Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/03 10:17:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR504702.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_SRR504702 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR504702_1.fastq.gz SRR504702_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Jan 03 10:17:30 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR504702.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	496,966,050
Mapped reads	449,651,148 / 90.48%
Unmapped reads	47,314,902 / 9.52%
Mapped paired reads	449,651,148 / 90.48%
Mapped reads, first in pair	226,318,458 / 45.54%
Mapped reads, second in pair	223,332,690 / 44.94%
Mapped reads, both in pair	443,064,648 / 89.15%
Mapped reads, singletons	6,586,500 / 1.33%
Secondary alignments	0
Supplementary alignments	2,305,963 / 0.46%
Read min/max/mean length	30 / 100 / 100.19
Duplicated reads (estimated)	108,002,187 / 21.73%
Duplication rate	21.82%
Clipped reads	58,676,914 / 11.81%

2.2. ACGT Content

Number/percentage of A's	11,586,231,772 / 26.54%
Number/percentage of C's	10,110,225,845 / 23.16%
Number/percentage of T's	11,549,815,265 / 26.45%
Number/percentage of G's	10,379,589,884 / 23.77%
Number/percentage of N's	37,234,169 / 0.09%

GC Percentage	46.93%

2.3. Coverage

Mean	14.1075
Standard Deviation	28.5332

2.4. Mapping Quality

Mean Mapping Quality	53.95

2.5. Insert size

Mean	29,700.67
Standard Deviation	1,631,956.22
P25/Median/P75	204 / 435 / 483

2.6. Mismatches and indels

General error rate	0.83%
Mismatches	356,245,960
Insertions	3,019,886
Mapped reads with at least one insertion	0.66%
Deletions	3,758,743
Mapped reads with at least one deletion	0.81%
Homopolymer indels	40.22%

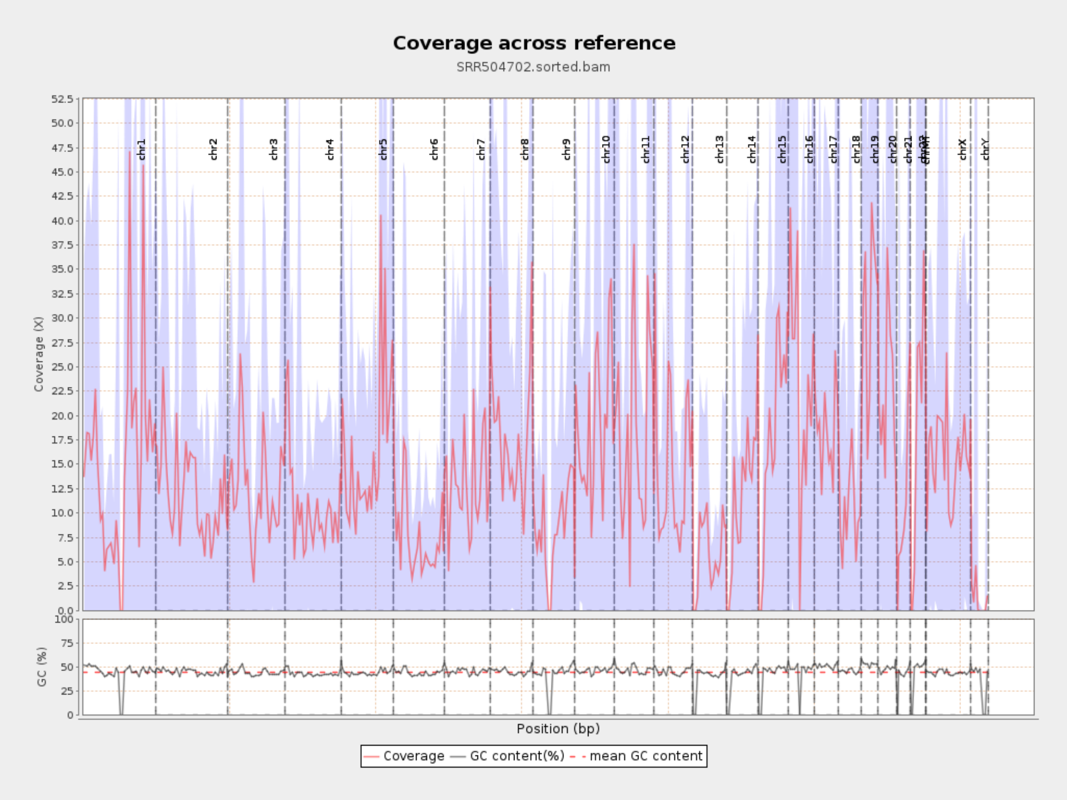
2.7. Chromosome stats

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

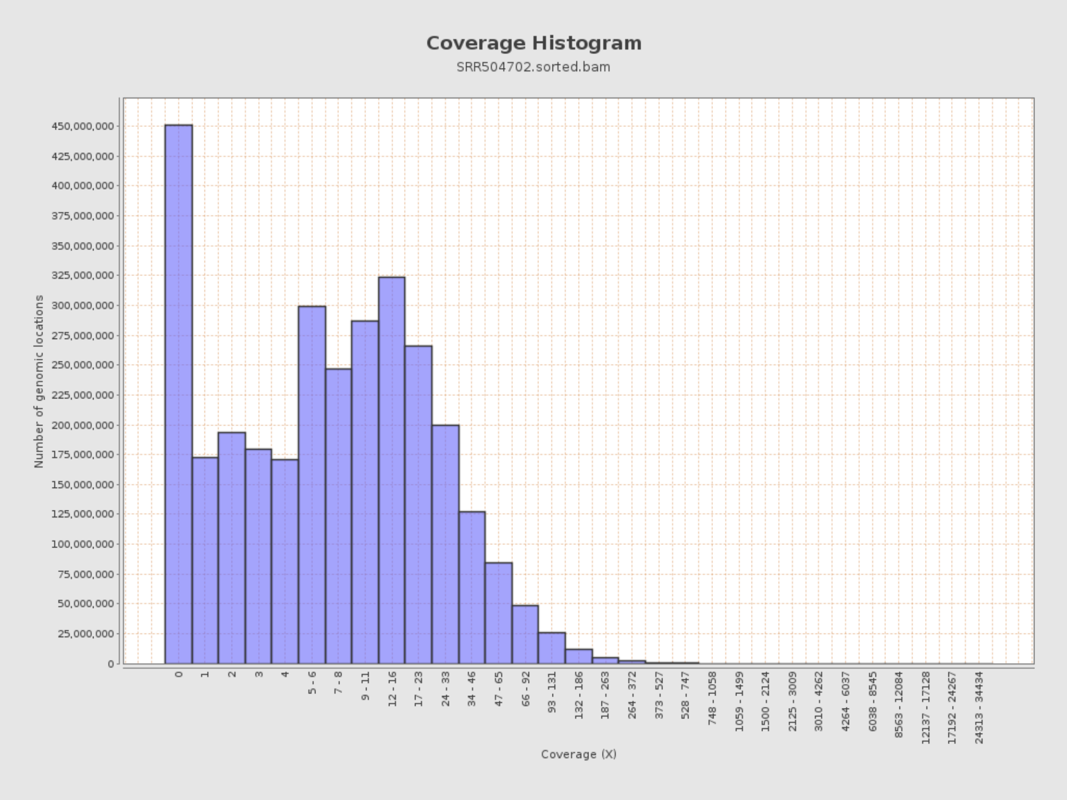
		bases	coverage	deviation
chr1	249250621	3829517971	15.3641	30.6586
chr2	243199373	2901575277	11.9309	18.8351
chr3	198022430	2470632683	12.4765	18.629
chr4	191154276	2023045206	10.5833	18.0091
chr5	180915260	3000987398	16.5878	24.9998
chr6	171115067	1251921584	7.3163	12.8128
chr7	159138663	2064827515	12.975	19.3026
chr8	146364022	2557722902	17.4751	30.8281
chr9	141213431	1189384928	8.4226	17.6018
chr10	135534747	2594281581	19.1411	28.2673
chr11	135006516	2498375156	18.5056	30.9113
chr12	133851895	1971304738	14.7275	24.7722
chr13	115169878	673269634	5.8459	9.6712
chr14	107349540	1230114609	11.459	17.5252
chr15	102531392	1767021655	17.234	27.4918
chr16	90354753	2094773352	23.1839	35.2348
chr17	81195210	1499474825	18.4675	29.4291
chr18	78077248	805934496	10.3223	82.9258
chr19	59128983	1821058374	30.7981	45.4073
chr20	63025520	1410249330	22.3758	30.672
chr21	48129895	549003469	11.4067	26.5123
chr22	51304566	955276865	18.6197	34.2494
chrMT	16571	330948	19.9715	7.566
chrX	155270560	2443616887	15.7378	22.3668

chrY	59373566	68652766	1.1563	39.9064

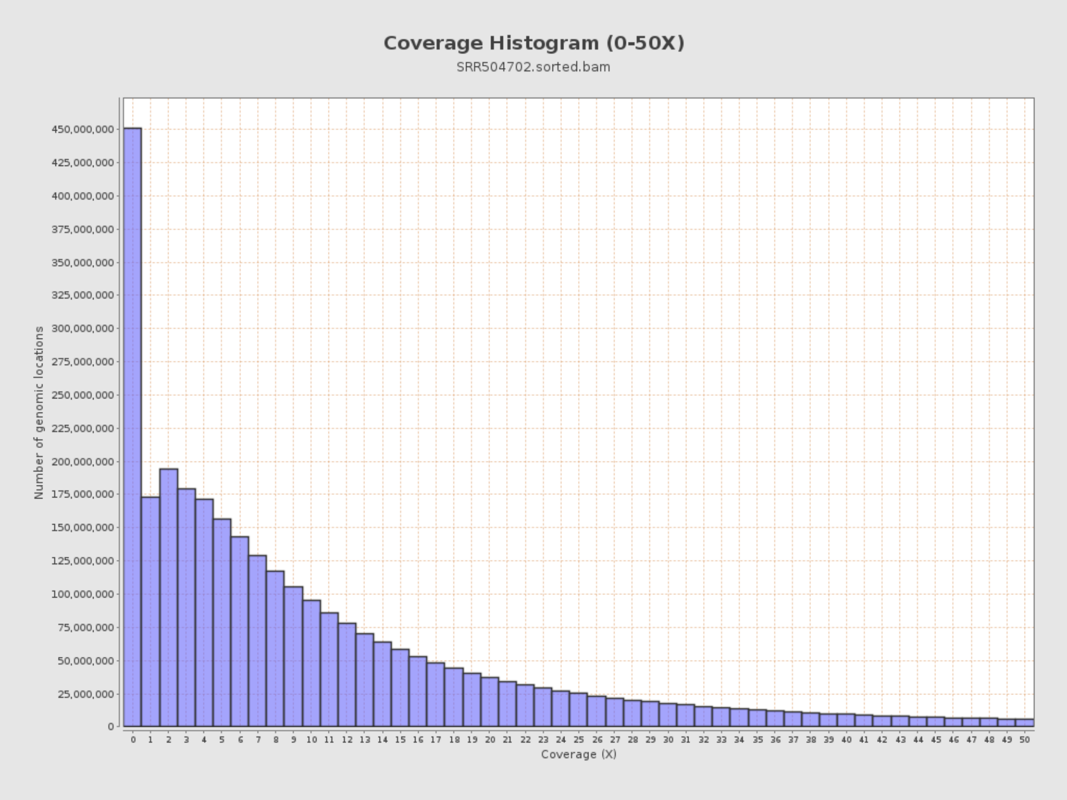
3. Results : Coverage across reference



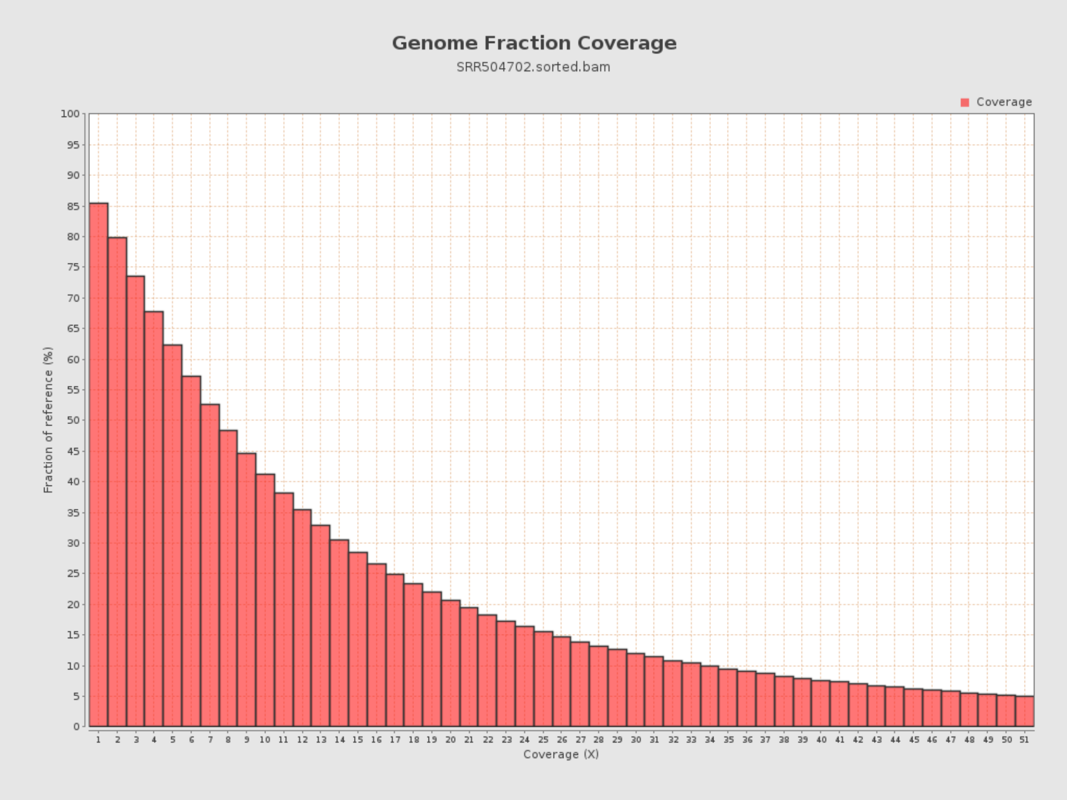
4. Results : Coverage Histogram



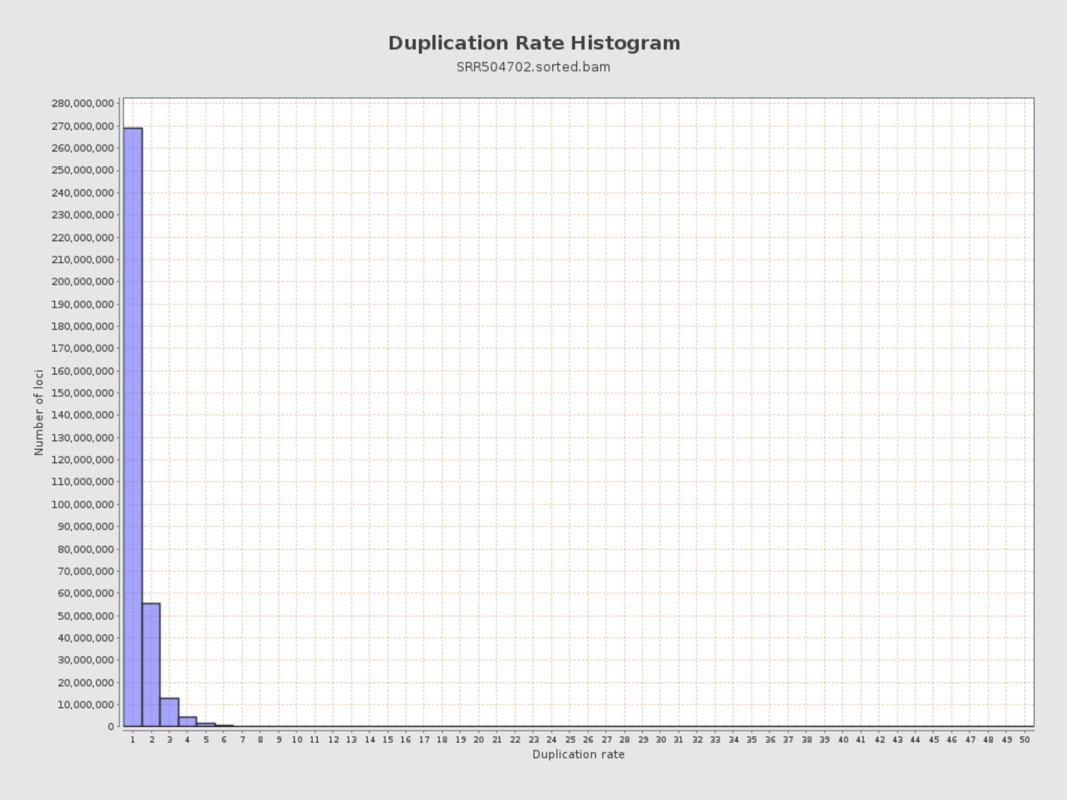
5. Results : Coverage Histogram (0-50X)



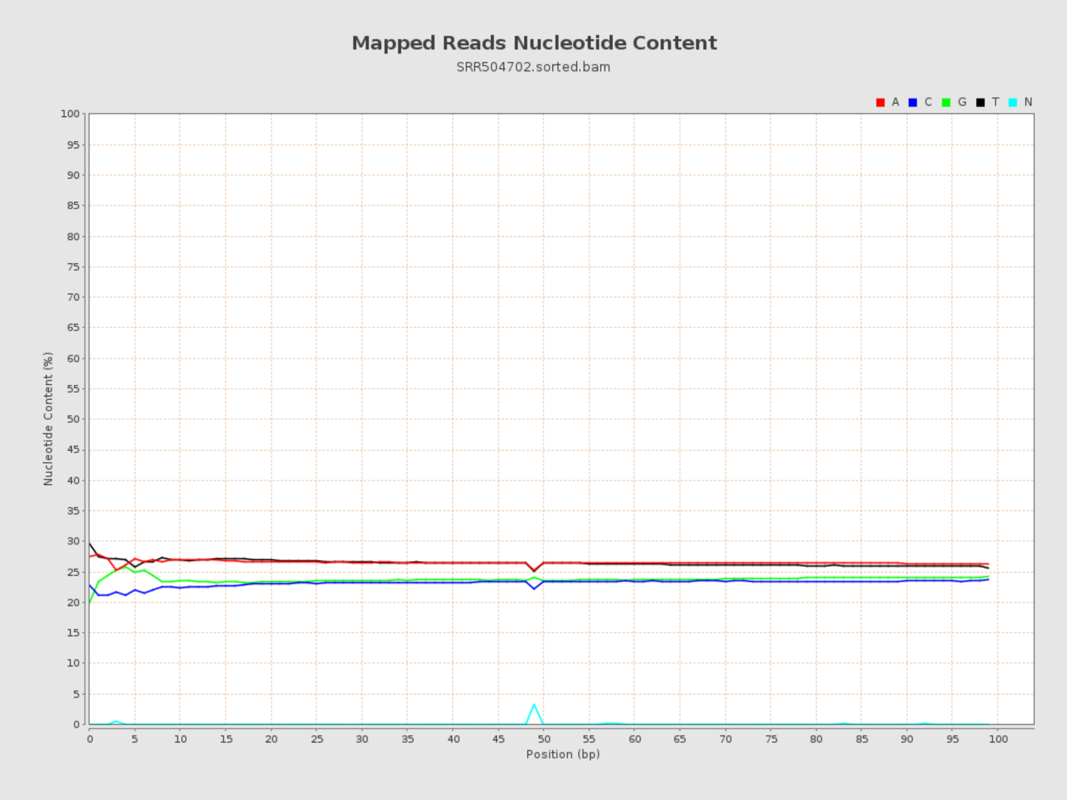
6. Results : Genome Fraction Coverage



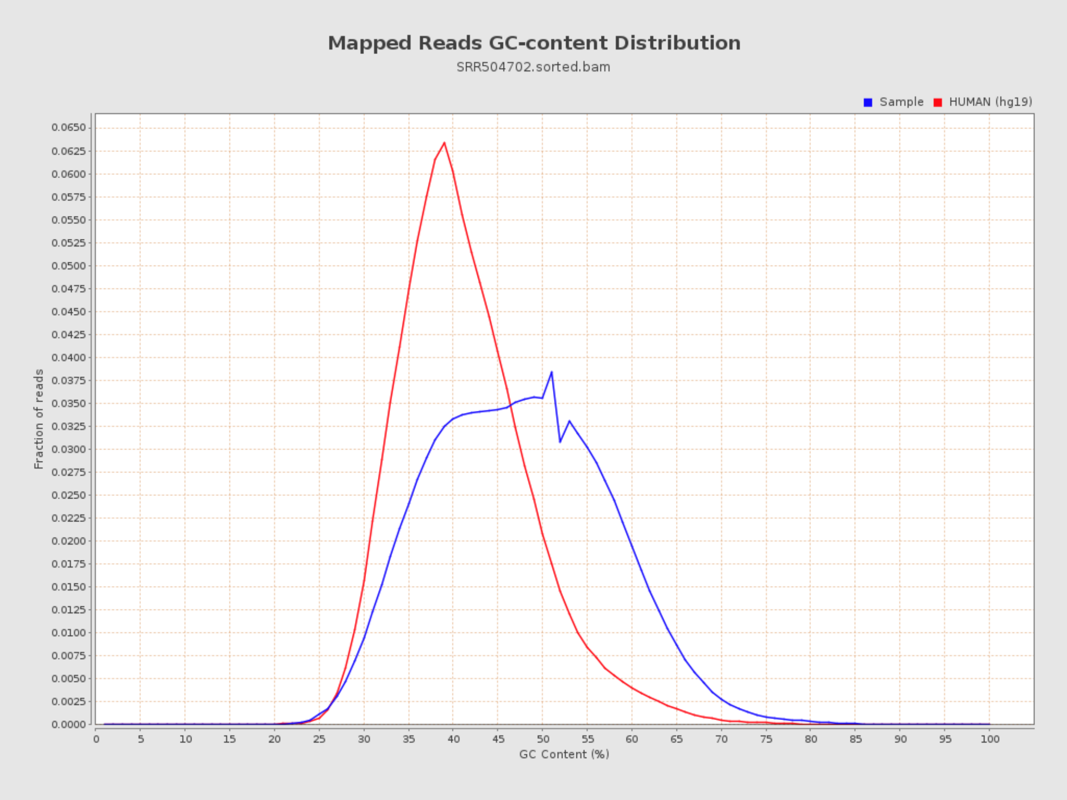
7. Results : Duplication Rate Histogram



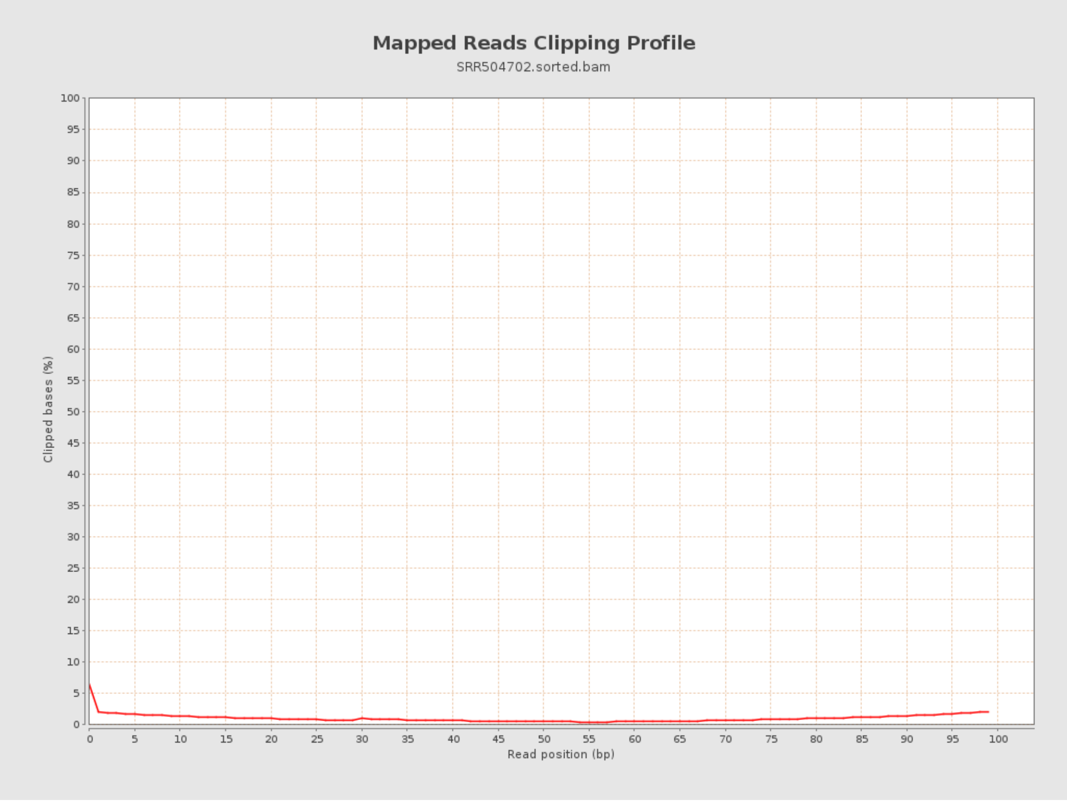
8. Results : Mapped Reads Nucleotide Content



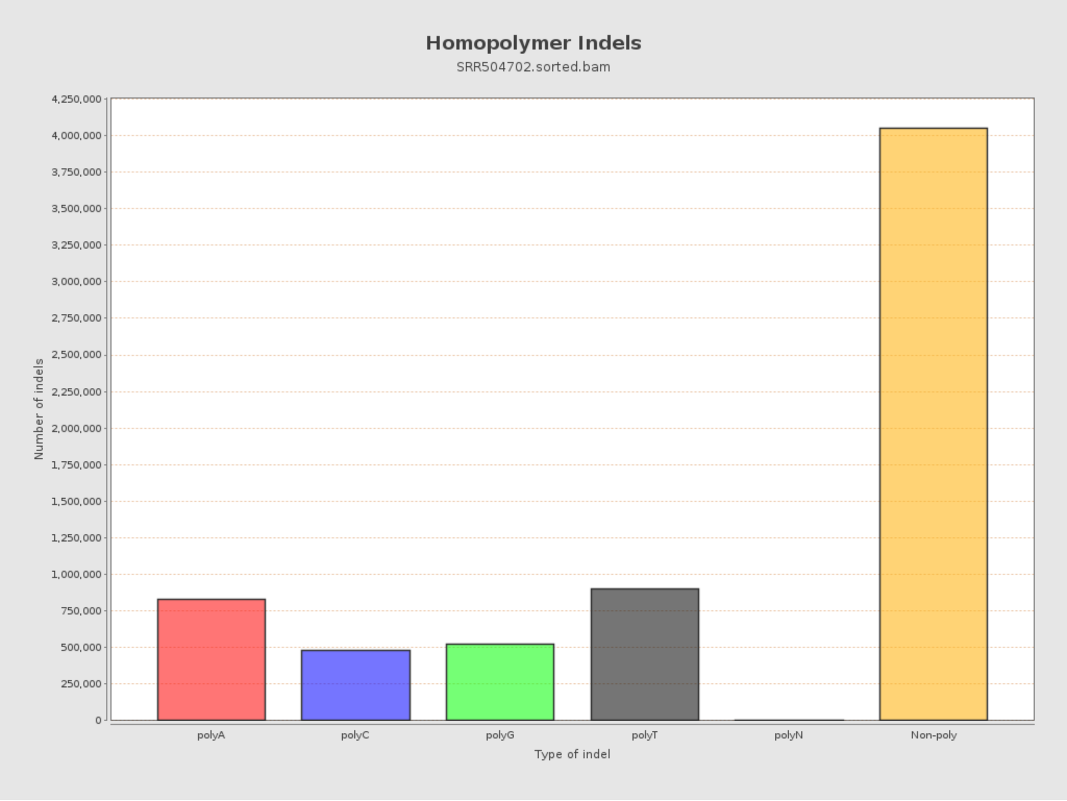
9. Results : Mapped Reads GC-content Distribution



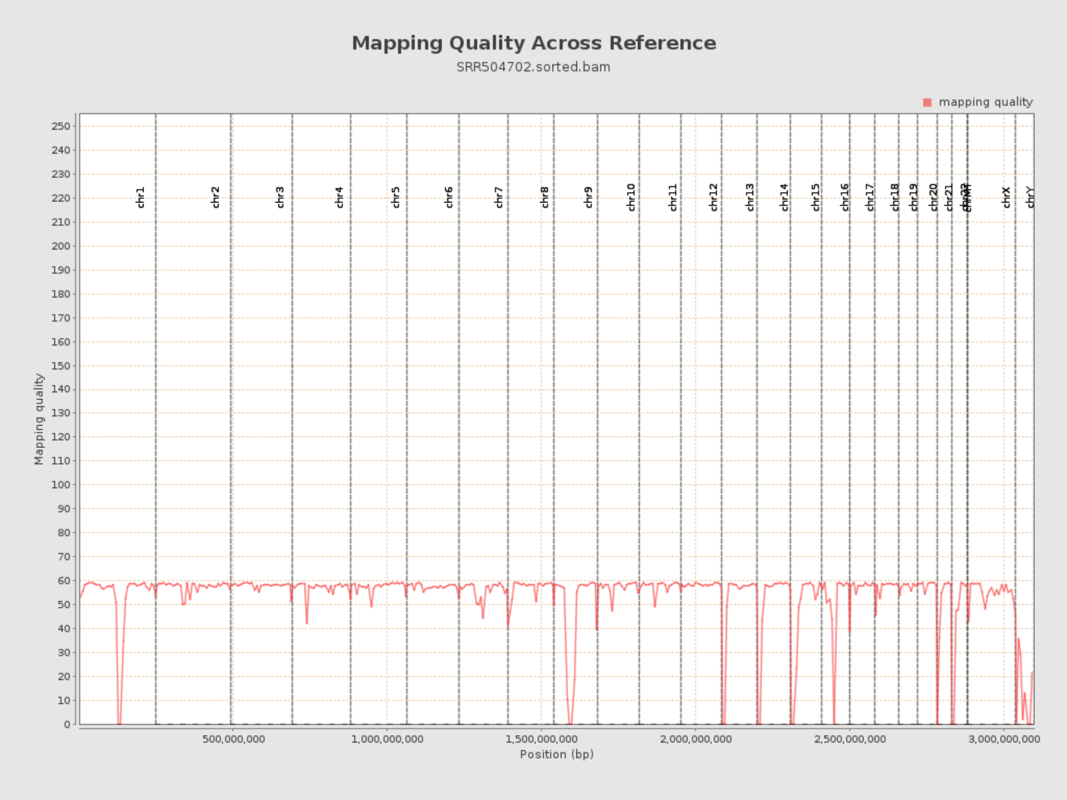
10. Results : Mapped Reads Clipping Profile



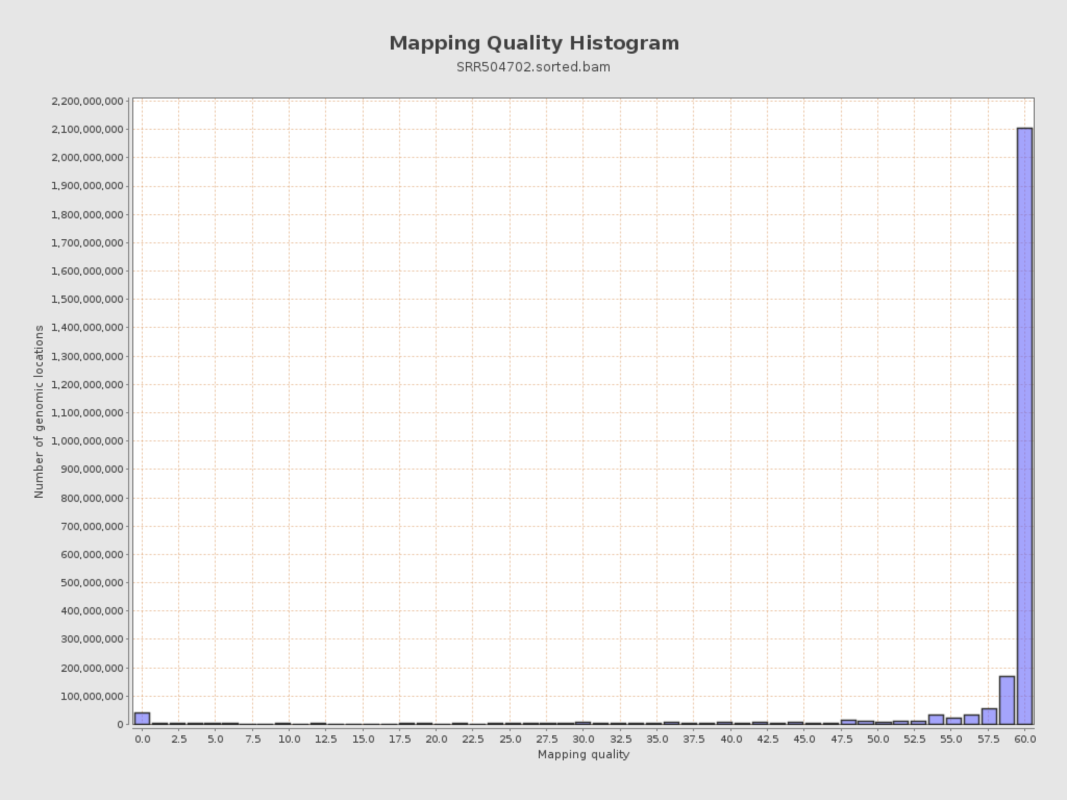
11. Results : Homopolymer Indels



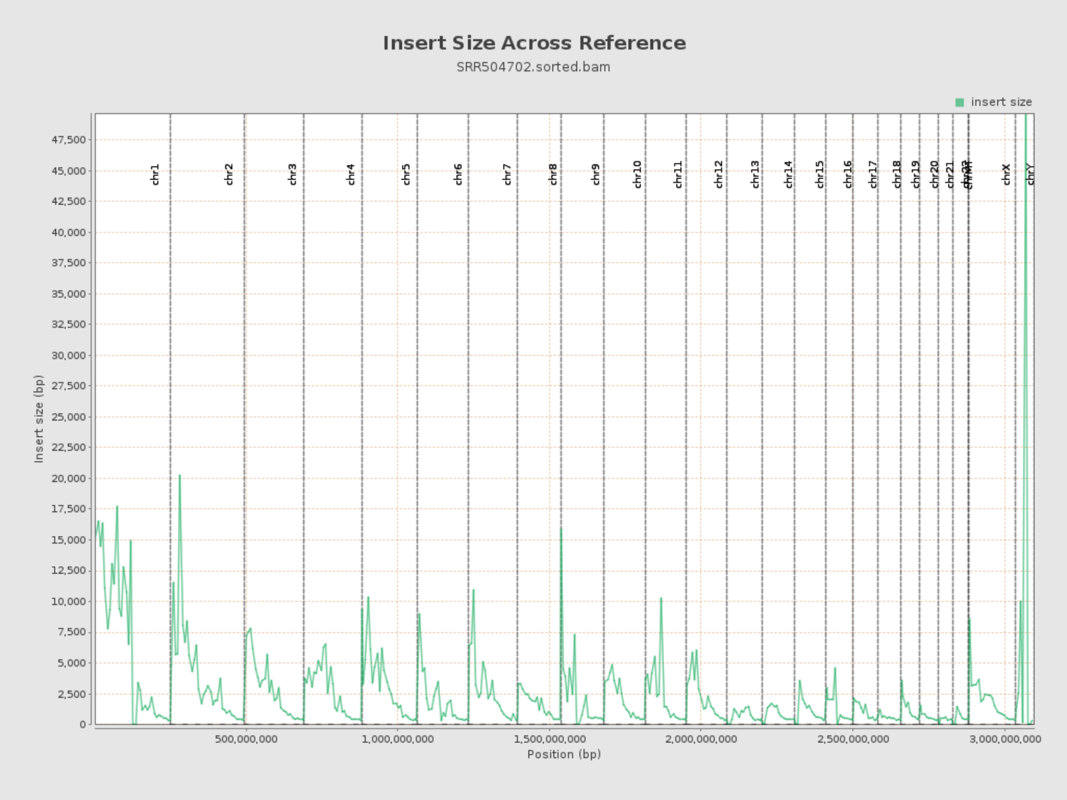
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram