

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/18 21:39:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618598.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_SRR618598 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618598_1.fastq.gz SRR618598_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Jan 18 21:39:26 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618598.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	45,053,364
Mapped reads	43,473,764 / 96.49%
Unmapped reads	1,579,600 / 3.51%
Mapped paired reads	43,473,764 / 96.49%
Mapped reads, first in pair	21,969,532 / 48.76%
Mapped reads, second in pair	21,504,232 / 47.73%
Mapped reads, both in pair	42,769,586 / 94.93%
Mapped reads, singletons	704,178 / 1.56%
Secondary alignments	0
Supplementary alignments	103,001 / 0.23%
Read min/max/mean length	30 / 100 / 100.09
Duplicated reads (estimated)	13,628,439 / 30.25%
Duplication rate	26.8%
Clipped reads	7,216,935 / 16.02%

2.2. ACGT Content

Number/percentage of A's	1,090,750,897 / 26.13%
Number/percentage of C's	972,739,732 / 23.3%
Number/percentage of T's	1,093,247,119 / 26.19%
Number/percentage of G's	1,017,831,333 / 24.38%
Number/percentage of N's	227,349 / 0.01%

GC Percentage	47.68%
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2.3. Coverage

Mean	1.3496
Standard Deviation	7.0405

2.4. Mapping Quality

Mean Mapping Quality	53.87
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2.5. Insert size

Mean	45,312.54
Standard Deviation	2,119,834.69
P25/Median/P75	177 / 204 / 242

2.6. Mismatches and indels

General error rate	1.36%
Mismatches	55,560,498
Insertions	803,065
Mapped reads with at least one insertion	1.81%
Deletions	2,321,747
Mapped reads with at least one deletion	5.19%
Homopolymer indels	52.6%

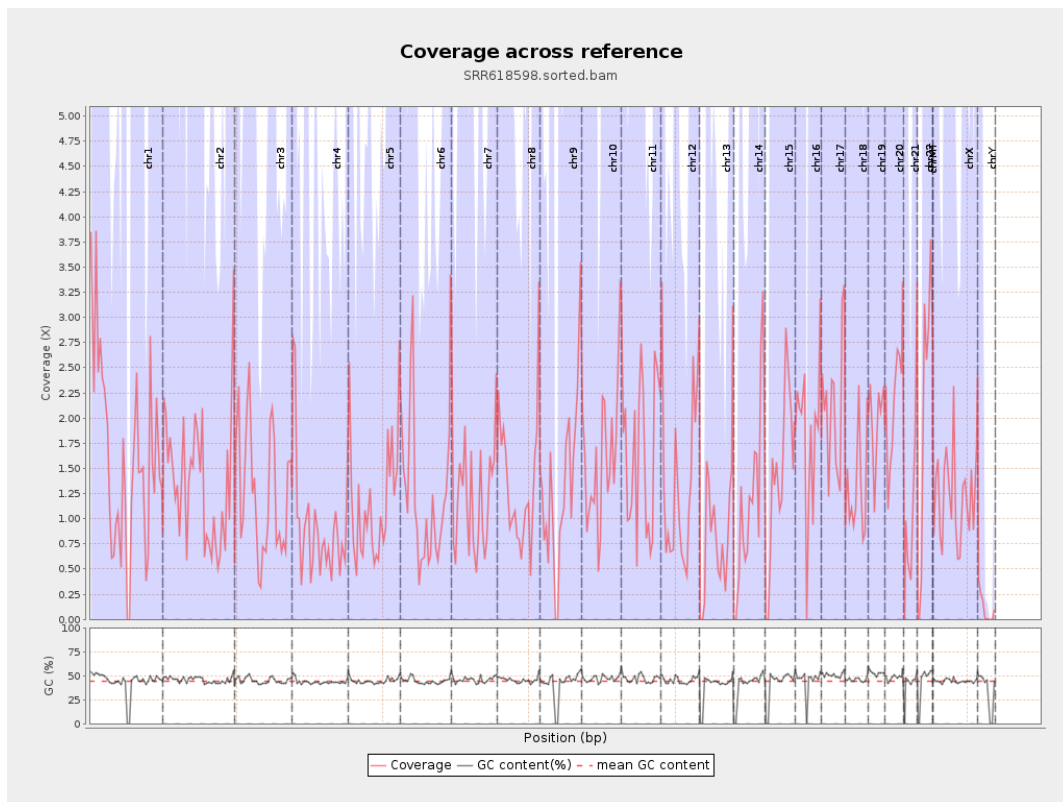
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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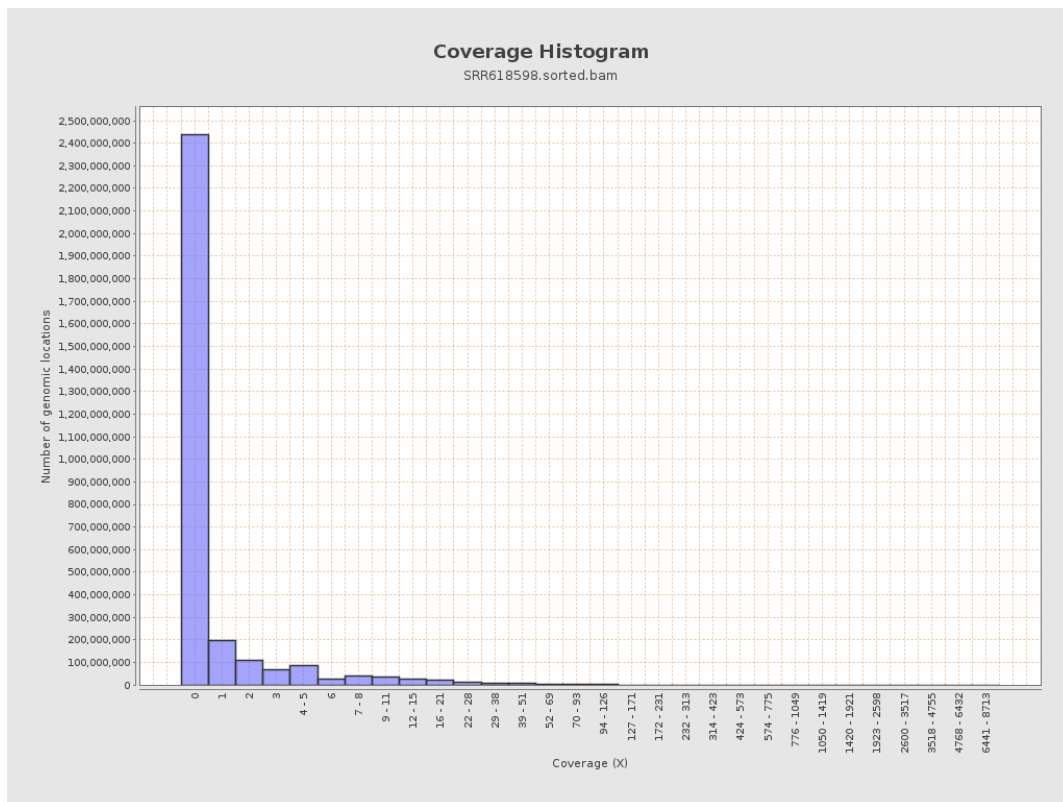
		bases	coverage	deviation
chr1	249250621	397488065	1.5947	7.4453
chr2	243199373	328879648	1.3523	8.0867
chr3	198022430	247171107	1.2482	5.4331
chr4	191154276	175171542	0.9164	4.9664
chr5	180915260	215449861	1.1909	5.1896
chr6	171115067	207947494	1.2152	5.3734
chr7	159138663	198649710	1.2483	5.582
chr8	146364022	194648972	1.3299	5.9553
chr9	141213431	185013055	1.3102	6.9567
chr10	135534747	213888811	1.5781	6.5718
chr11	135006516	223876527	1.6583	7.1841
chr12	133851895	183028408	1.3674	6.144
chr13	115169878	94023466	0.8164	3.8831
chr14	107349540	127249997	1.1854	5.7928
chr15	102531392	147366987	1.4373	6.712
chr16	90354753	165368382	1.8302	16.4733
chr17	81195210	168898567	2.0802	8.6778
chr18	78077248	98578428	1.2626	6.0499
chr19	59128983	114804664	1.9416	9.0526
chr20	63025520	134552313	2.1349	8.0185
chr21	48129895	54640221	1.1353	10.8895
chr22	51304566	104478180	2.0364	9.032
chrMT	16571	30471	1.8388	6.8851
chrX	155270560	190387826	1.2262	5.0514

chrY	59373566	6363355	0.1072	5.7067
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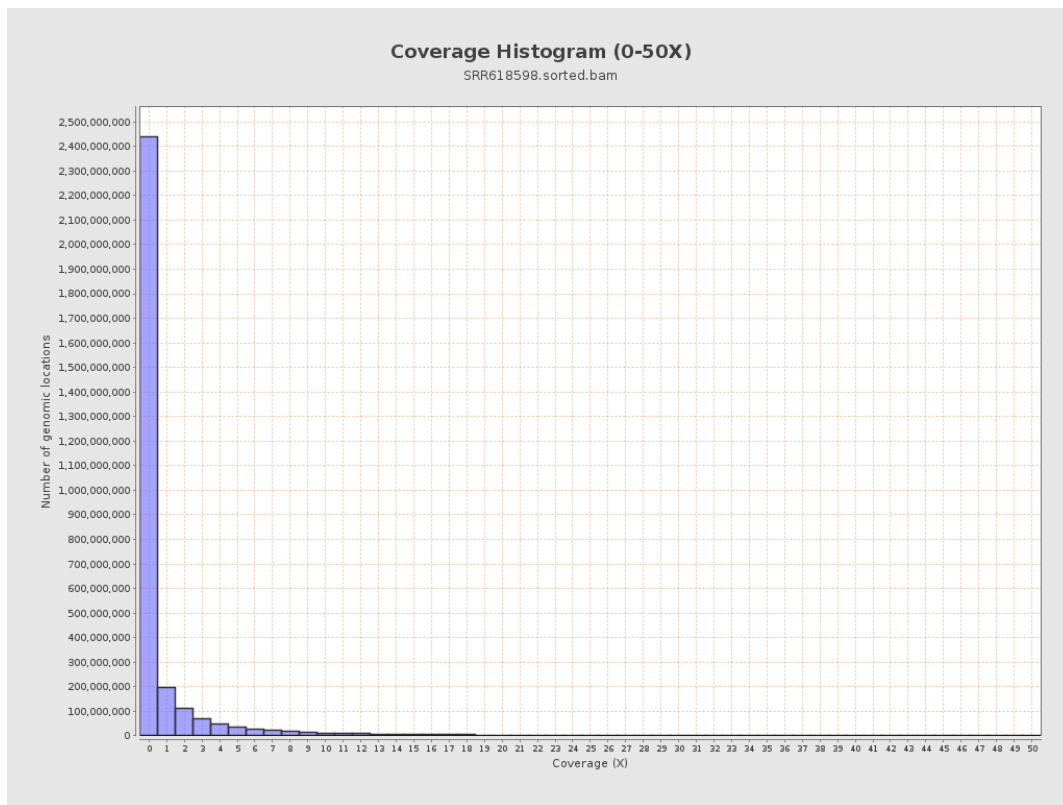
3. Results : Coverage across reference



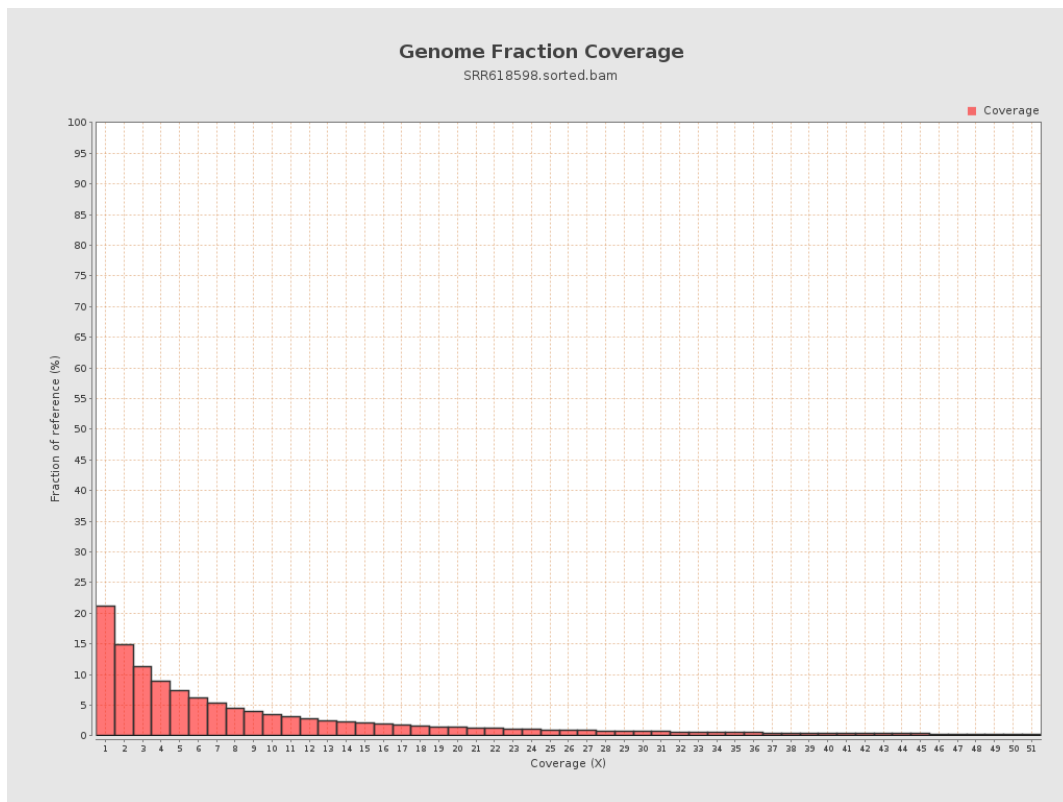
4. Results : Coverage Histogram



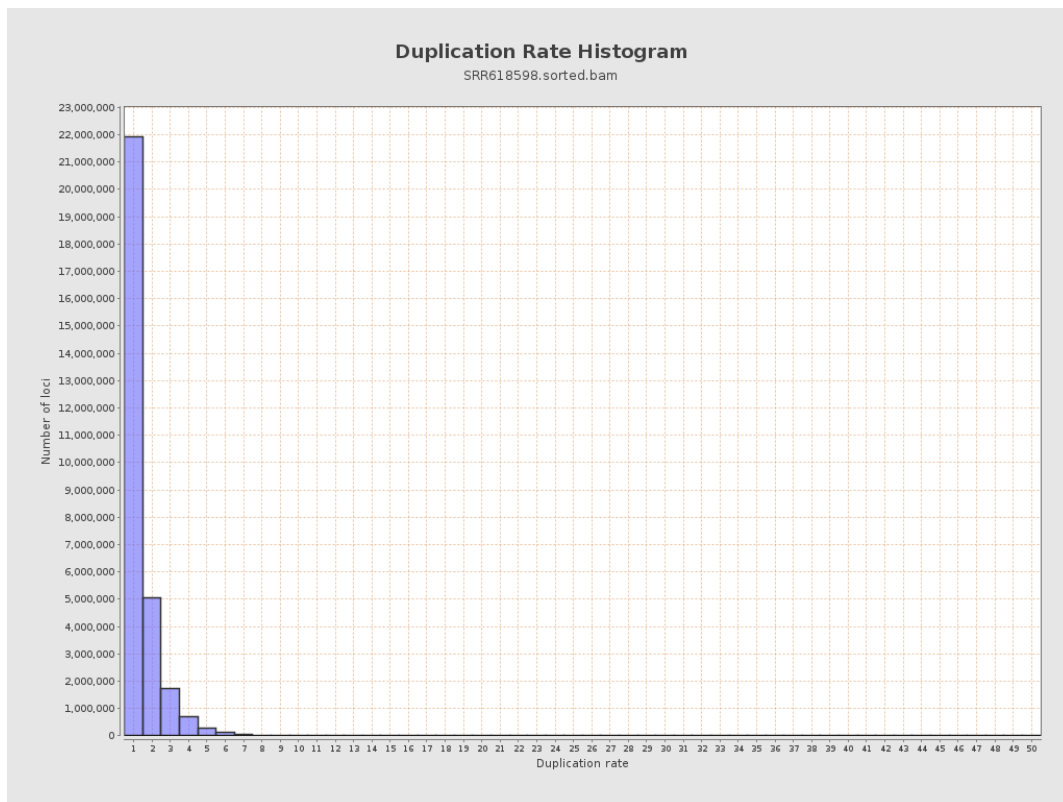
5. Results : Coverage Histogram (0-50X)



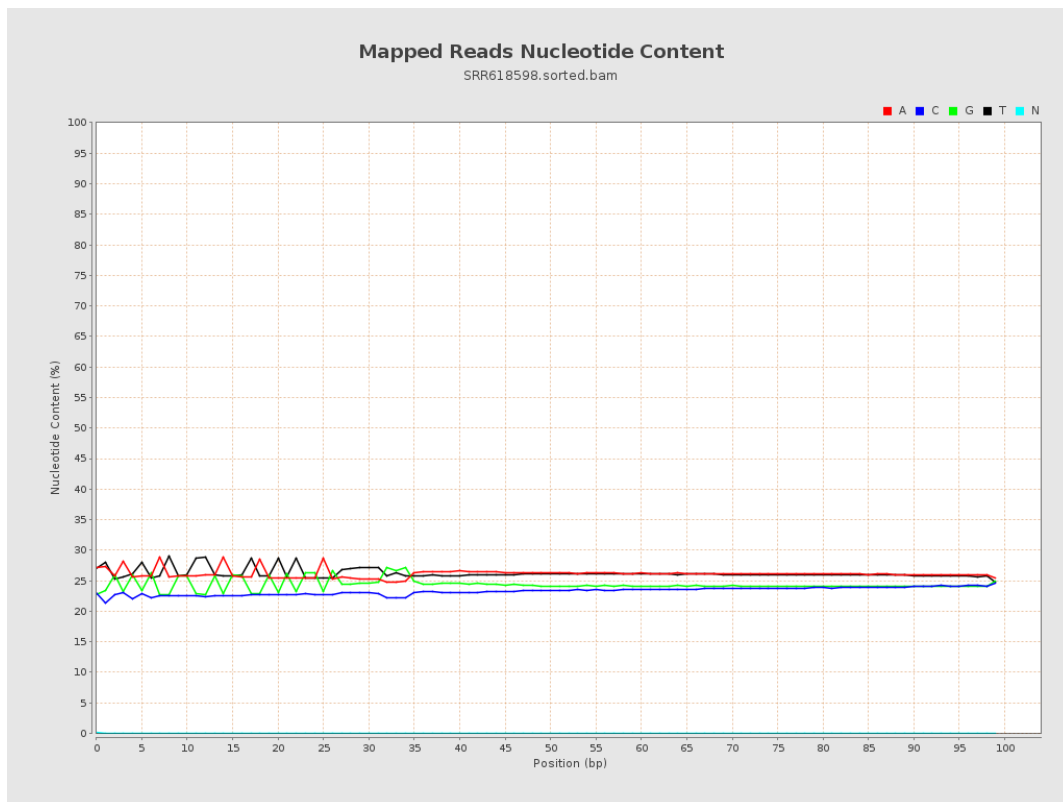
6. Results : Genome Fraction Coverage



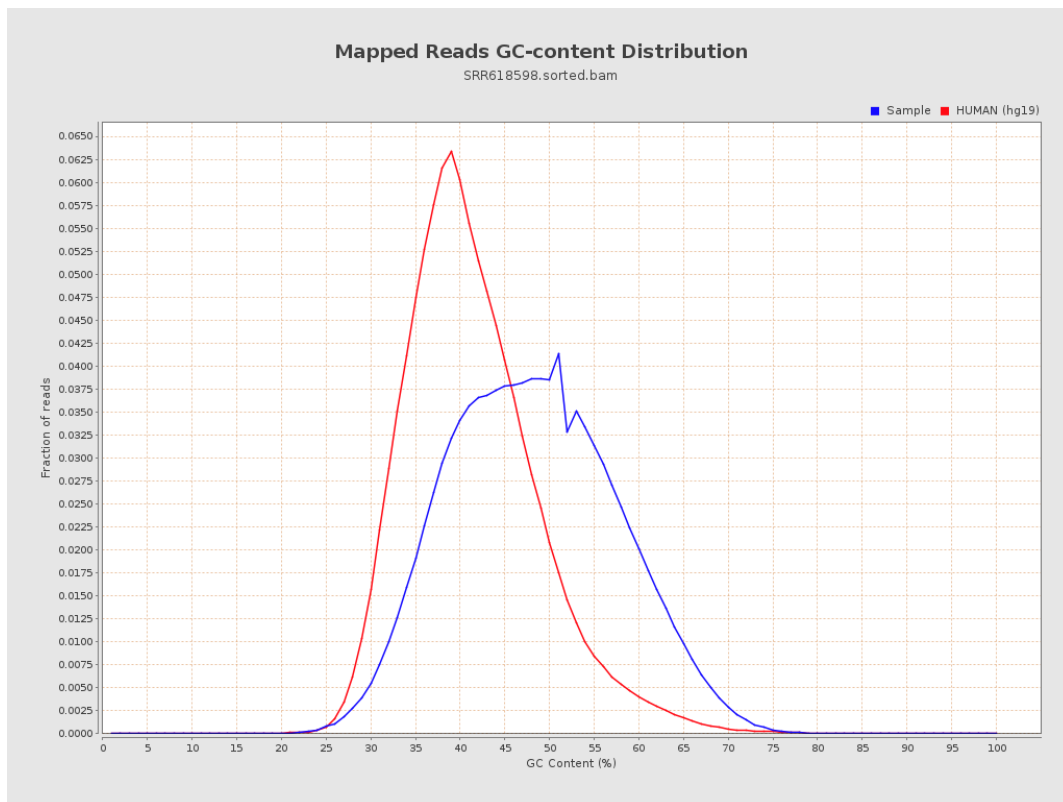
7. Results : Duplication Rate Histogram



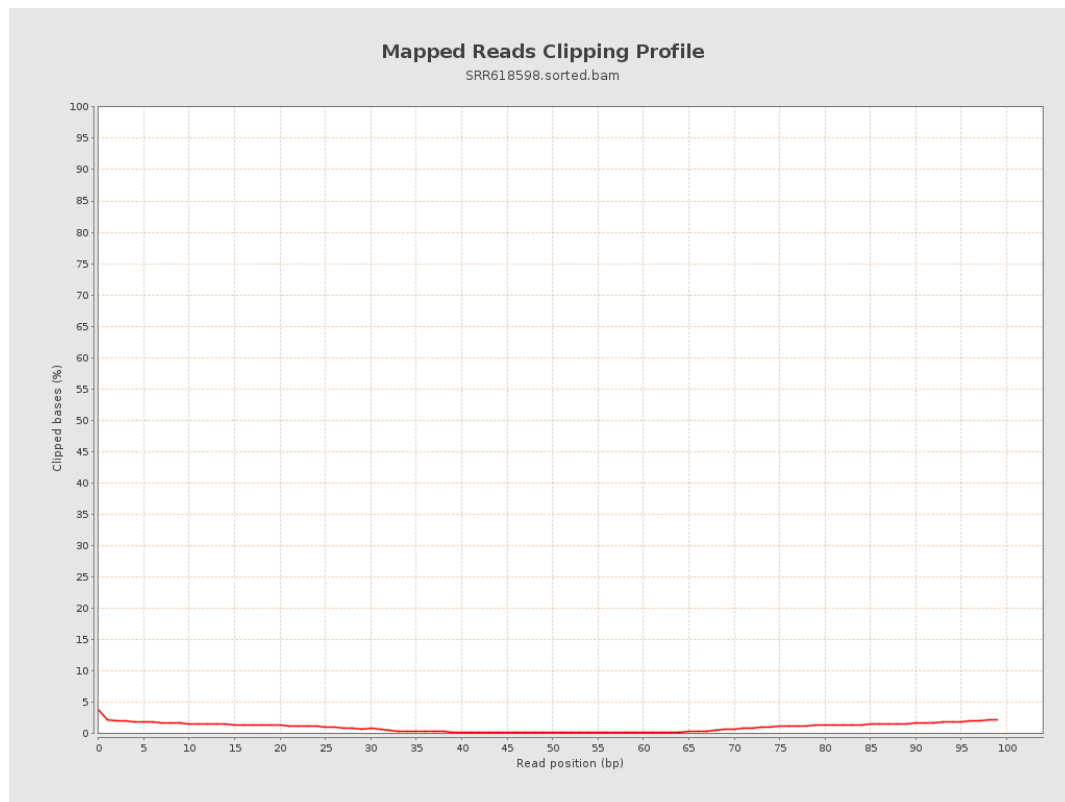
8. Results : Mapped Reads Nucleotide Content



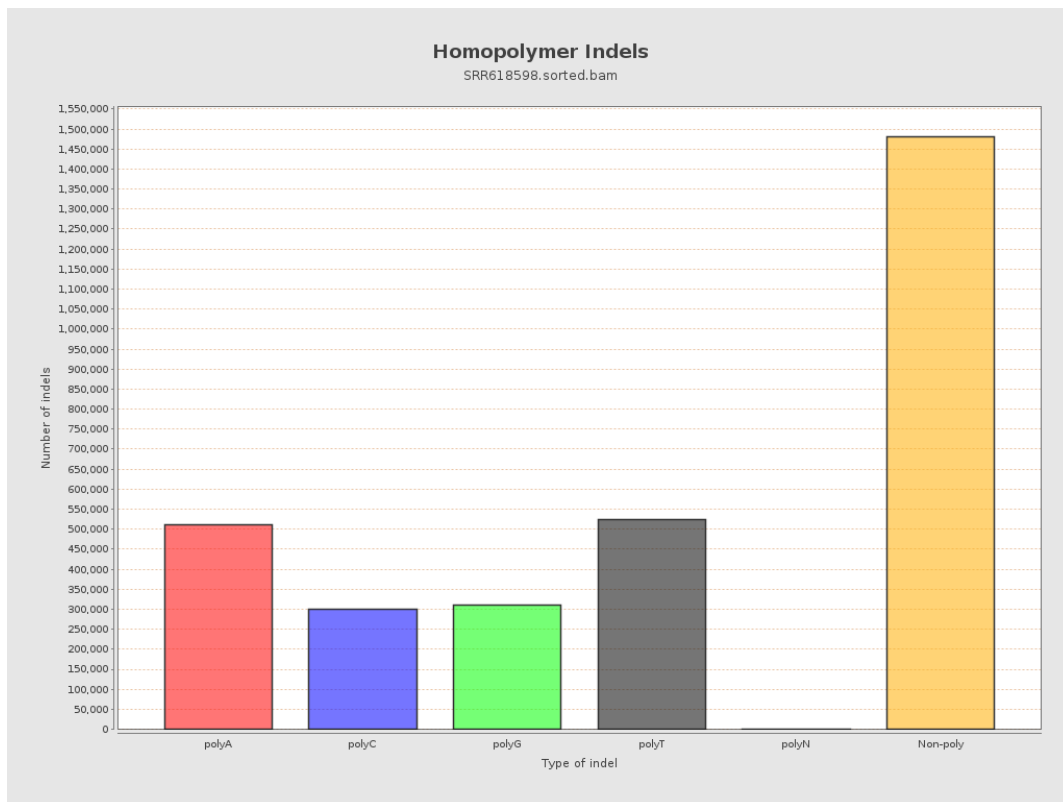
9. Results : Mapped Reads GC-content Distribution



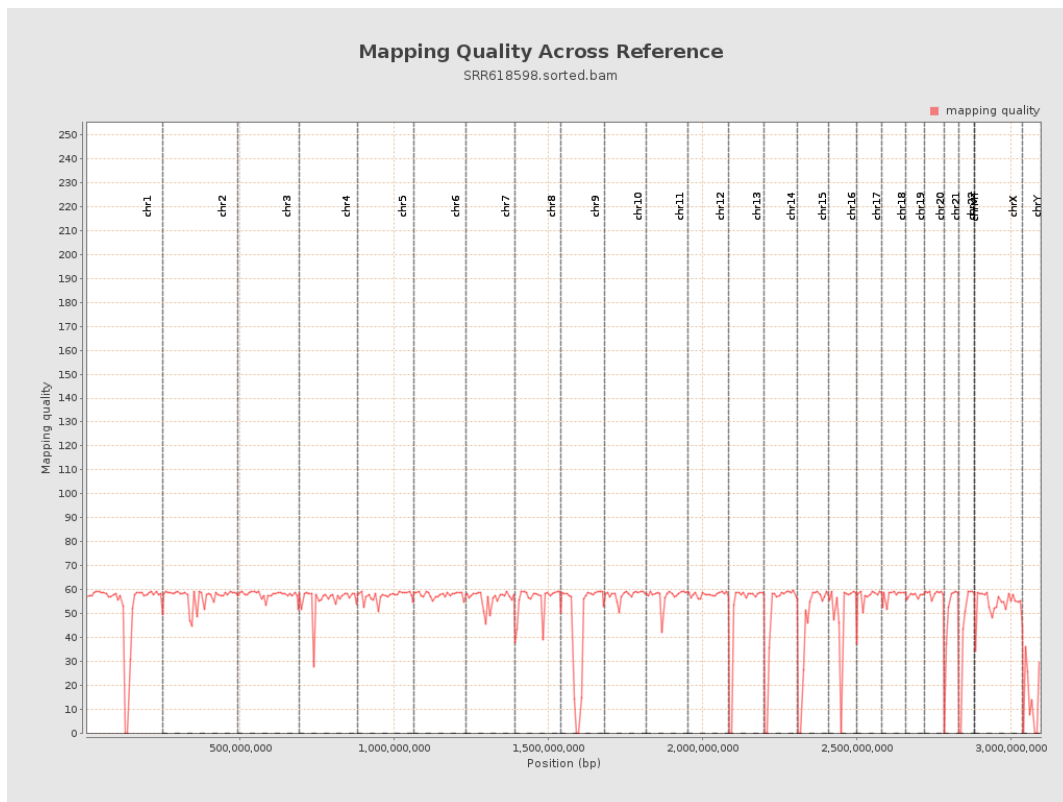
10. Results : Mapped Reads Clipping Profile



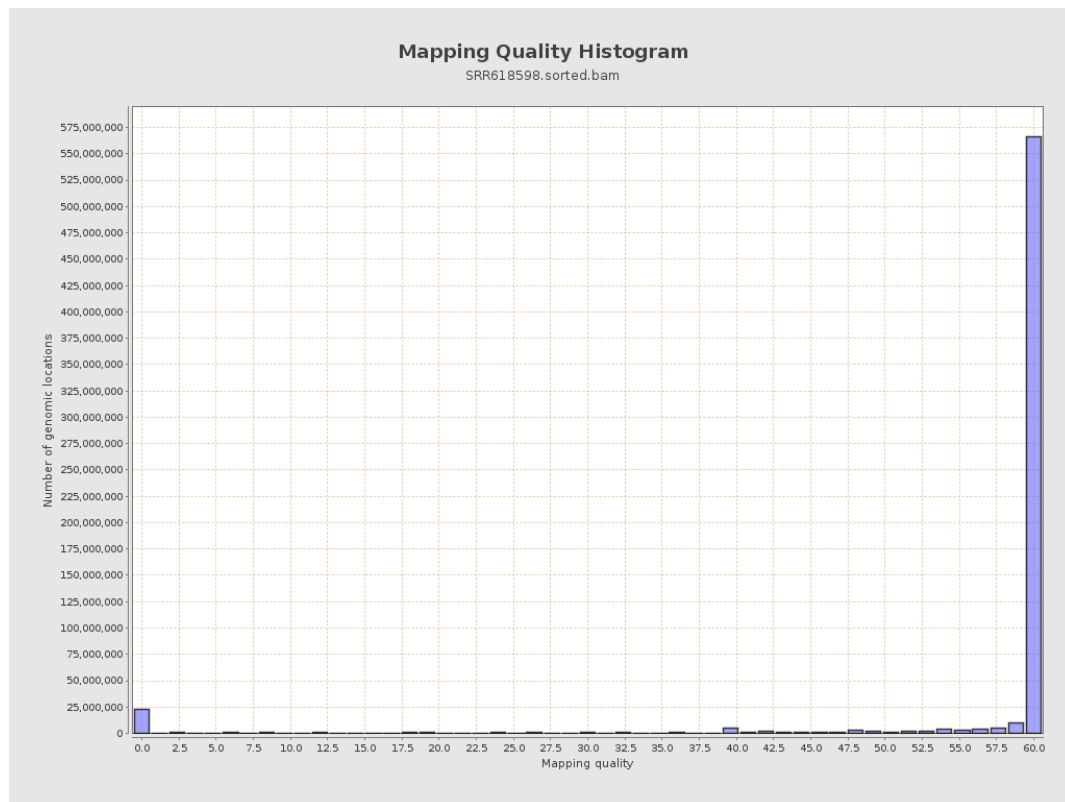
11. Results : Homopolymer Indels



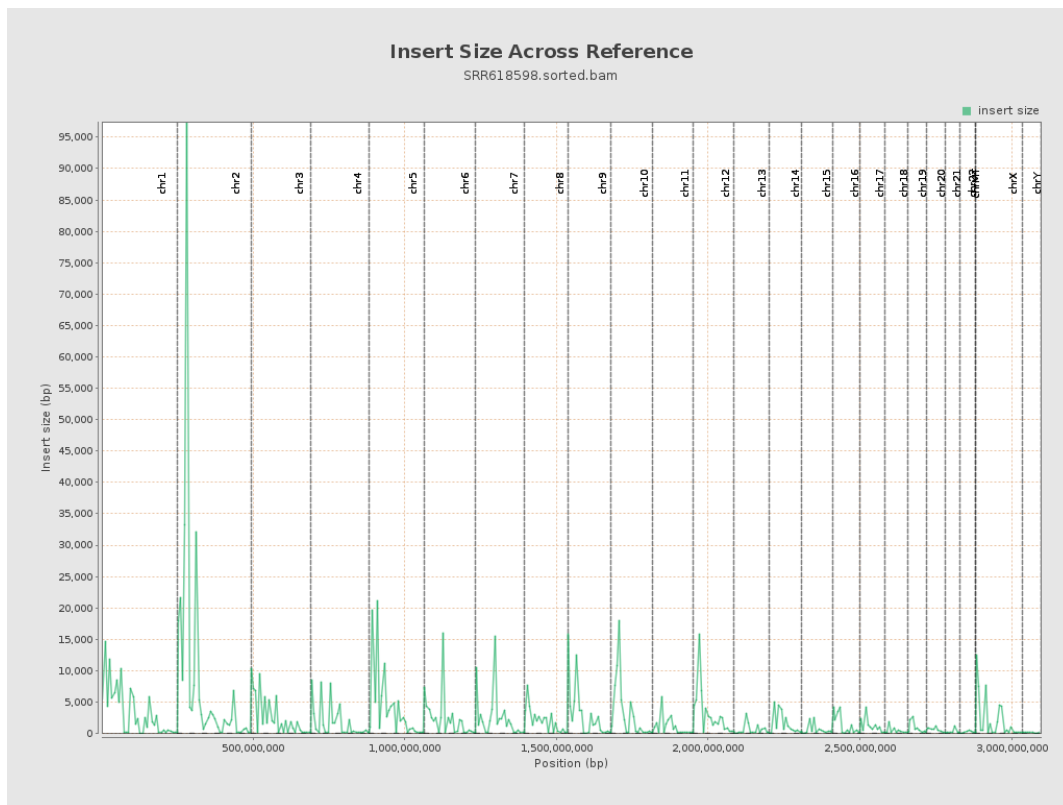
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

