.8388
chr5	180915260	266519240	1.4732	5.0753
chr6	171115067	249152266	1.4561	5.5672
chr7	159138663	227411301	1.429	5.4656
chr8	146364022	239059063	1.6333	5.7573
chr9	141213431	205902223	1.4581	8.7401
chr10	135534747	236145466	1.7423	8.134
chr11	135006516	241487883	1.7887	6.1157
chr12	133851895	208301075	1.5562	5.586
chr13	115169878	118595977	1.0297	3.882
chr14	107349540	141616172	1.3192	4.9914
chr15	102531392	150746858	1.4703	5.2223
chr16	90354753	169612739	1.8772	10.4673
chr17	81195210	157327543	1.9376	7.6192
chr18	78077248	119596610	1.5318	10.5666
chr19	59128983	94760872	1.6026	6.0774
chr20	63025520	135565697	2.151	6.8185
chr21	48129895	61893784	1.286	14.335
chr22	51304566	86593688	1.6878	6.5191
chrMT	16571	41820	2.5237	7.6396
chrX	155270560	257503085	1.6584	5.2742

chrY	59373566	9374567	0.1579	5.1594
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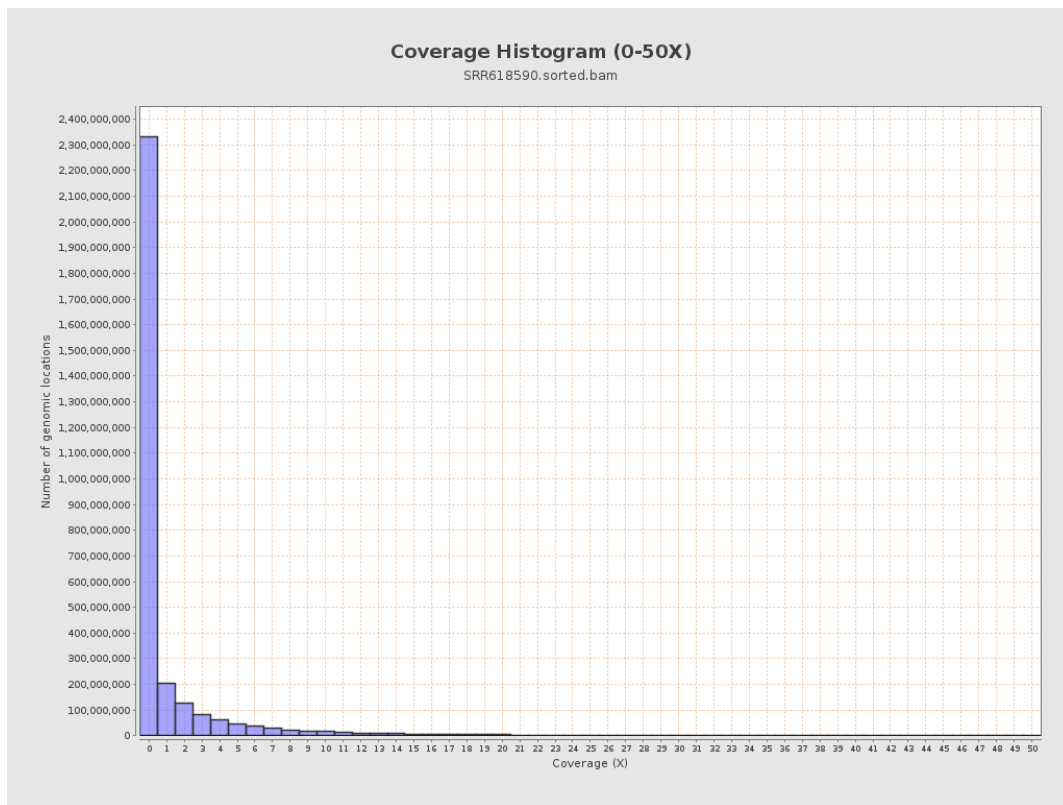
3. Results : Coverage across reference



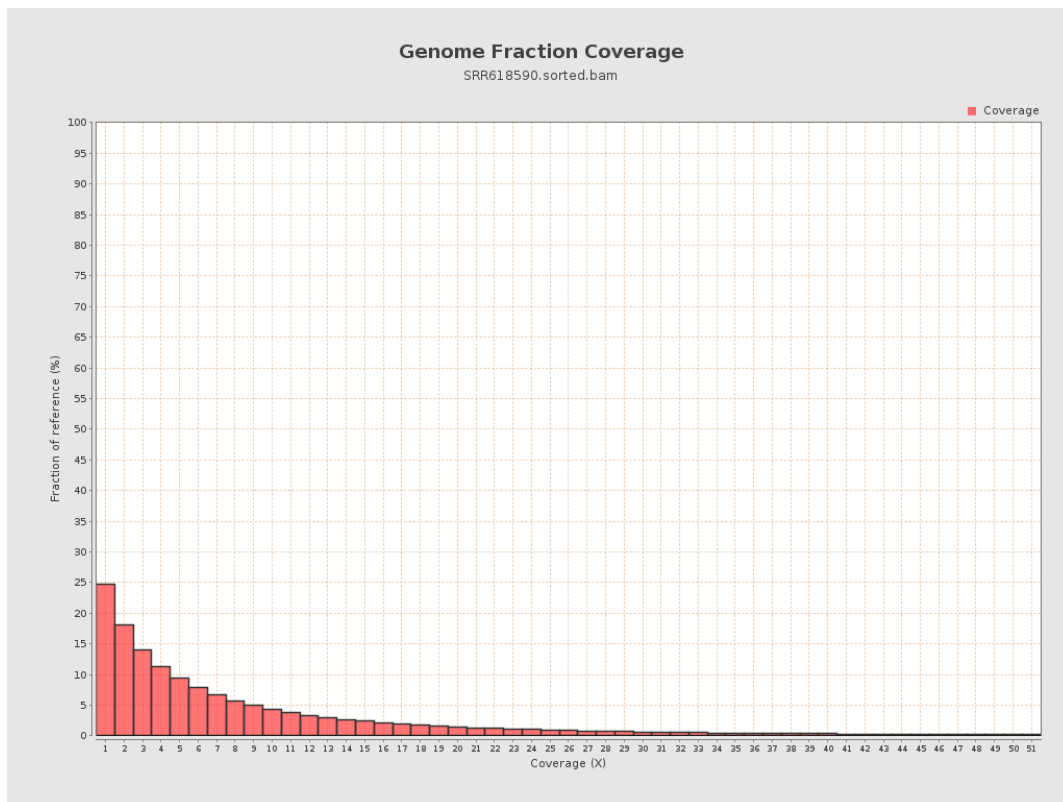
4. Results : Coverage Histogram



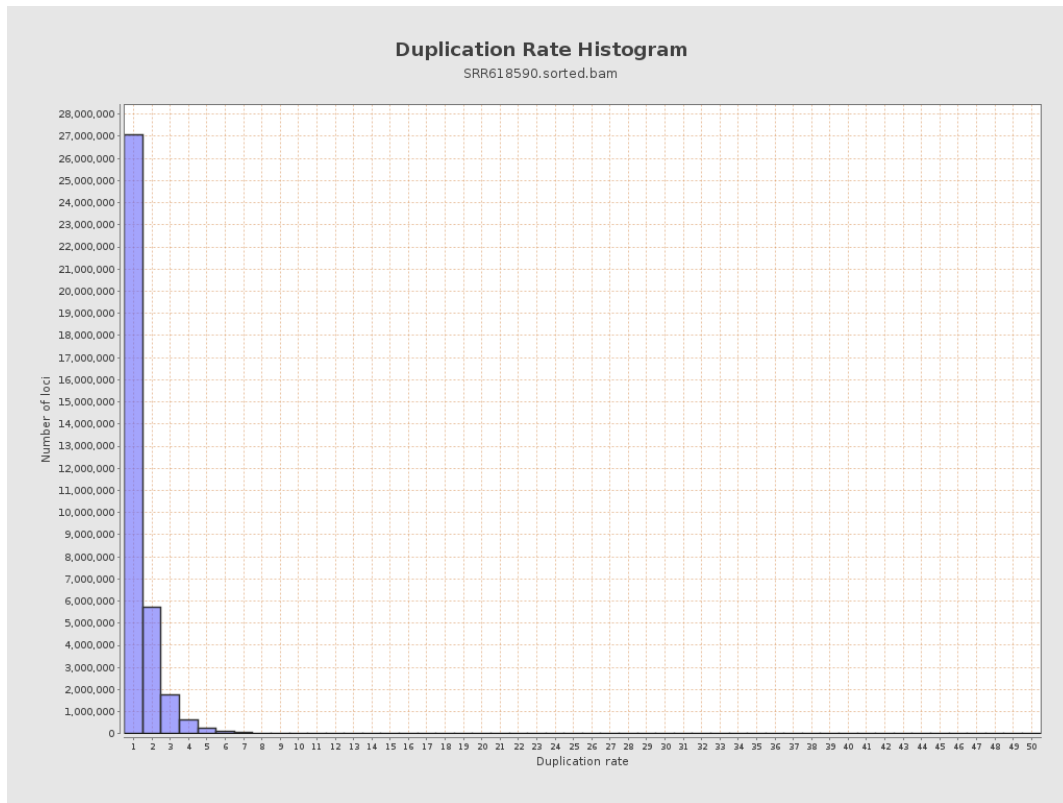
5. Results : Coverage Histogram (0-50X)



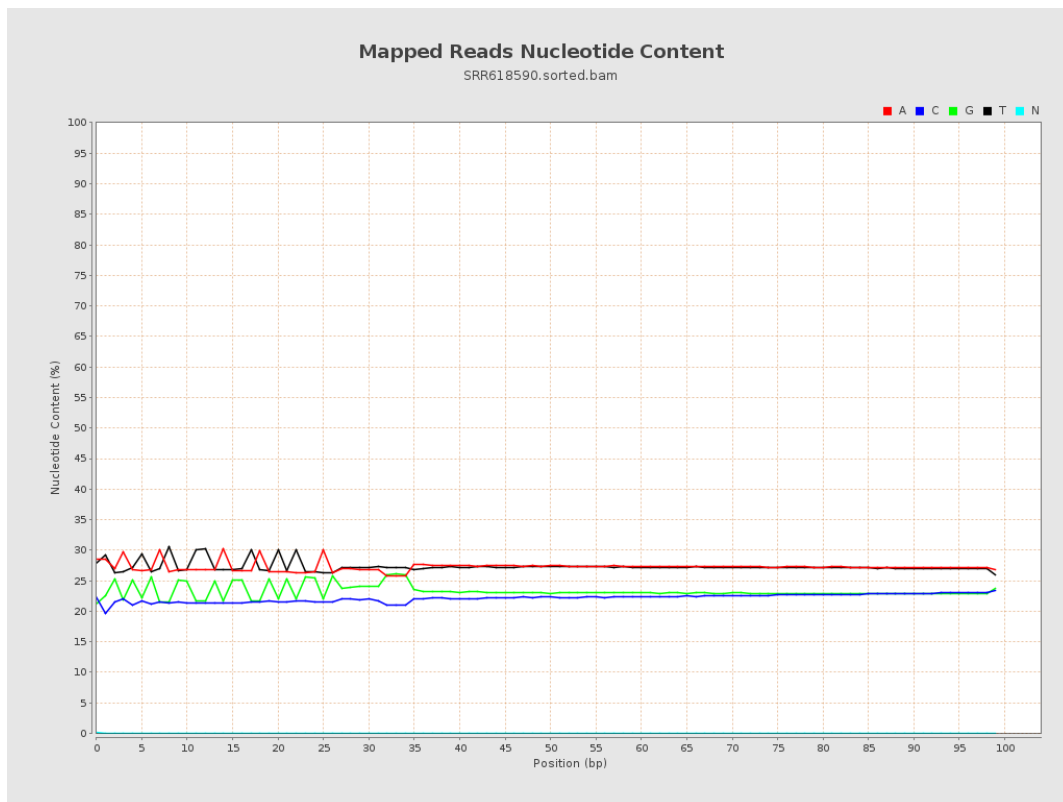
6. Results : Genome Fraction Coverage



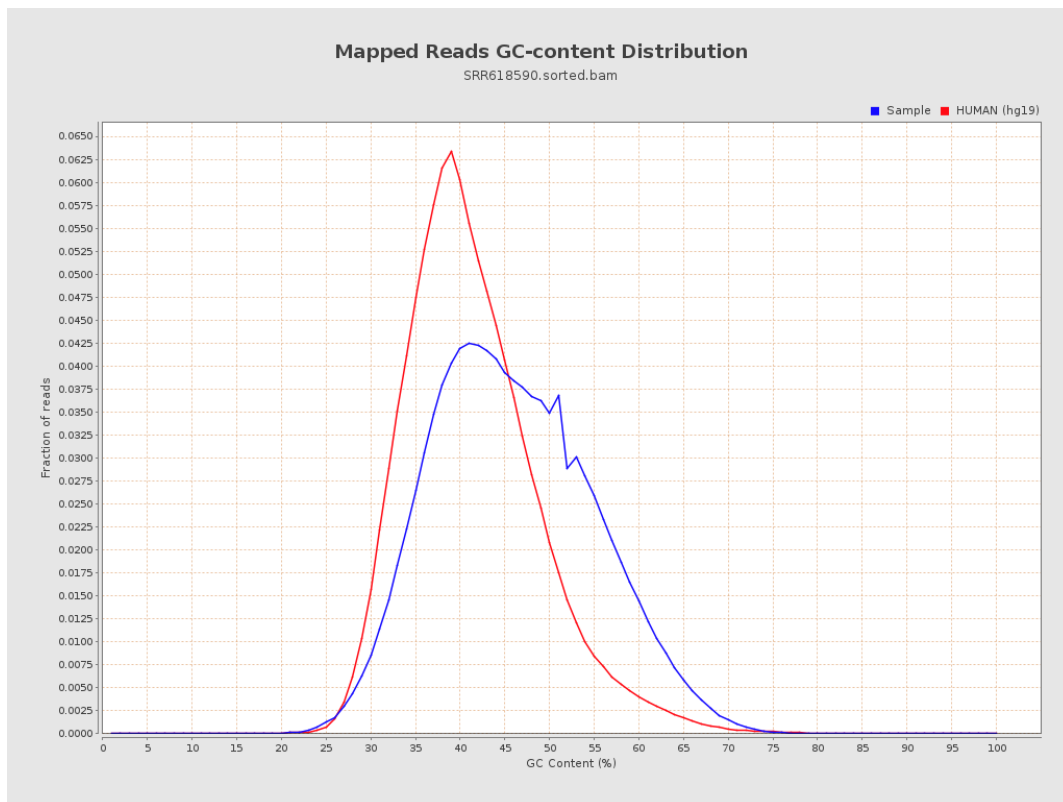
7. Results : Duplication Rate Histogram



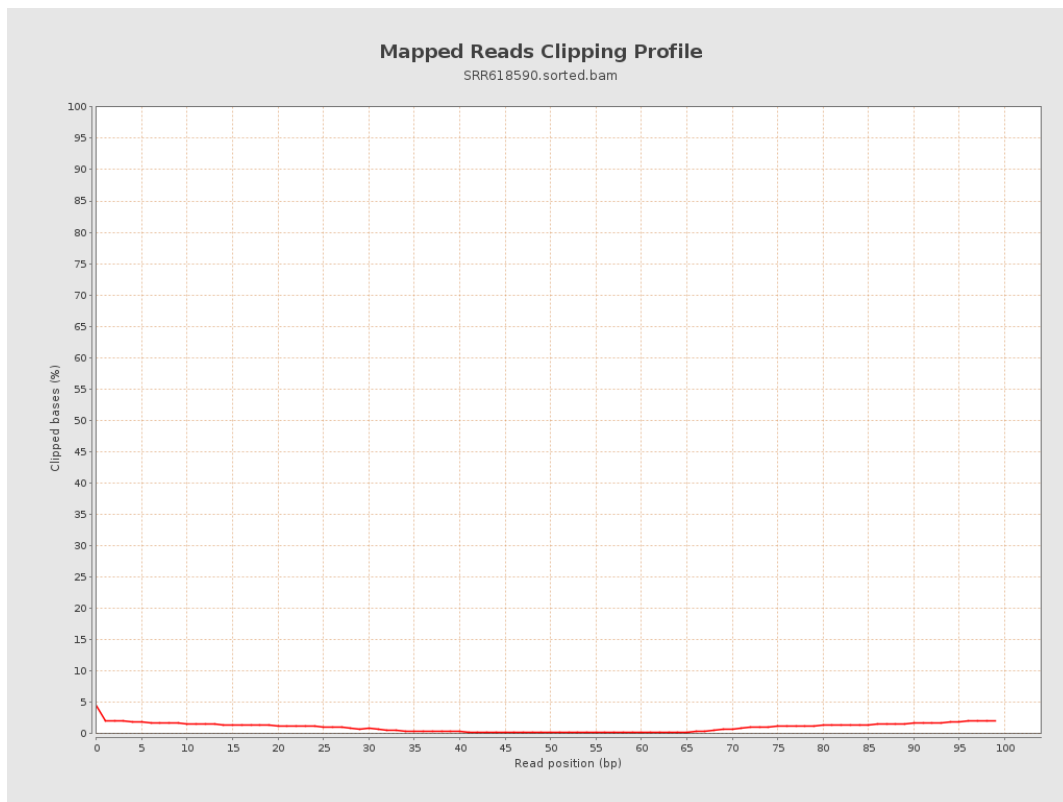
8. Results : Mapped Reads Nucleotide Content



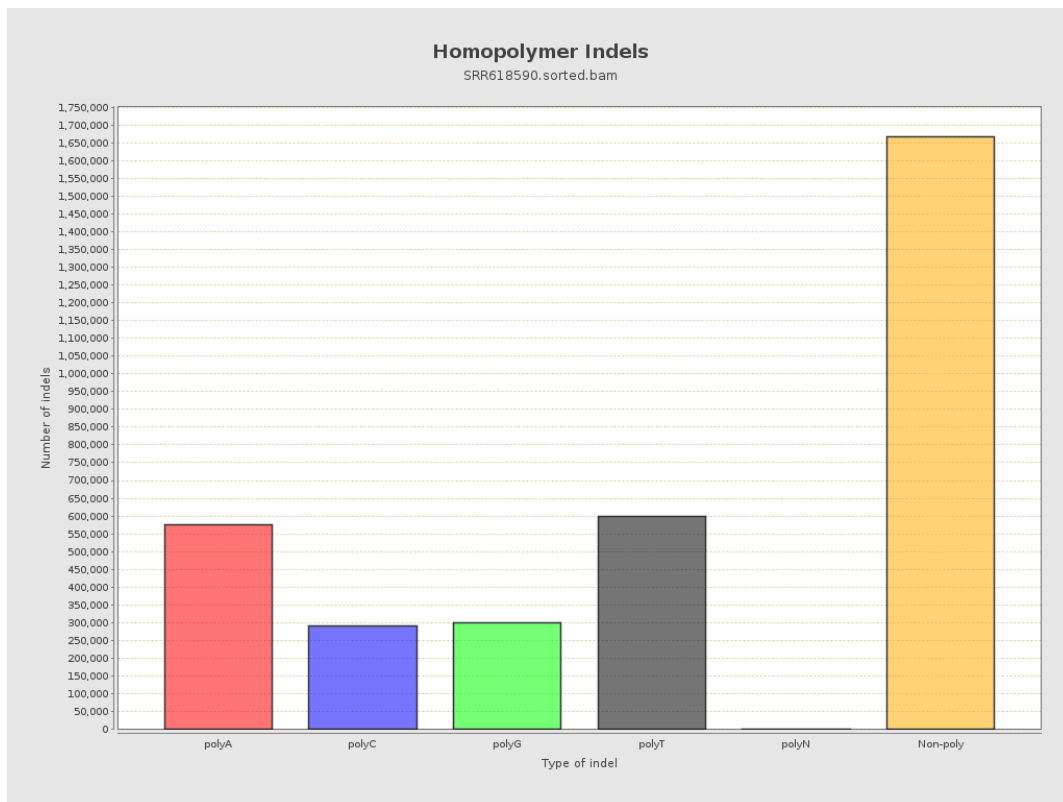
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



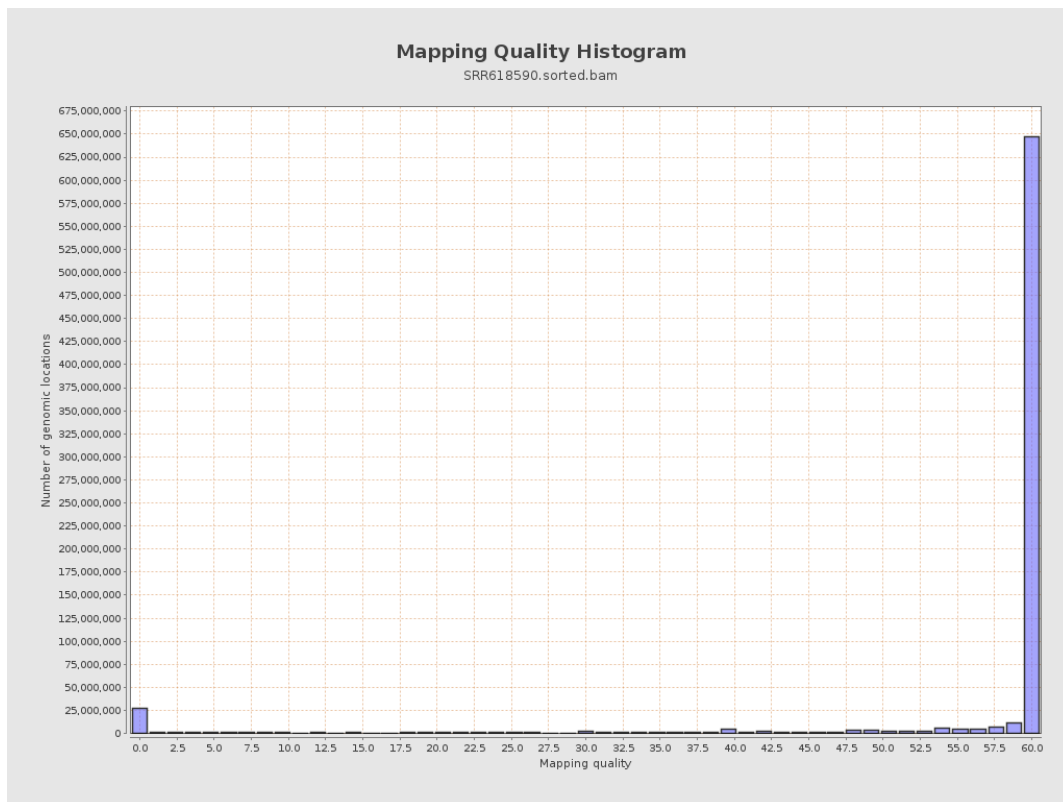
11. Results : Homopolymer Indels



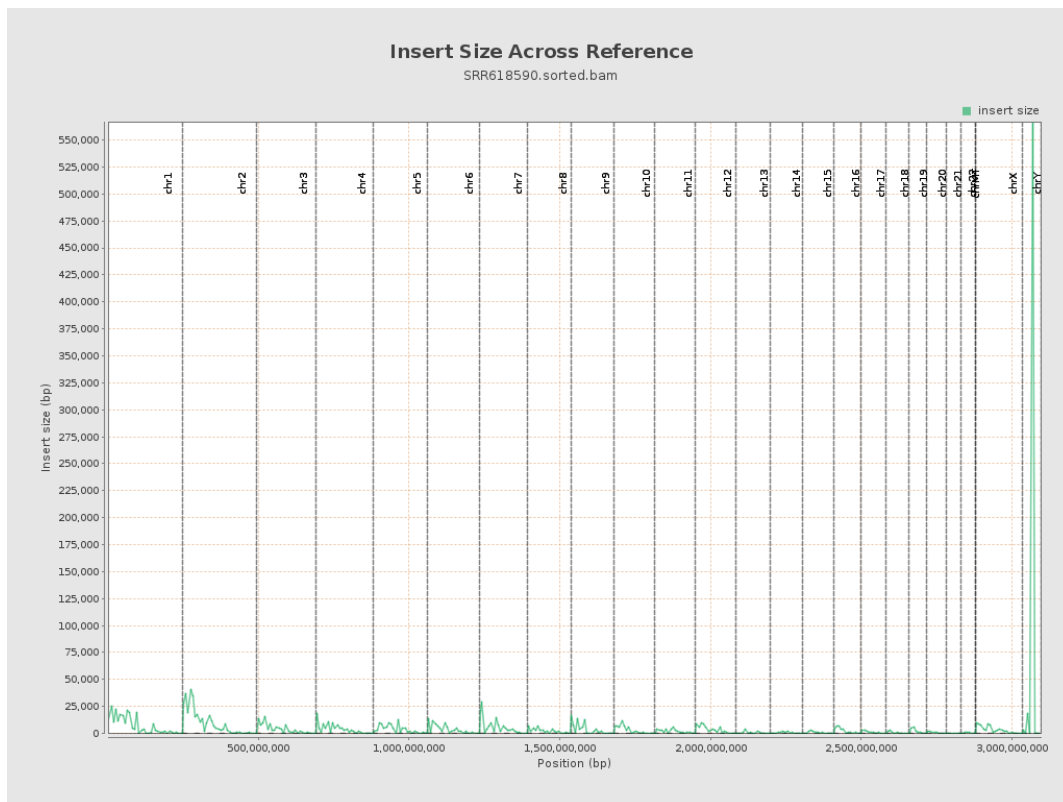
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

