Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/03 22:44:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR504704.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_SRR504704 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR504704_1.fastq.gz SRR504704_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Jan 03 22:44:15 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR504704.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	494,695,710
Mapped reads	446,834,233 / 90.33%
Unmapped reads	47,861,477 / 9.67%
Mapped paired reads	446,834,233 / 90.33%
Mapped reads, first in pair	225,282,406 / 45.54%
Mapped reads, second in pair	221,551,827 / 44.79%
Mapped reads, both in pair	439,790,730 / 88.9%
Mapped reads, singletons	7,043,503 / 1.42%
Secondary alignments	0
Supplementary alignments	2,283,239 / 0.46%
Read min/max/mean length	30 / 100 / 100.19
Duplicated reads (estimated)	118,150,163 / 23.88%
Duplication rate	23.23%
Clipped reads	38,406,916 / 7.76%

2.2. ACGT Content

Number/percentage of A's	11,616,553,312 / 26.47%
Number/percentage of C's	10,218,099,782 / 23.29%
Number/percentage of T's	11,632,311,395 / 26.51%
Number/percentage of G's	10,386,123,611 / 23.67%
Number/percentage of N's	26,581,066 / 0.06%

GC Percentage	46.96%

2.3. Coverage

Mean	14.1774
Standard Deviation	33.8161

2.4. Mapping Quality

Mean Mapping Quality	53.79

2.5. Insert size

Mean	43,126.14
Standard Deviation	1,940,920.1
P25/Median/P75	375 / 410 / 450

2.6. Mismatches and indels

General error rate	0.71%
Mismatches	304,560,628
Insertions	3,021,793
Mapped reads with at least one insertion	0.66%
Deletions	3,786,527
Mapped reads with at least one deletion	0.83%
Homopolymer indels	41.14%

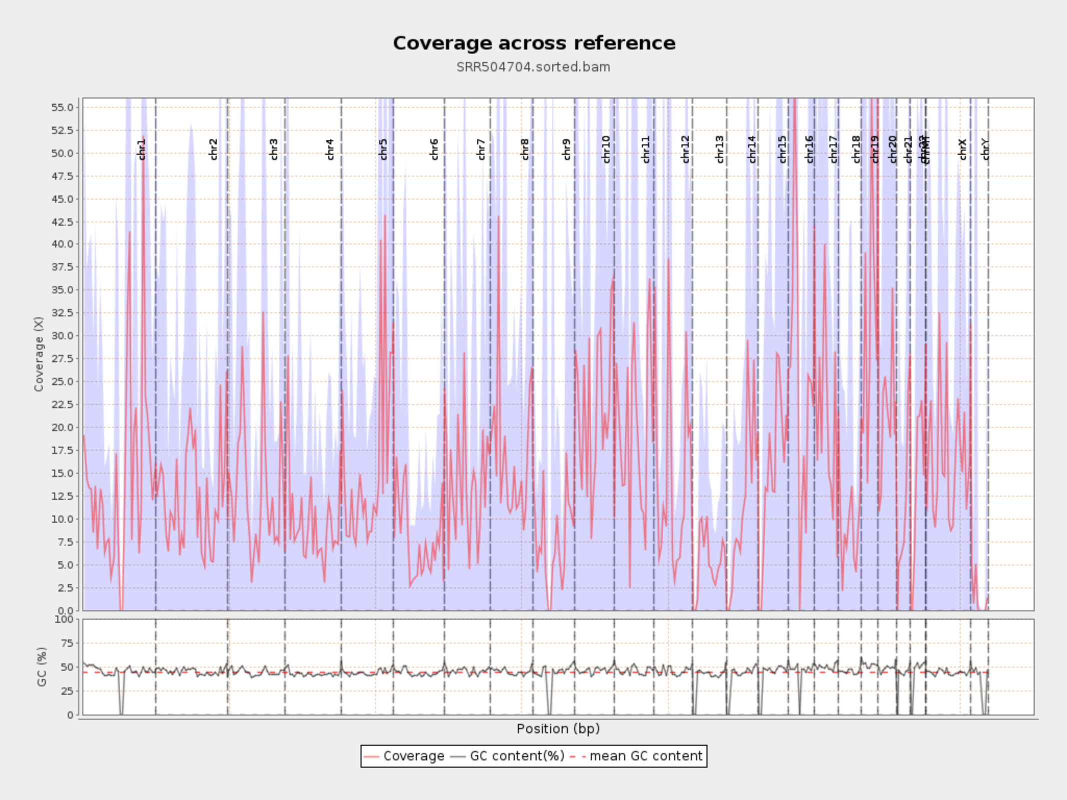
2.7. Chromosome stats

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

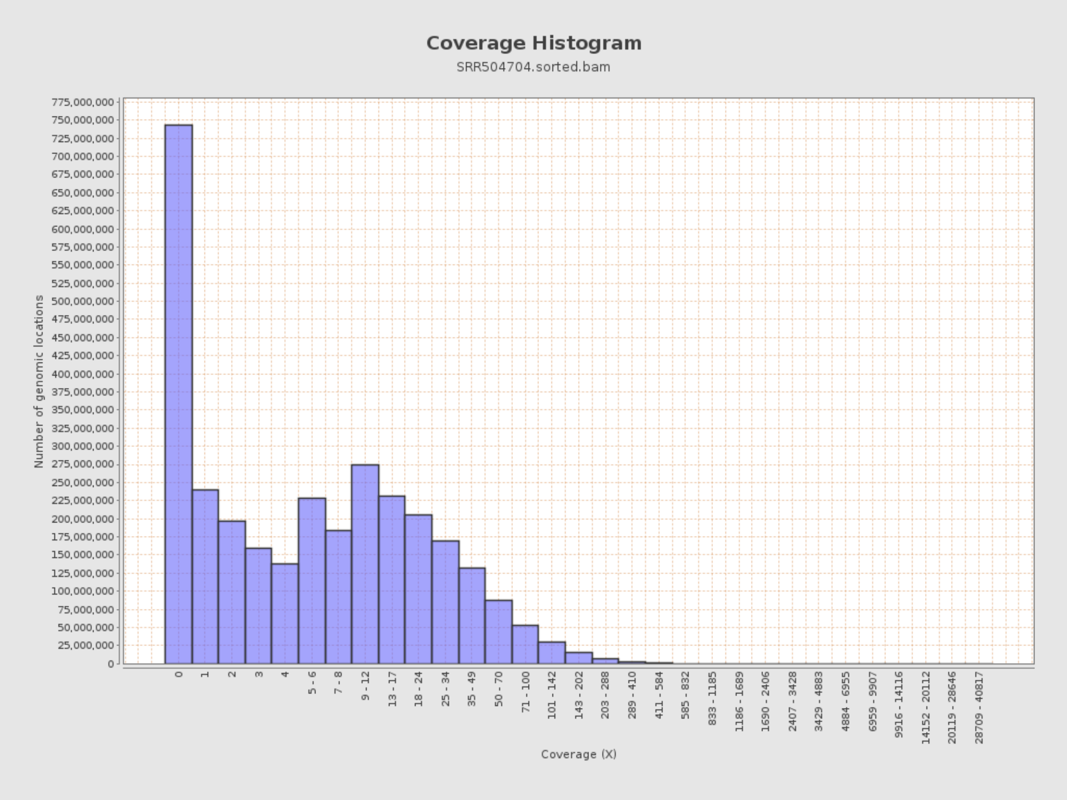
		bases	coverage	deviation
chr1	249250621	3615970742	14.5074	30.9851
chr2	243199373	2996738657	12.3221	23.6704
chr3	198022430	2555552443	12.9054	24.6004
chr4	191154276	1881060120	9.8405	17.6967
chr5	180915260	2865202931	15.8373	30.7226
chr6	171115067	1324499403	7.7404	15.5204
chr7	159138663	2248126164	14.1268	24.3884
chr8	146364022	2463864595	16.8338	33.2611
chr9	141213431	1051265988	7.4445	27.7474
chr10	135534747	2983361959	22.0118	35.3098
chr11	135006516	2632170206	19.4966	35.7699
chr12	133851895	1997143687	14.9205	35.356
chr13	115169878	612736082	5.3203	10.8067
chr14	107349540	1267049839	11.803	23.3718
chr15	102531392	1558593186	15.2011	29.7912
chr16	90354753	2208851656	24.4464	41.2636
chr17	81195210	1720656079	21.1916	40.2984
chr18	78077248	682660436	8.7434	97.121
chr19	59128983	1893224064	32.0185	59.791
chr20	63025520	1352961426	21.4669	35.0883
chr21	48129895	560690016	11.6495	25.1098
chr22	51304566	724918999	14.1297	29.3135
chrMT	16571	193266	11.6629	17.8468
chrX	155270560	2609375913	16.8053	28.1717

chrY	59373566	82084260	1.3825	47.8062

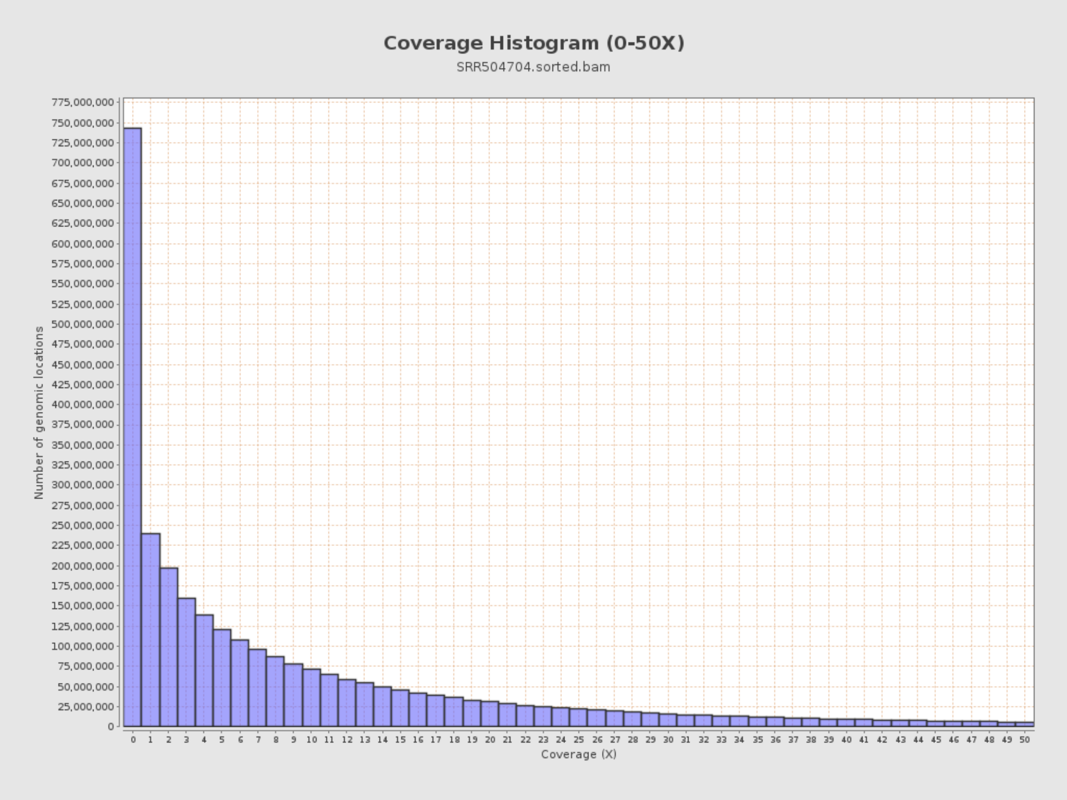
3. Results : Coverage across reference



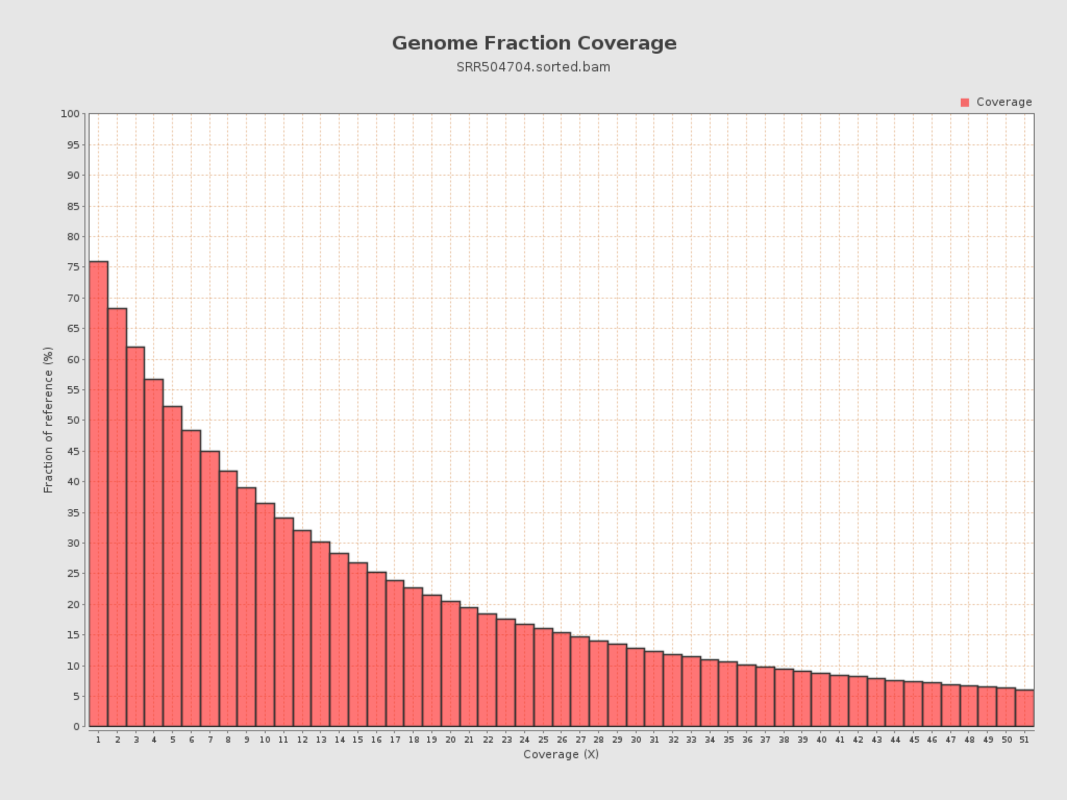
4. Results : Coverage Histogram



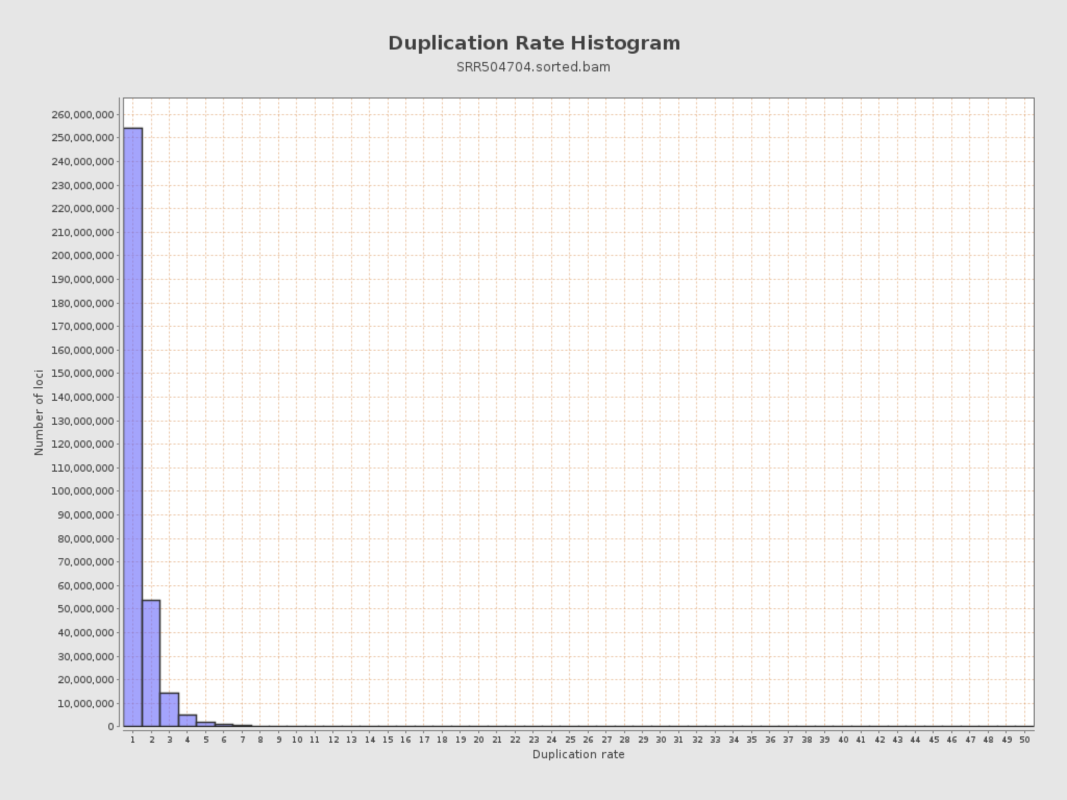
5. Results : Coverage Histogram (0-50X)



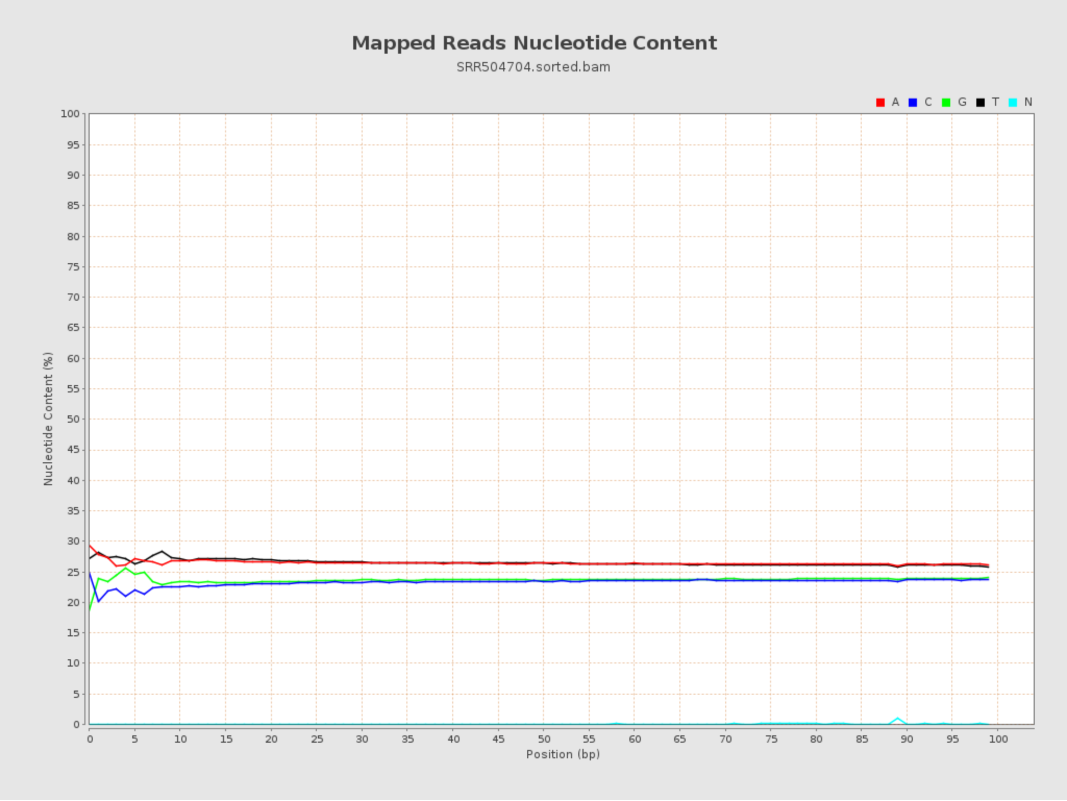
6. Results : Genome Fraction Coverage



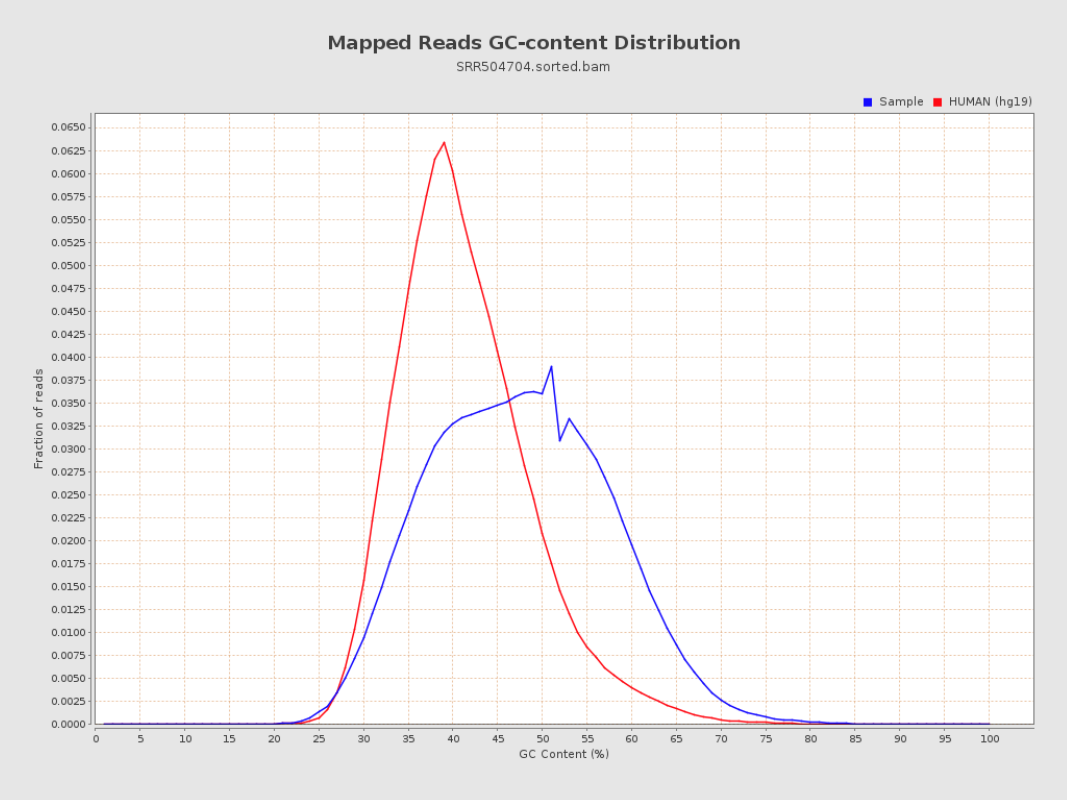
7. Results : Duplication Rate Histogram



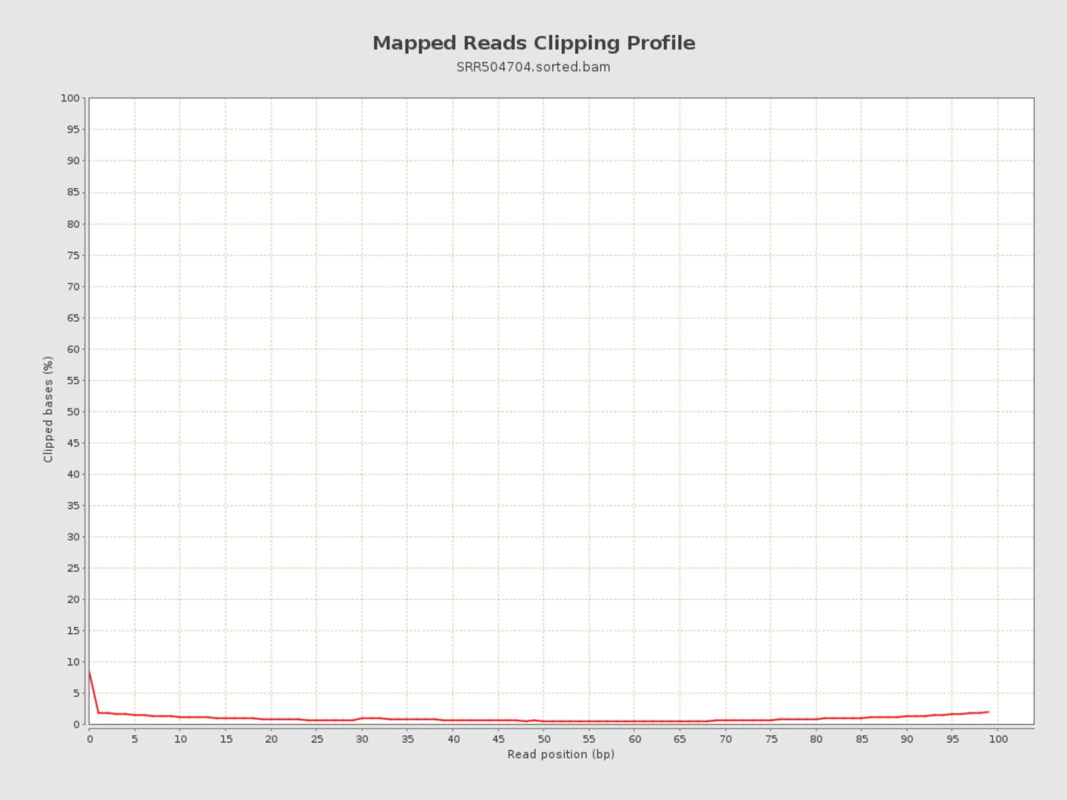
8. Results : Mapped Reads Nucleotide Content



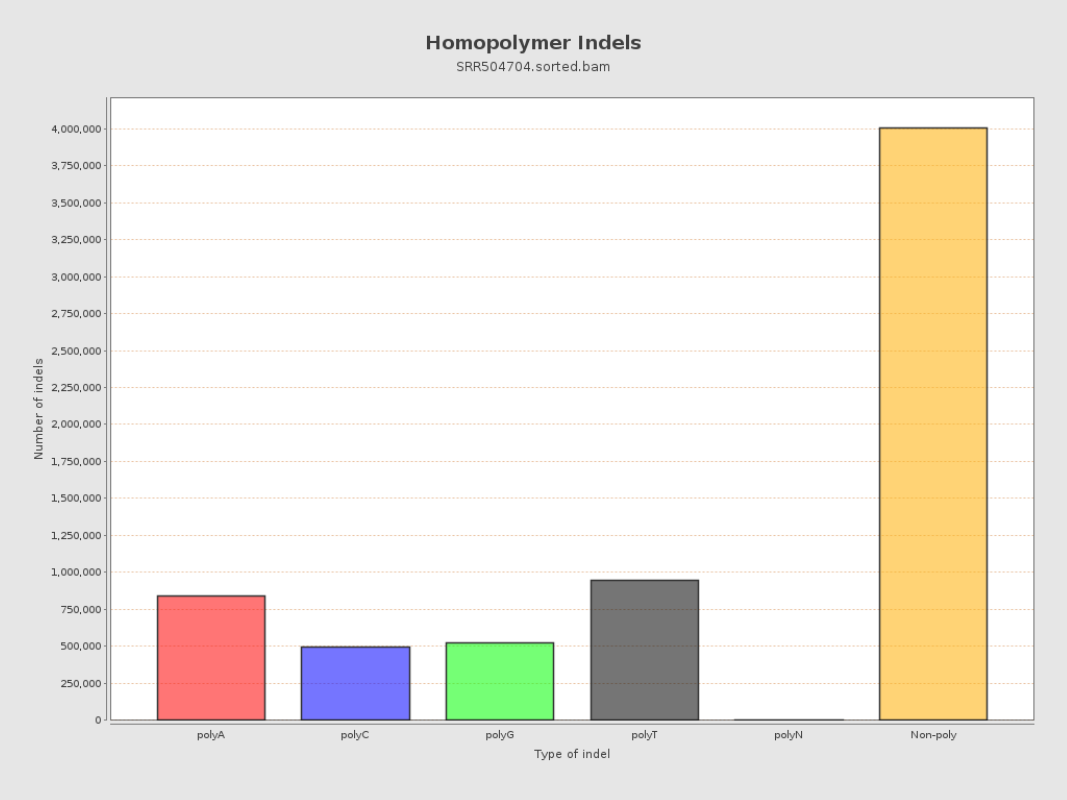
9. Results : Mapped Reads GC-content Distribution



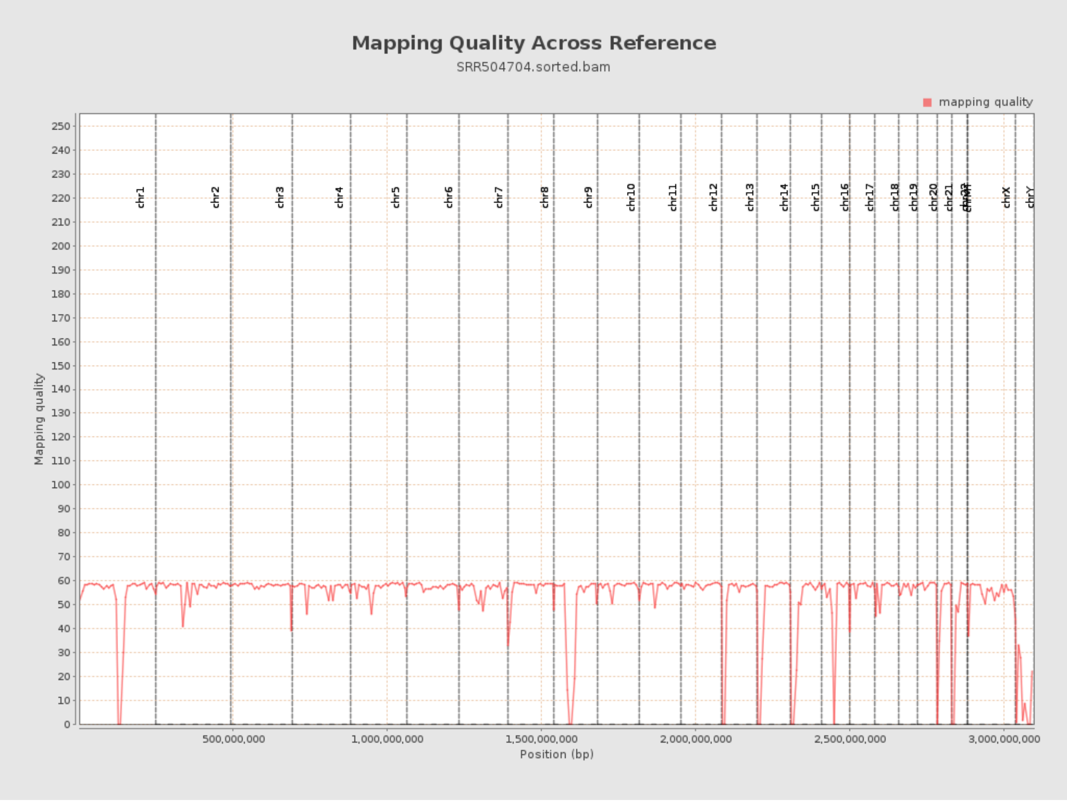
10. Results : Mapped Reads Clipping Profile



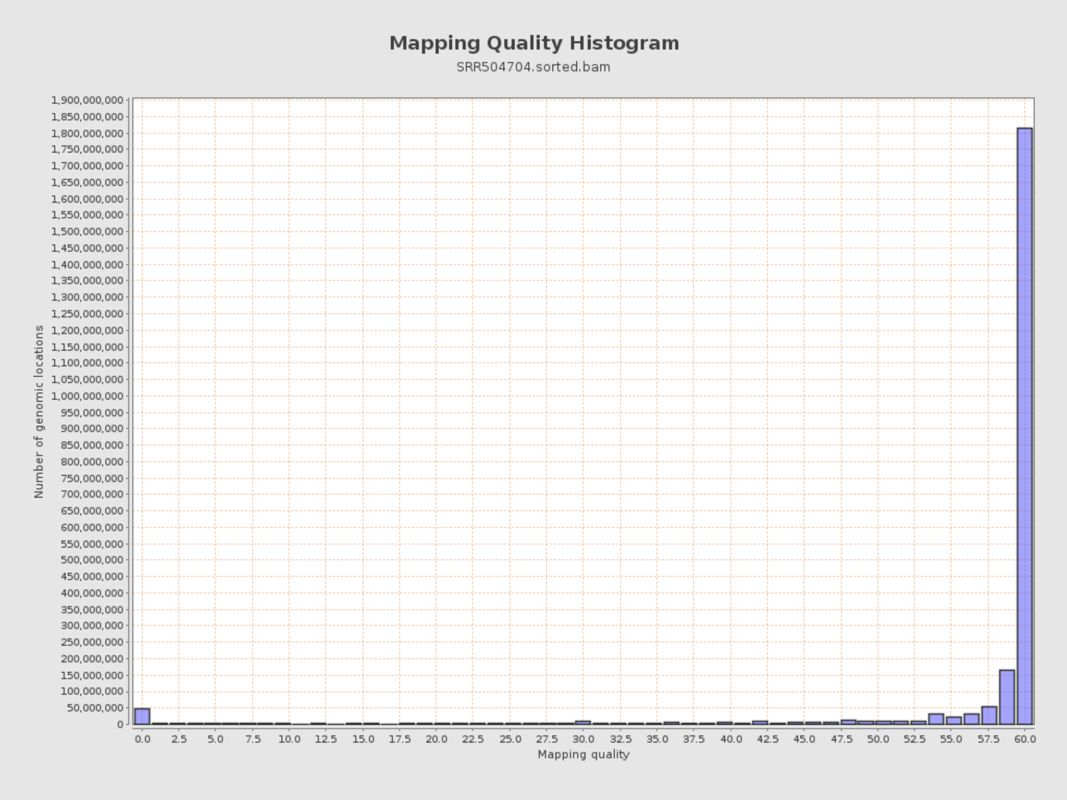
11. Results : Homopolymer Indels



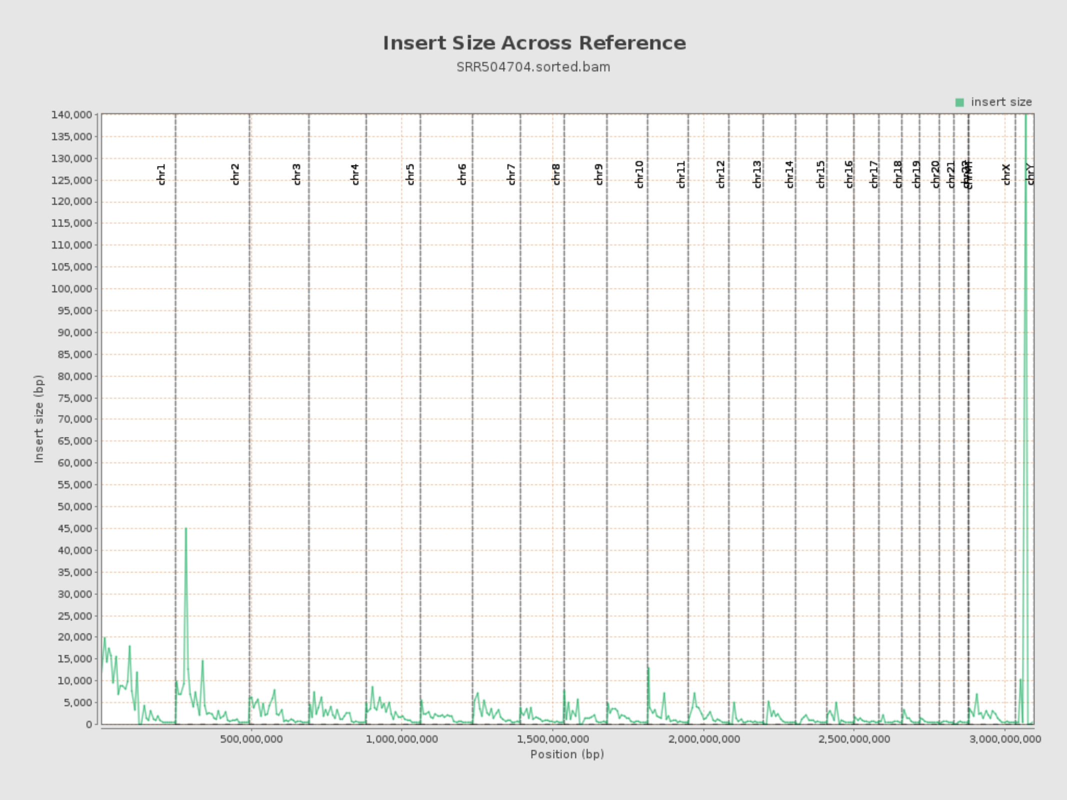
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram