Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/03 03:44:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR504701.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_SRR504701 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR504701_1.fastq.gz SRR504701_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Jan 03 03:44:53 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR504701.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	517,802,328
Mapped reads	468,321,567 / 90.44%
Unmapped reads	49,480,761 / 9.56%
Mapped paired reads	468,321,567 / 90.44%
Mapped reads, first in pair	236,082,132 / 45.59%
Mapped reads, second in pair	232,239,435 / 44.85%
Mapped reads, both in pair	460,704,842 / 88.97%
Mapped reads, singletons	7,616,725 / 1.47%
Secondary alignments	0
Supplementary alignments	2,402,489 / 0.46%
Read min/max/mean length	30 / 100 / 100.19
Duplicated reads (estimated)	115,196,186 / 22.25%
Duplication rate	22.32%
Clipped reads	61,549,239 / 11.89%

2.2. ACGT Content

Number/percentage of A's	12,075,540,856 / 26.56%
Number/percentage of C's	10,524,956,257 / 23.15%
Number/percentage of T's	12,041,955,853 / 26.49%
Number/percentage of G's	10,790,925,128 / 23.74%
Number/percentage of N's	23,645,593 / 0.05%

GC Percentage	46.89%

2.3. Coverage

Mean	14.6871
Standard Deviation	29.7329

2.4. Mapping Quality

Mean Mapping Quality	53.95

2.5. Insert size

Mean	30,070.86
Standard Deviation	1,647,802.69
P25/Median/P75	204 / 435 / 483

2.6. Mismatches and indels

General error rate	0.76%
Mismatches	337,180,837
Insertions	3,134,308
Mapped reads with at least one insertion	0.65%
Deletions	3,910,248
Mapped reads with at least one deletion	0.81%
Homopolymer indels	40.28%

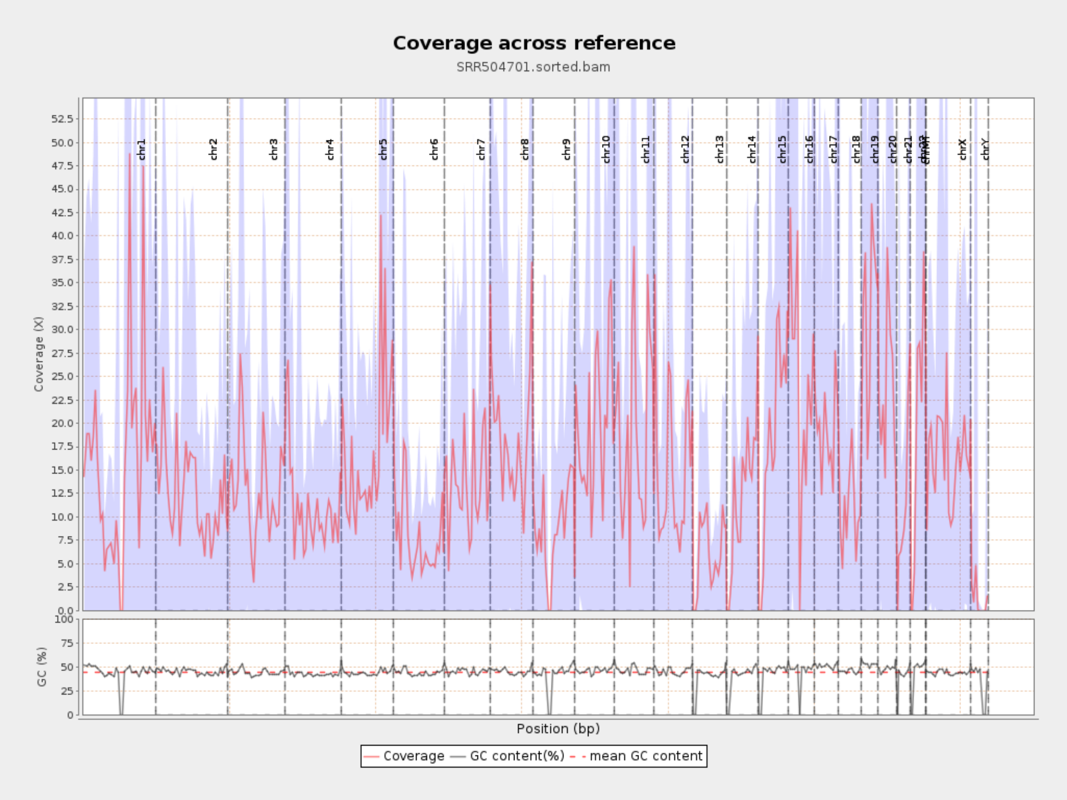
2.7. Chromosome stats

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

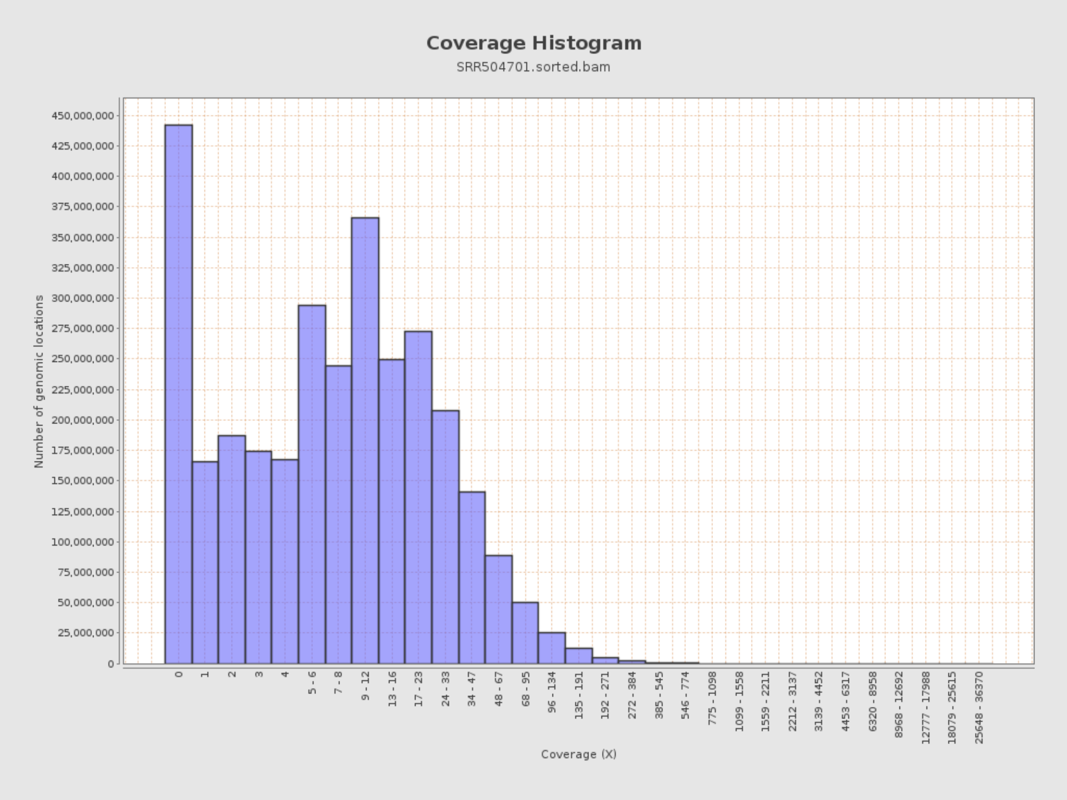
		bases	coverage	deviation
chr1	249250621	3983987119	15.9839	31.84
chr2	243199373	3022033176	12.4262	19.6071
chr3	198022430	2571365835	12.9852	19.3282
chr4	191154276	2108114384	11.0283	18.709
chr5	180915260	3126205344	17.2799	25.9848
chr6	171115067	1303372801	7.6169	13.2892
chr7	159138663	2151721628	13.521	20.0653
chr8	146364022	2664703505	18.206	32.0253
chr9	141213431	1238198879	8.7683	18.2915
chr10	135534747	2700777273	19.9268	29.4236
chr11	135006516	2601304738	19.268	32.0775
chr12	133851895	2052157200	15.3316	25.7162
chr13	115169878	701270431	6.089	10.0296
chr14	107349540	1281986139	11.9422	18.2358
chr15	102531392	1841206782	17.9575	28.5808
chr16	90354753	2179327526	24.1197	36.625
chr17	81195210	1558617008	19.1959	30.5628
chr18	78077248	839841545	10.7565	87.3204
chr19	59128983	1891120767	31.983	47.0894
chr20	63025520	1467404083	23.2827	31.8445
chr21	48129895	570780056	11.8592	27.406
chr22	51304566	993986892	19.3742	35.6039
chrMT	16571	339720	20.5009	8.0985
chrX	155270560	2545181080	16.3919	23.263

chrY	59373566	71661822	1.207	41.6314

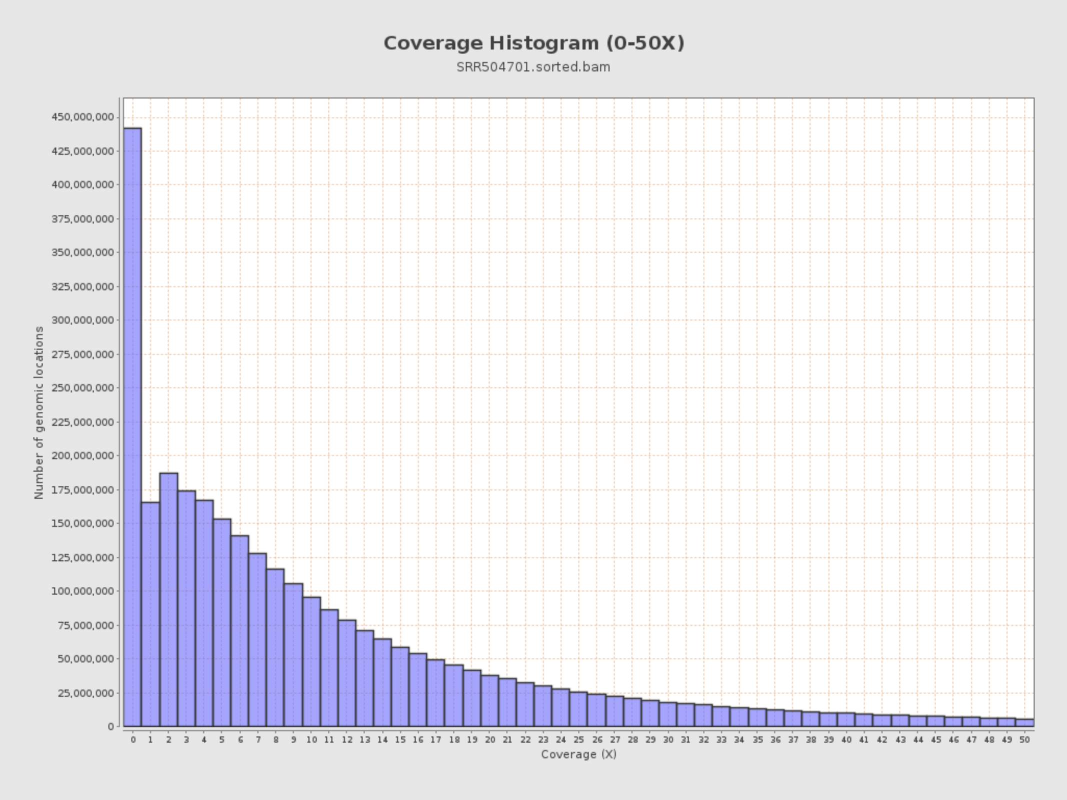
3. Results : Coverage across reference



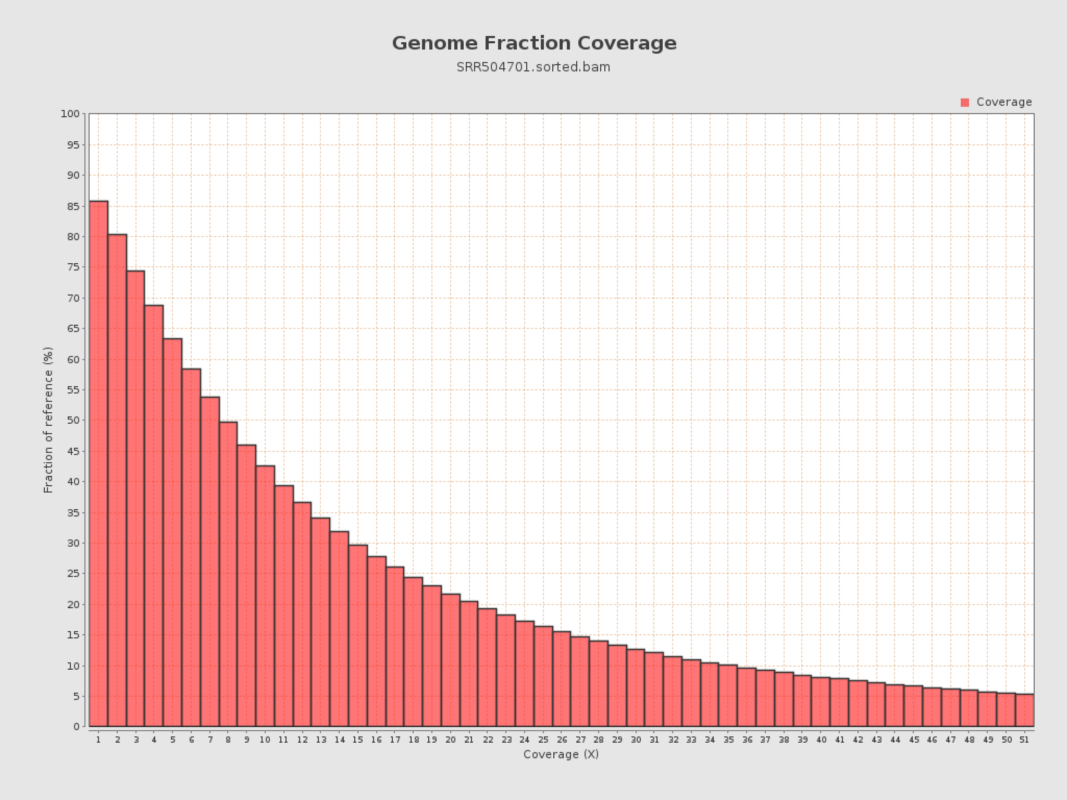
4. Results : Coverage Histogram



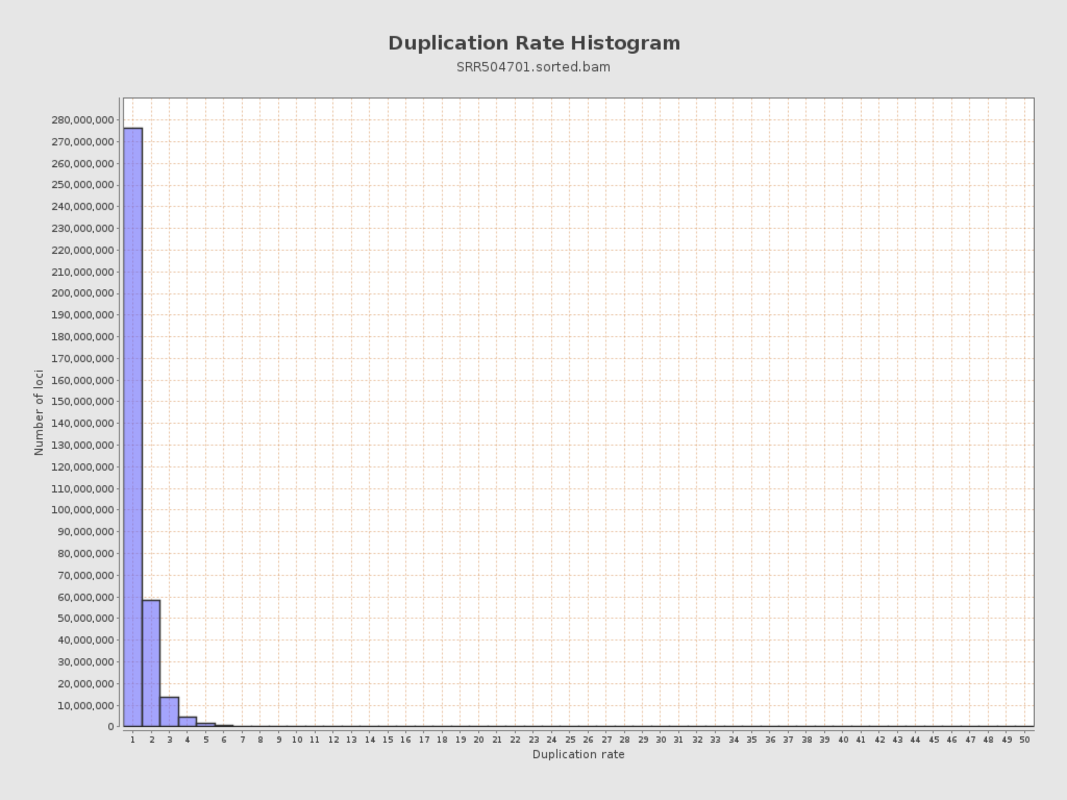
5. Results : Coverage Histogram (0-50X)



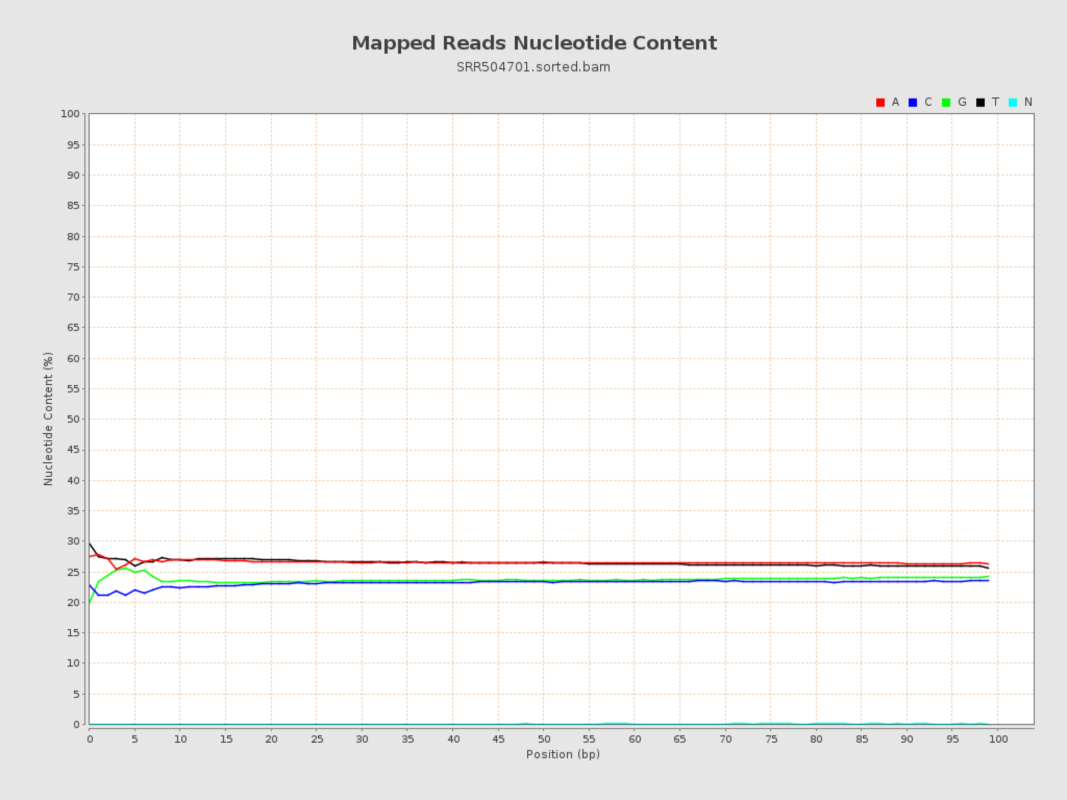
6. Results : Genome Fraction Coverage



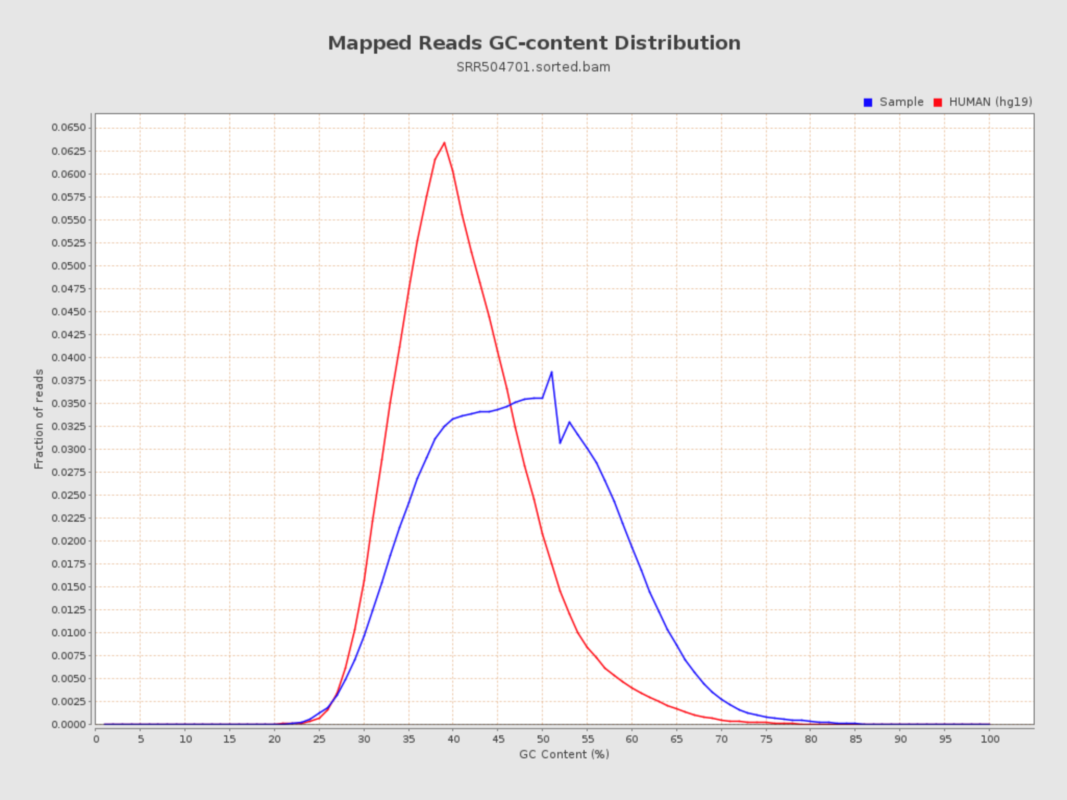
7. Results : Duplication Rate Histogram



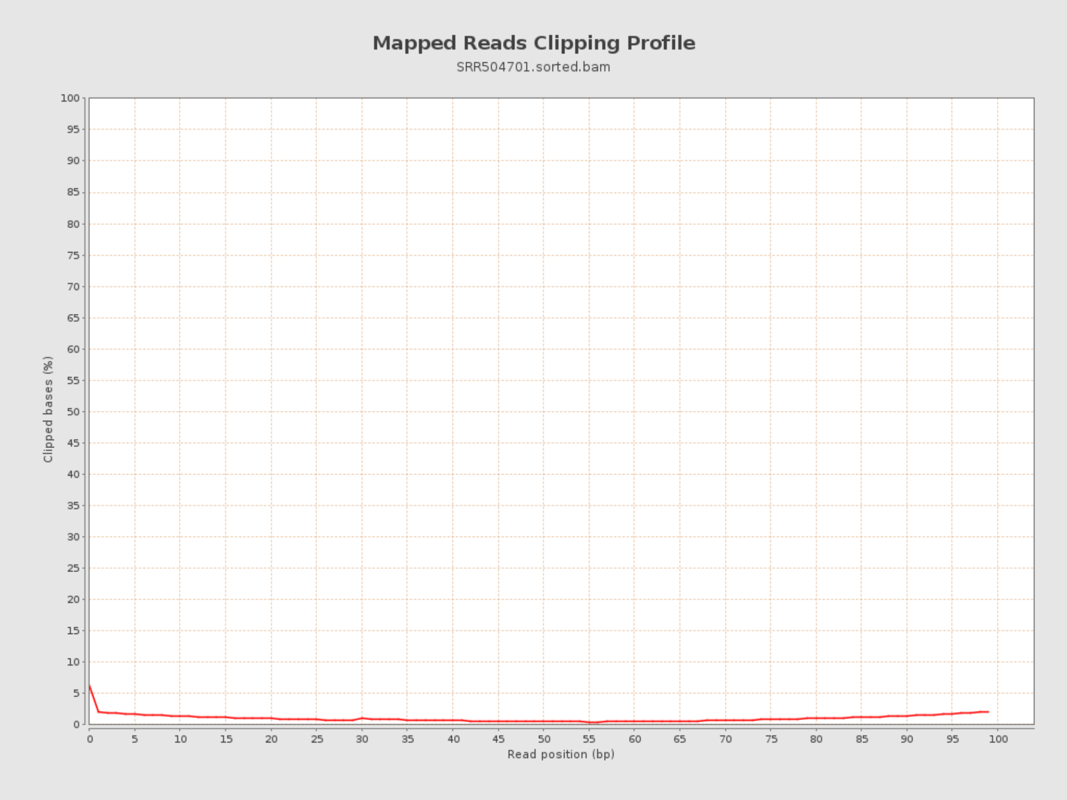
8. Results : Mapped Reads Nucleotide Content



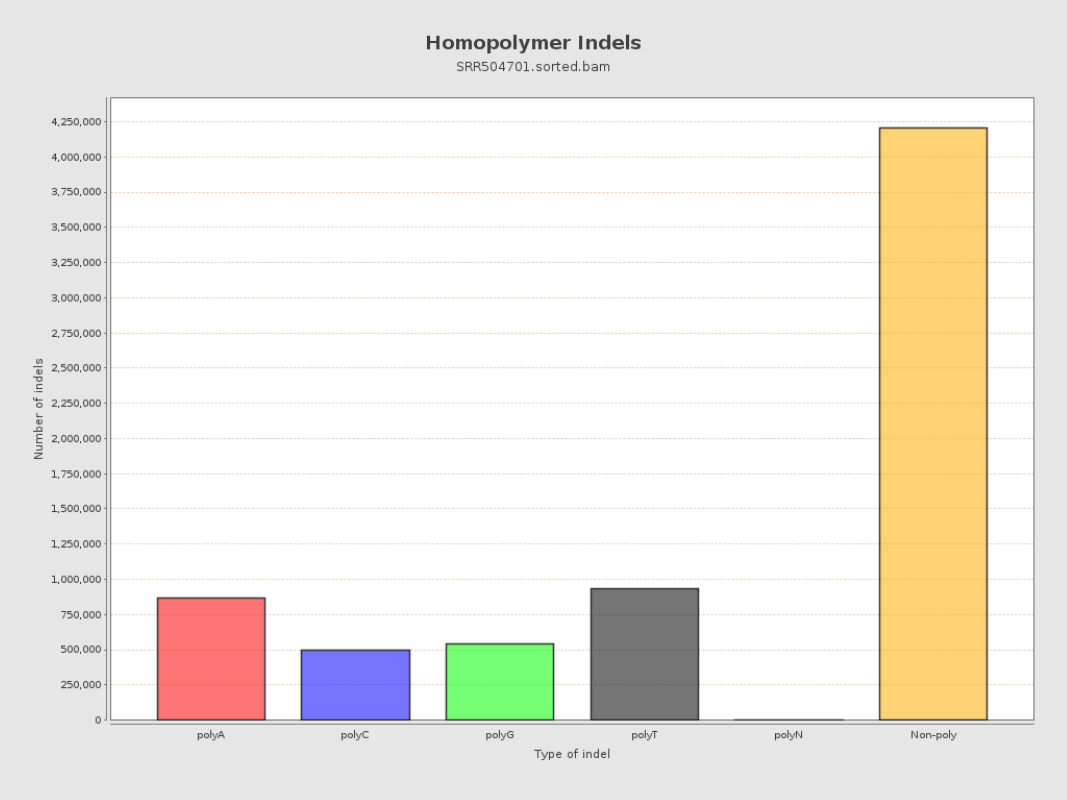
9. Results : Mapped Reads GC-content Distribution



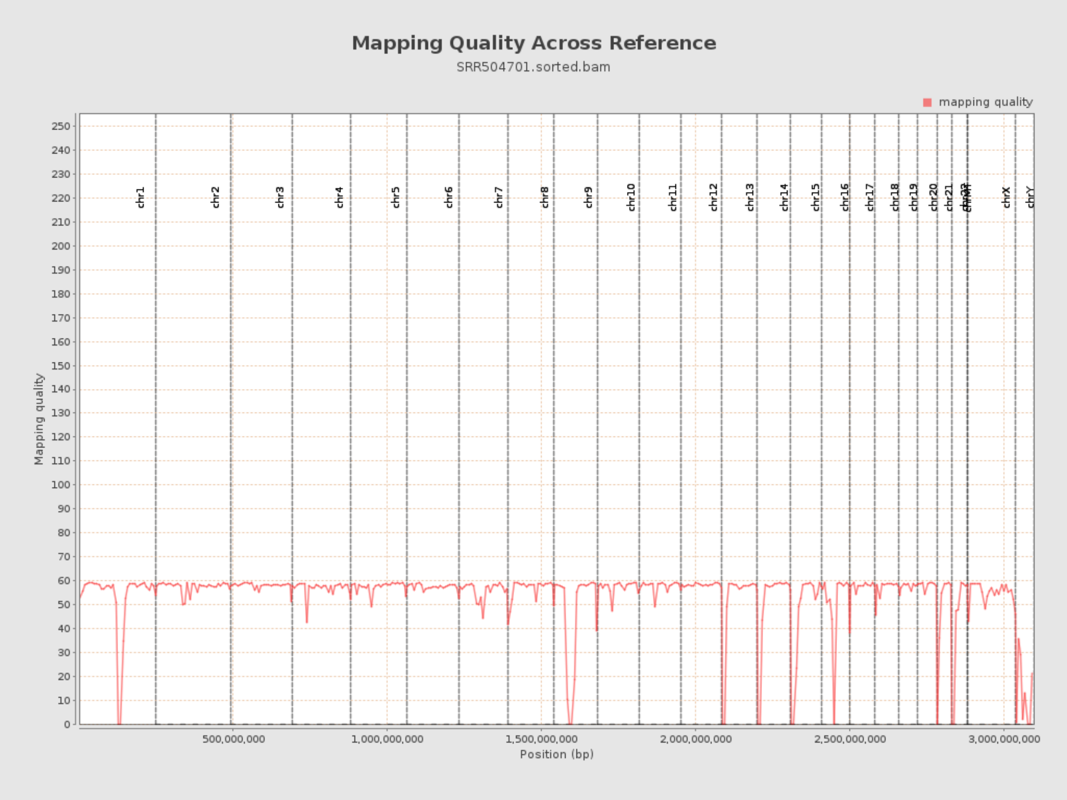
10. Results : Mapped Reads Clipping Profile



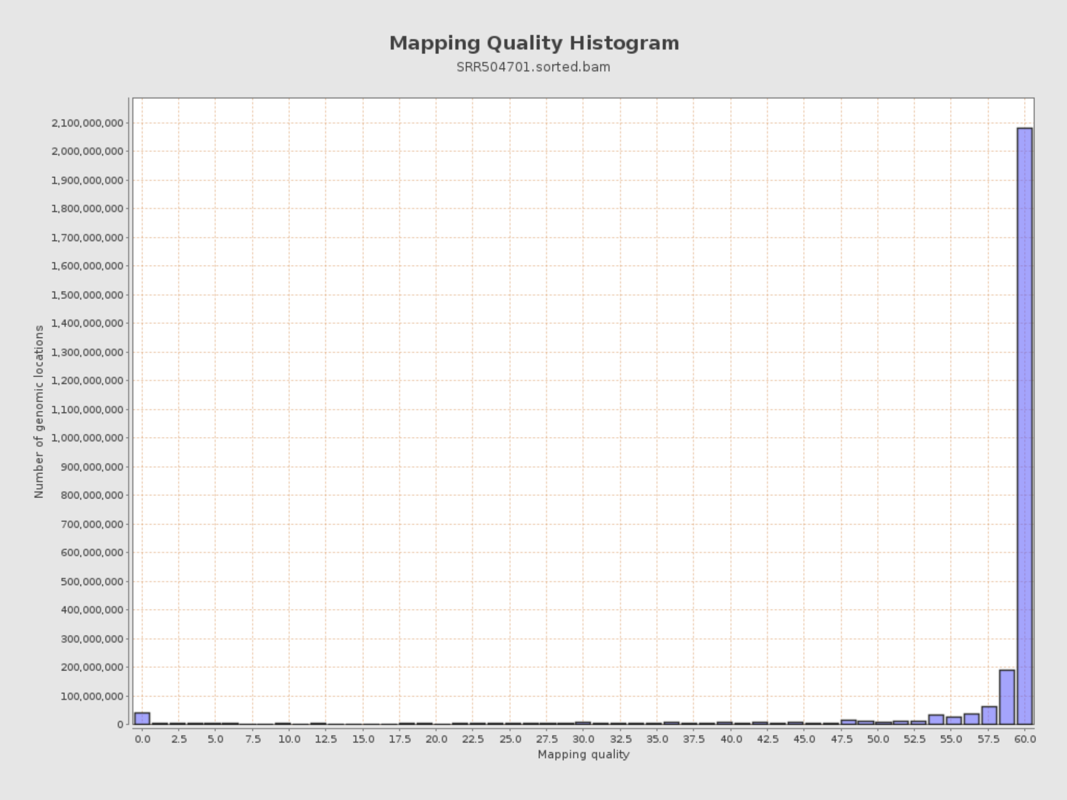
11. Results : Homopolymer Indels



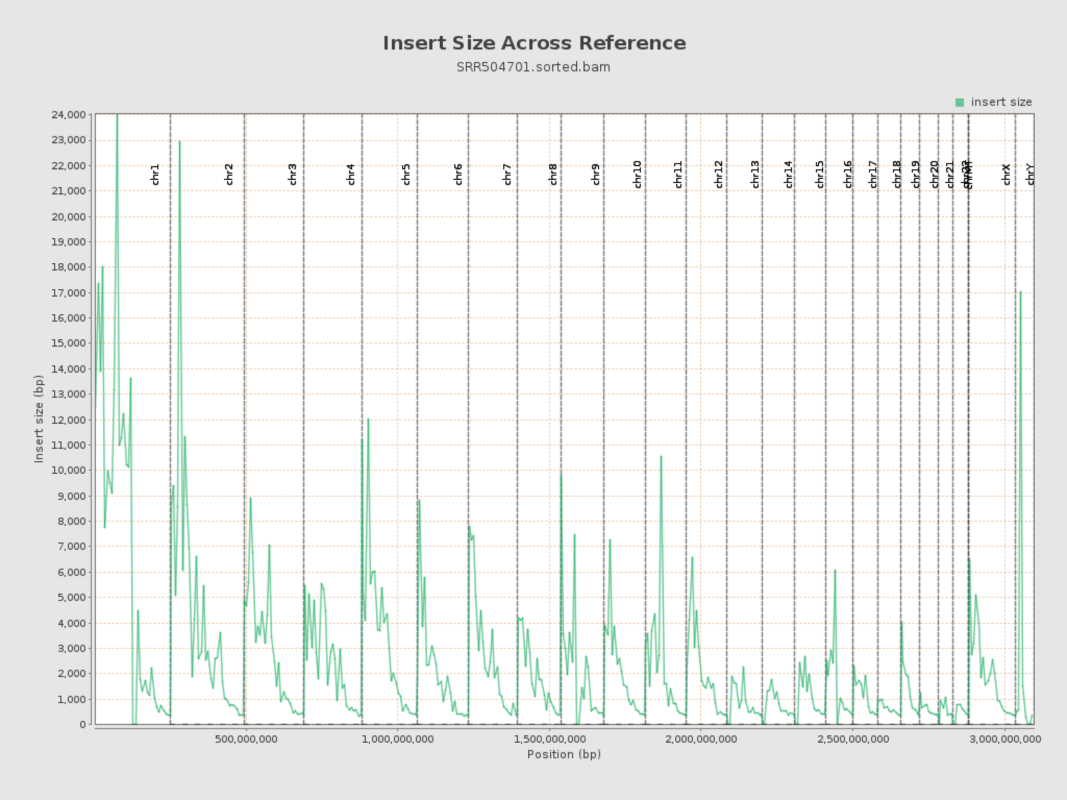
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram