Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/31 00:45:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR504630.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_SRR504630 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR504630_1.fastq.gz SRR504630_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 31 00:45:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR504630.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	598,059,300
Mapped reads	514,938,517 / 86.1%
Unmapped reads	83,120,783 / 13.9%
Mapped paired reads	514,938,517 / 86.1%
Mapped reads, first in pair	262,262,954 / 43.85%
Mapped reads, second in pair	252,675,563 / 42.25%
Mapped reads, both in pair	492,232,572 / 82.3%
Mapped reads, singletons	22,705,945 / 3.8%
Secondary alignments	0
Supplementary alignments	4,491,211 / 0.75%
Read min/max/mean length	30 / 100 / 100.3
Duplicated reads (estimated)	183,324,794 / 30.65%
Duplication rate	23.99%
Clipped reads	121,841,282 / 20.37%

2.2. ACGT Content

Number/percentage of A's	13,179,309,780 / 27.21%
Number/percentage of C's	10,995,431,604 / 22.7%
Number/percentage of T's	13,338,506,029 / 27.53%
Number/percentage of G's	10,903,379,605 / 22.51%
Number/percentage of N's	26,032,787 / 0.05%

GC Percentage	45.21%

2.3. Coverage

Mean	15.6612
Standard Deviation	331.6805

2.4. Mapping Quality

Mean Mapping Quality	51.56

2.5. Insert size

Mean	102,675.94
Standard Deviation	2,977,552.56
P25/Median/P75	308 / 353 / 406

2.6. Mismatches and indels

General error rate	2.59%
Mismatches	1,202,603,085
Insertions	13,298,845
Mapped reads with at least one insertion	2.41%
Deletions	12,221,971
Mapped reads with at least one deletion	2.22%
Homopolymer indels	33.18%

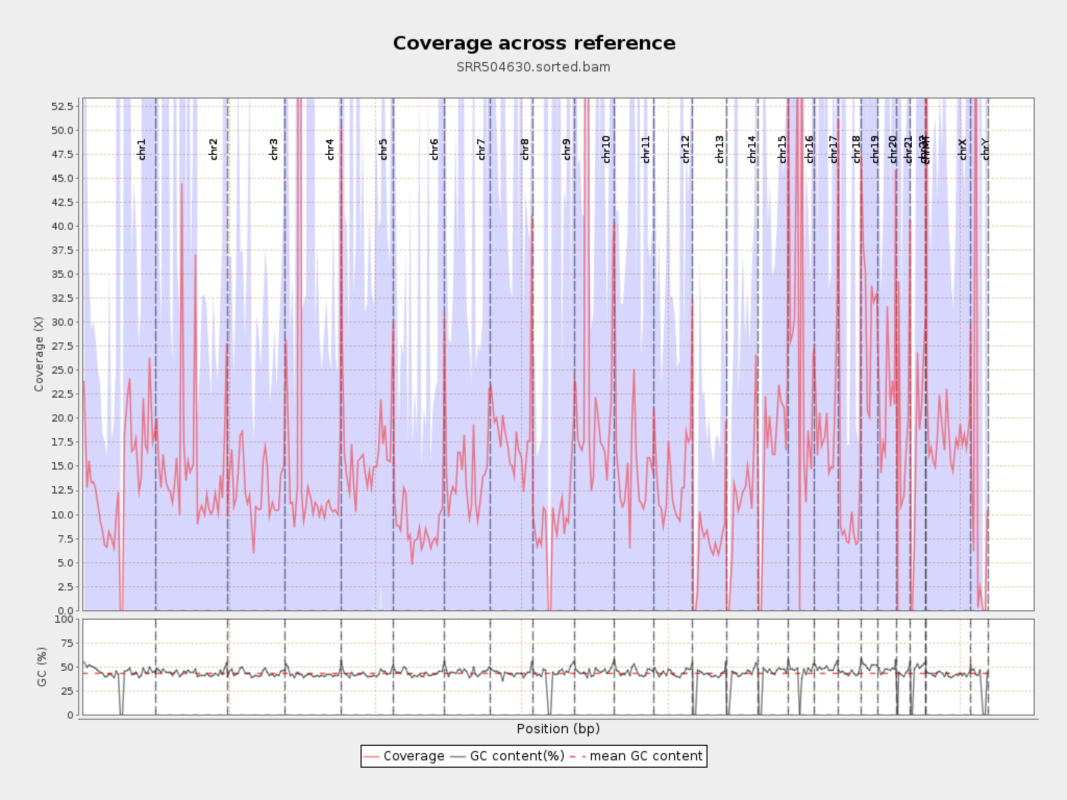
2.7. Chromosome stats

Name	**Length**	**Mapped**	**Mean**	**Standard**

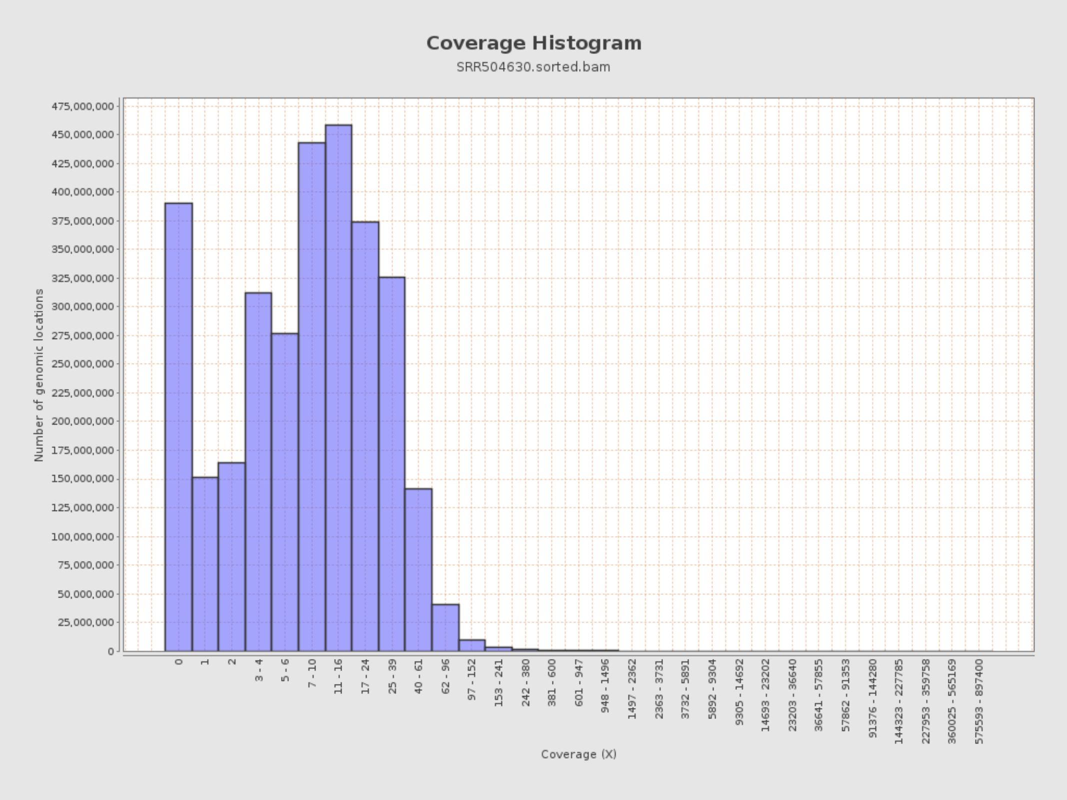
		bases	**coverage**	**deviation**
chr1	249250621	3426367585	13.7467	111.0932
chr2	243199373	3664985279	15.0699	340.6215
chr3	198022430	2506071598	12.6555	38.6572
chr4	191154276	3513778042	18.3819	840.4667
chr5	180915260	3012445590	16.6511	47.4274
chr6	171115067	1450550223	8.477	34.4862
chr7	159138663	2284735538	14.3569	53.5914
chr8	146364022	2706389363	18.4908	252.094
chr9	141213431	1271727445	9.0057	159.7006
chr10	135534747	3618988671	26.7016	814.4388
chr11	135006516	1971299421	14.6015	39.2253
chr12	133851895	1839014315	13.7392	34.2662
chr13	115169878	756671396	6.57	16.5476
chr14	107349540	1249616741	11.6406	40.7186
chr15	102531392	1653667300	16.1284	26.9732
chr16	90354753	2556975912	28.2993	332.8318
chr17	81195210	1540690099	18.9751	107.4241
chr18	78077248	805585354	10.3178	420.3603
chr19	59128983	1841894857	31.1505	67.3997
chr20	63025520	1415630767	22.4612	229.4316
chr21	48129895	921168869	19.1392	303.6227
chr22	51304566	839213214	16.3575	43.6696
chrMT	16571	16227398	979.2649	455.2408
chrX	155270560	2823346357	18.1834	36.9539

chrY	59373566	795180800	13.3928	781.3129

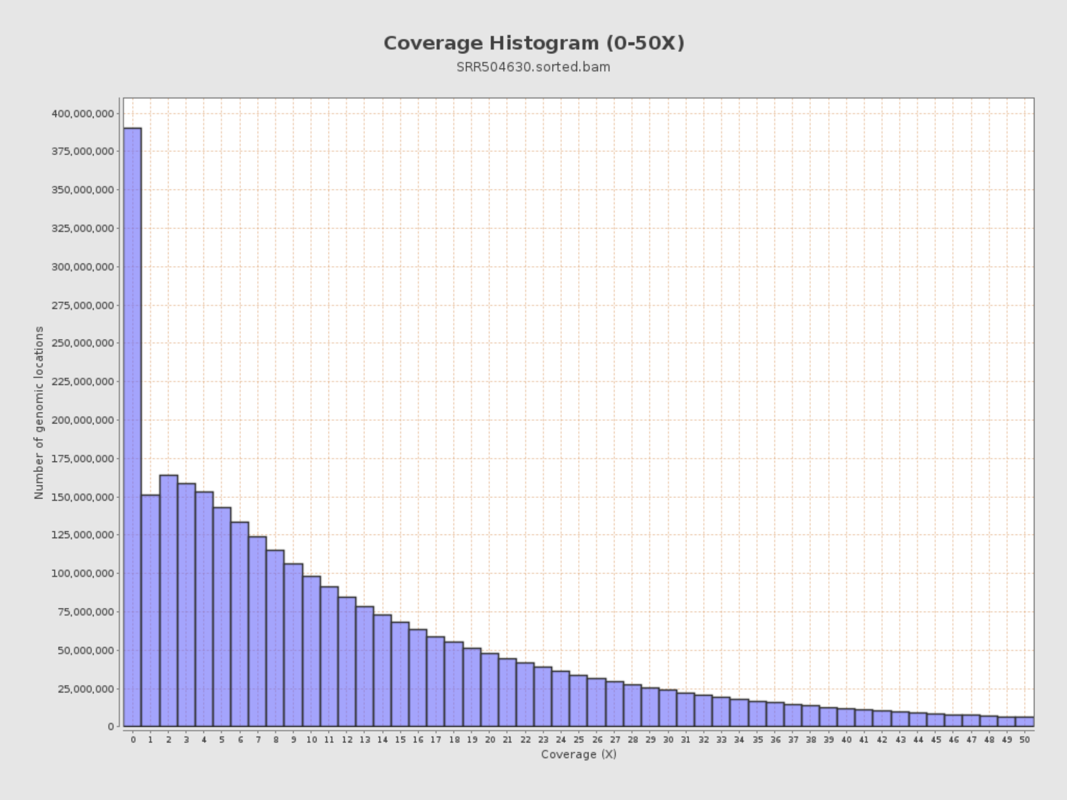
3. Results : Coverage across reference



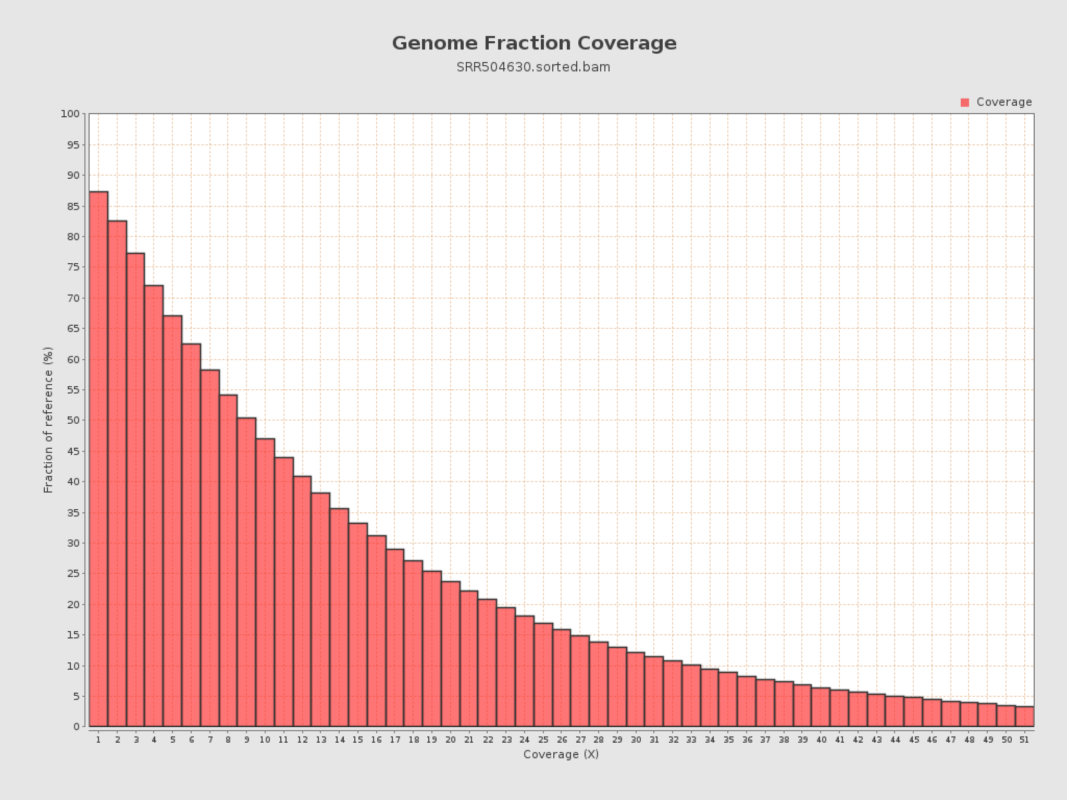
4. Results : Coverage Histogram



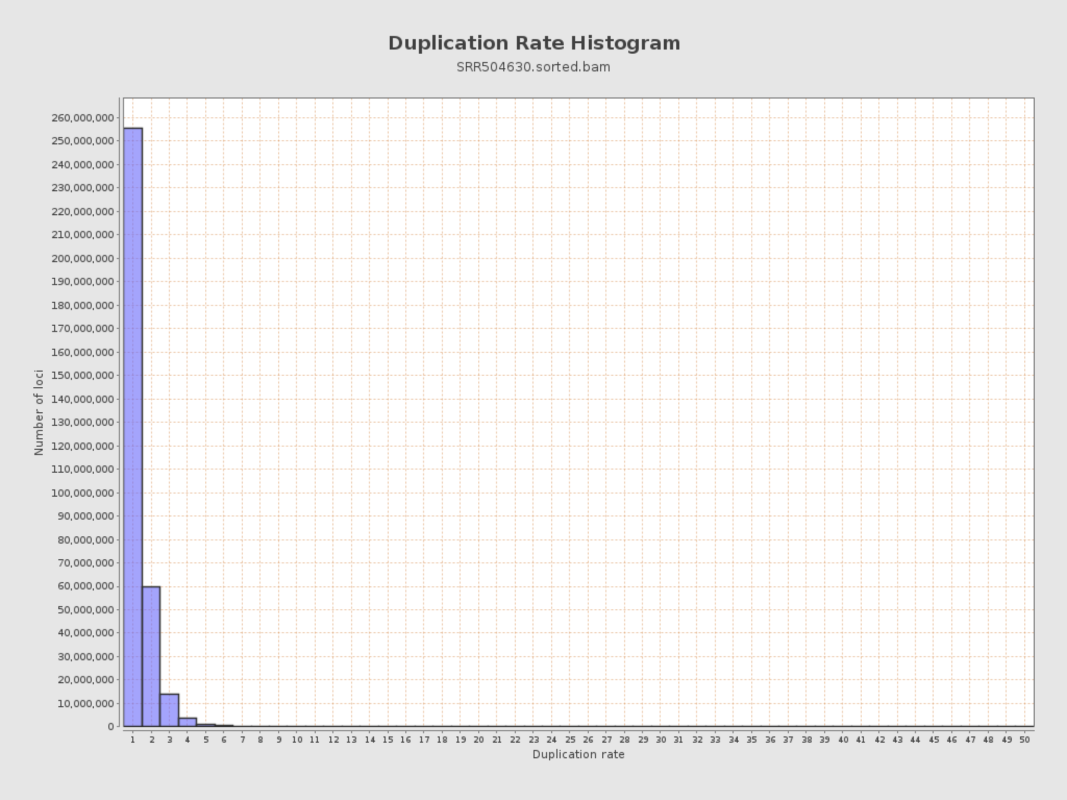
5. Results : Coverage Histogram (0-50X)



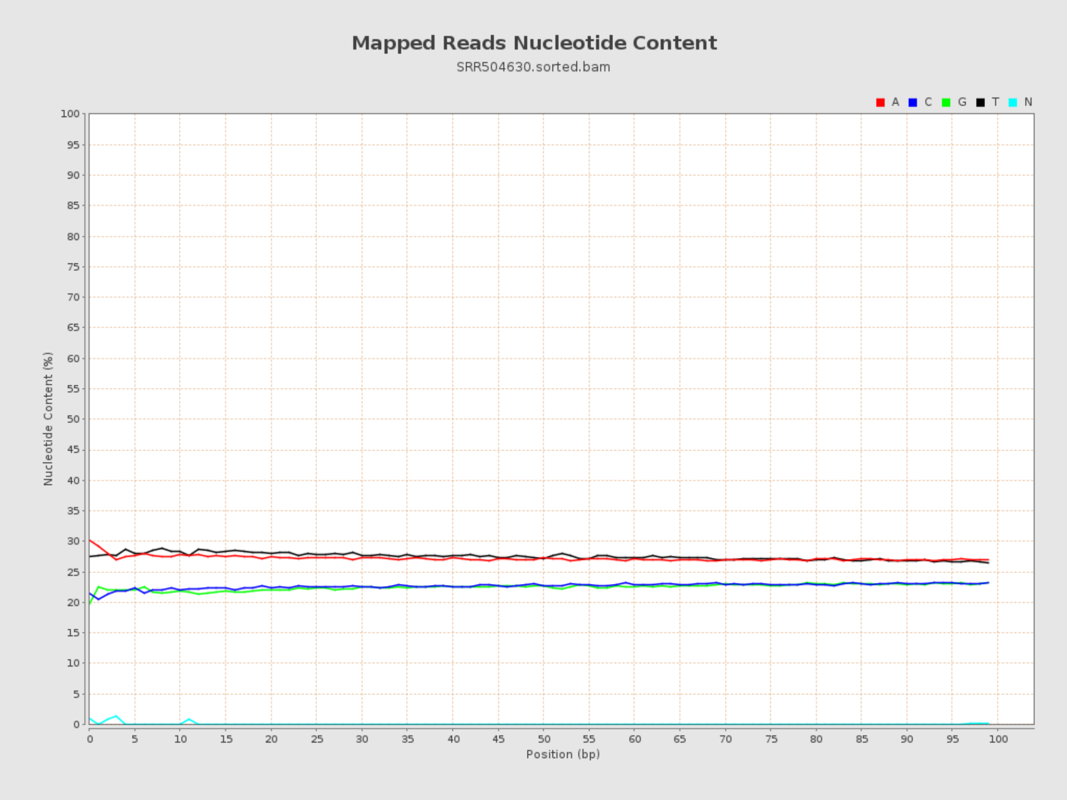
6. Results : Genome Fraction Coverage



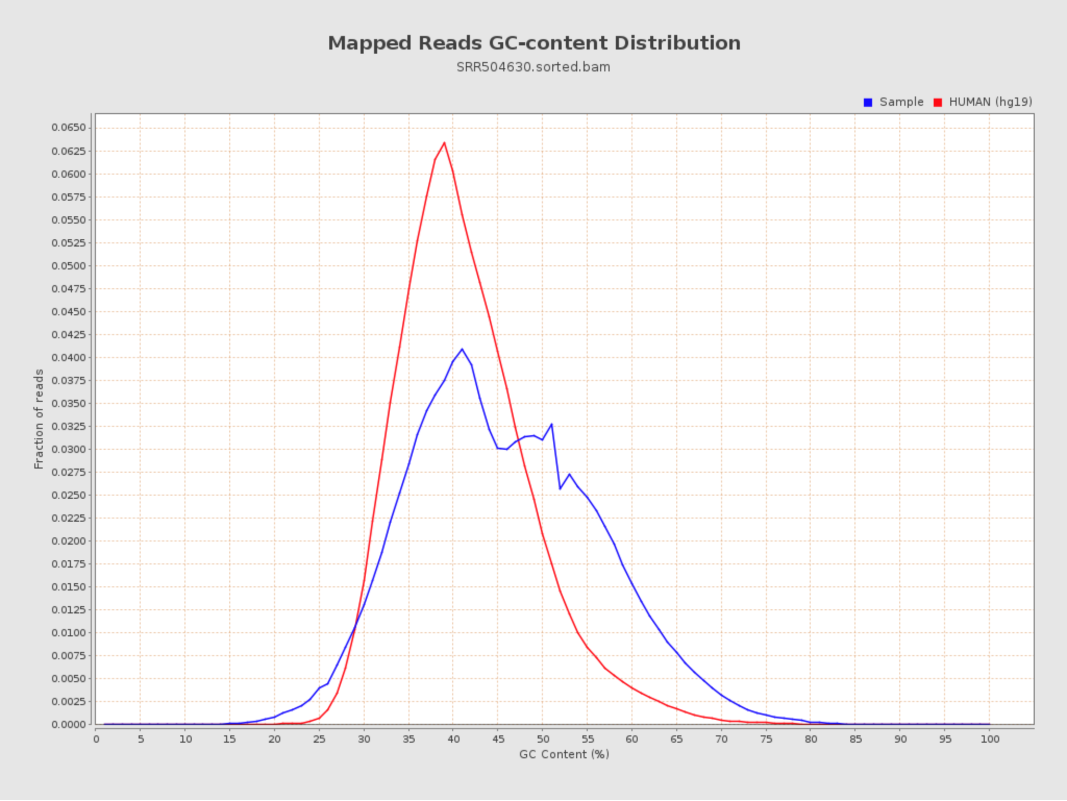
7. Results : Duplication Rate Histogram



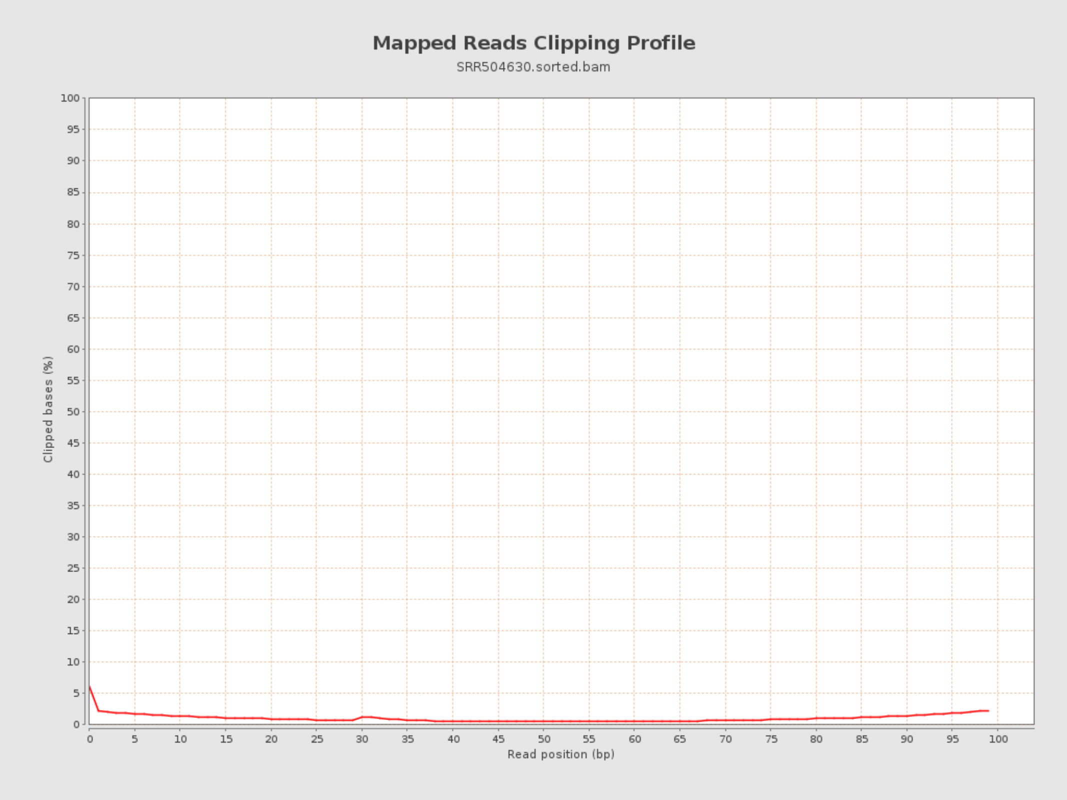
8. Results : Mapped Reads Nucleotide Content



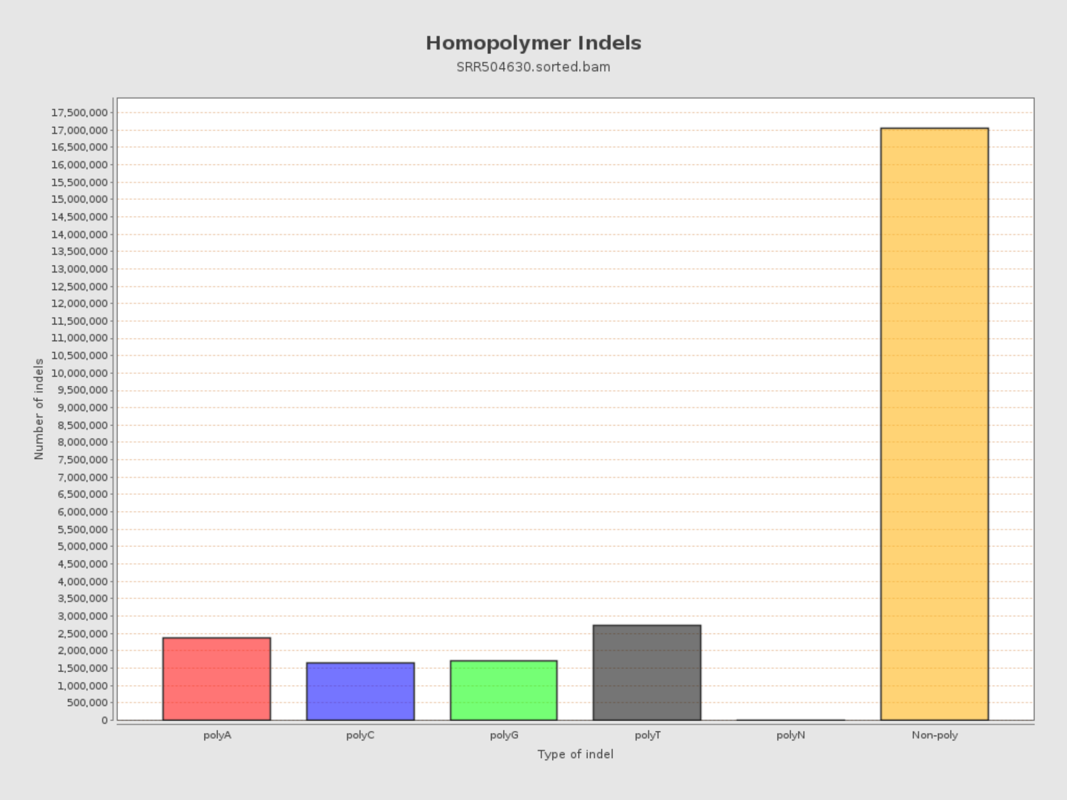
9. Results : Mapped Reads GC-content Distribution



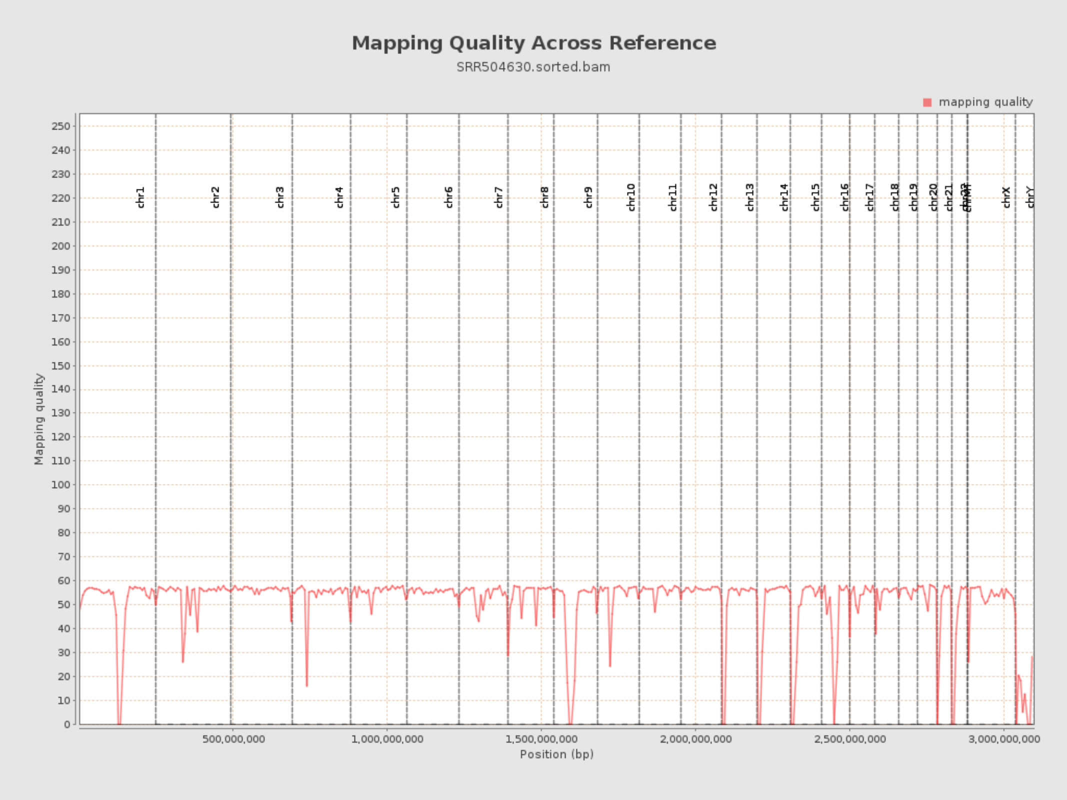
10. Results : Mapped Reads Clipping Profile



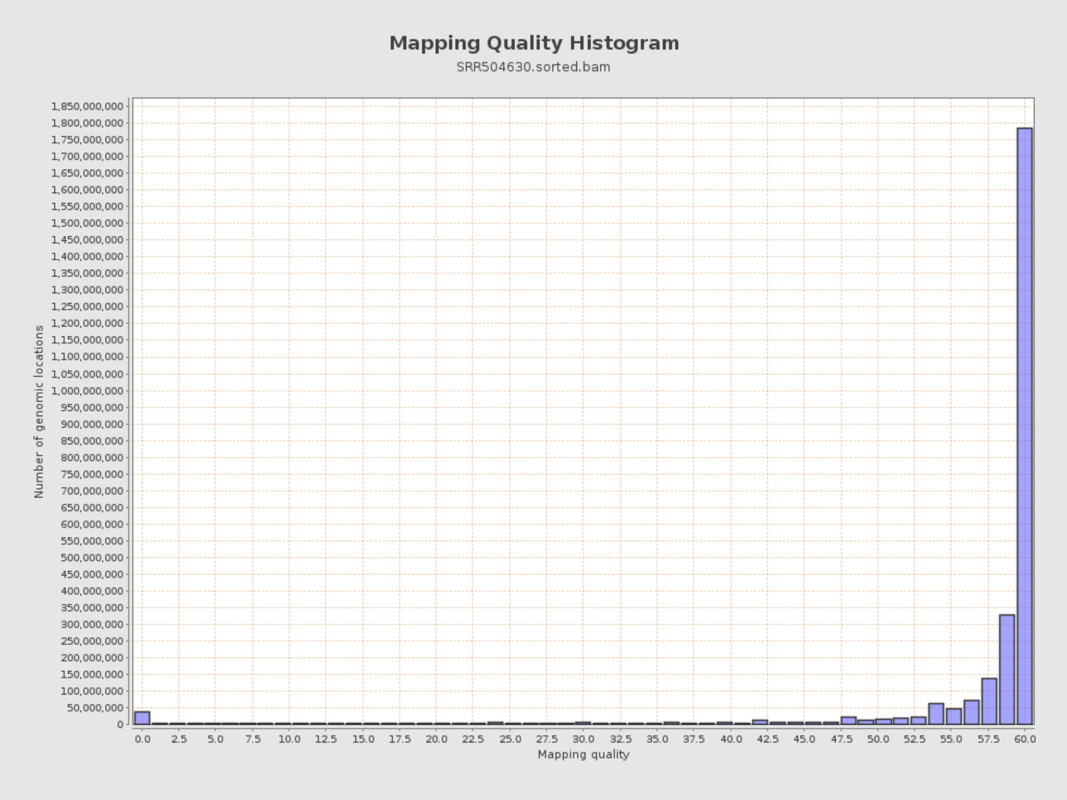
11. Results : Homopolymer Indels



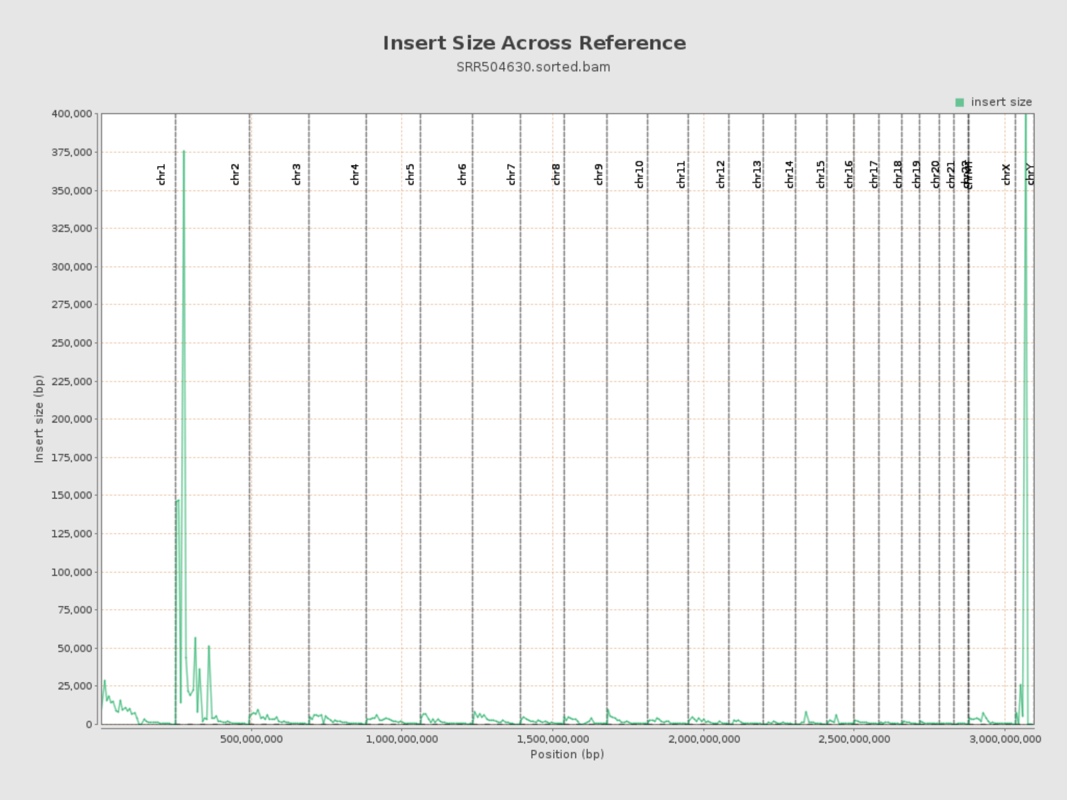
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram