Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/03 16:31:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR504703.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_SRR504703 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR504703_1.fastq.gz SRR504703_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Jan 03 16:31:21 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR504703.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	498,300,510
Mapped reads	451,655,631 / 90.64%
Unmapped reads	46,644,879 / 9.36%
Mapped paired reads	451,655,631 / 90.64%
Mapped reads, first in pair	226,795,588 / 45.51%
Mapped reads, second in pair	224,860,043 / 45.13%
Mapped reads, both in pair	446,268,380 / 89.56%
Mapped reads, singletons	5,387,251 / 1.08%
Secondary alignments	0
Supplementary alignments	2,289,623 / 0.46%
Read min/max/mean length	30 / 100 / 100.19
Duplicated reads (estimated)	119,941,344 / 24.07%
Duplication rate	23.36%
Clipped reads	39,103,842 / 7.85%

2.2. ACGT Content

Number/percentage of A's	11,746,503,168 / 26.48%
Number/percentage of C's	10,324,609,297 / 23.28%
Number/percentage of T's	11,765,913,513 / 26.53%
Number/percentage of G's	10,493,343,921 / 23.66%
Number/percentage of N's	22,813,194 / 0.05%

GC Percentage	46.94%

2.3. Coverage

Mean	14.3304
Standard Deviation	34.0863

2.4. Mapping Quality

Mean Mapping Quality	53.81

2.5. Insert size

Mean	42,949.99
Standard Deviation	1,932,946.21
P25/Median/P75	375 / 410 / 450

2.6. Mismatches and indels

General error rate	0.72%
Mismatches	311,357,709
Insertions	3,033,525
Mapped reads with at least one insertion	0.66%
Deletions	3,823,273
Mapped reads with at least one deletion	0.83%
Homopolymer indels	41.12%

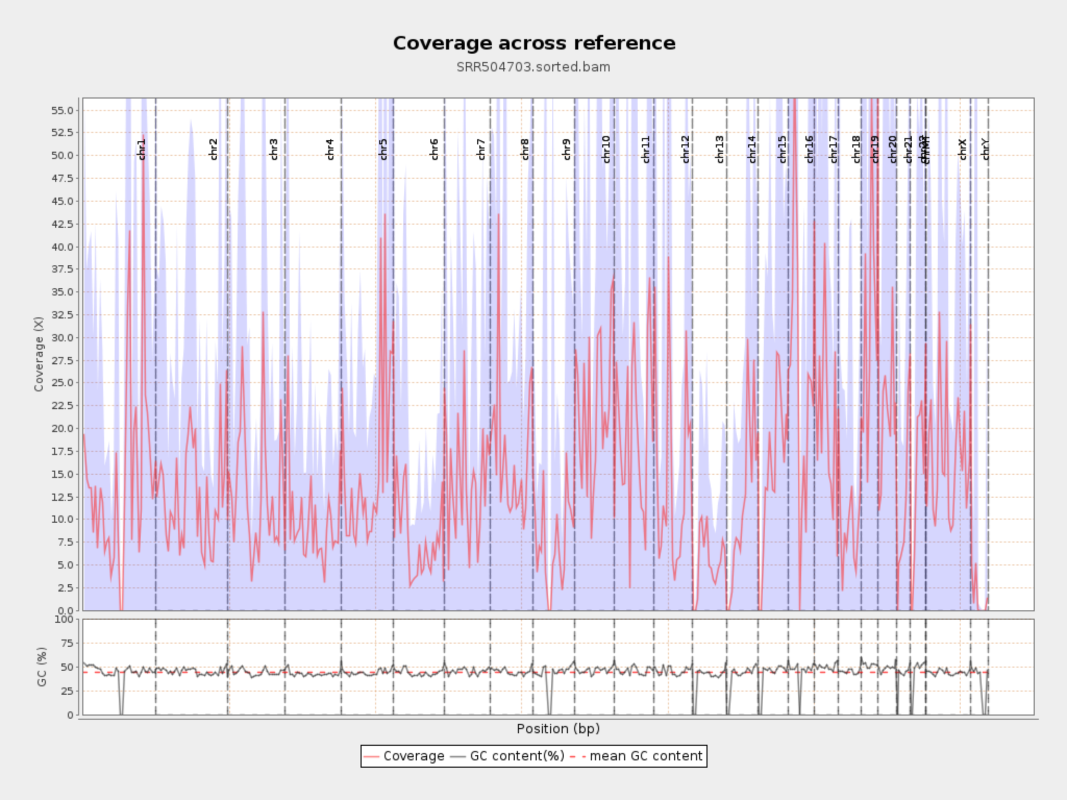
2.7. Chromosome stats

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

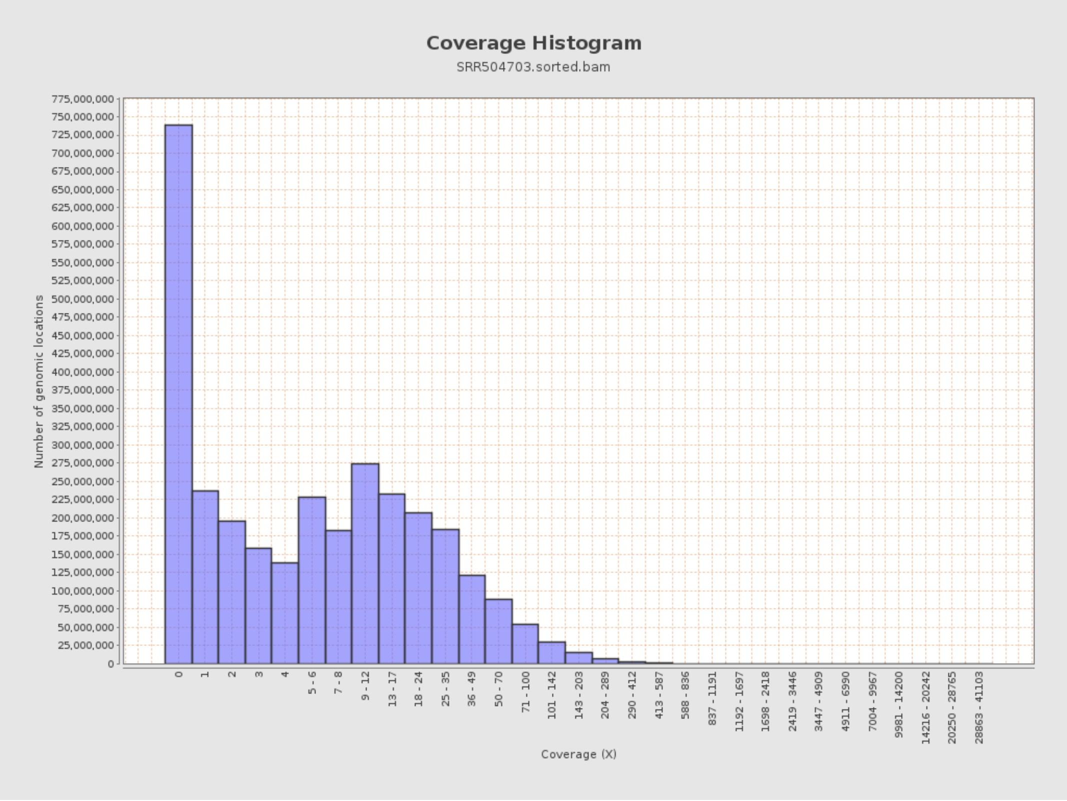
		bases	coverage	deviation
chr1	249250621	3655175812	14.6647	31.2082
chr2	243199373	3029942741	12.4587	23.5372
chr3	198022430	2585300301	13.0556	24.7646
chr4	191154276	1905621485	9.969	17.8184
chr5	180915260	2900108356	16.0302	30.9428
chr6	171115067	1340371531	7.8332	15.6379
chr7	159138663	2272091953	14.2774	24.5723
chr8	146364022	2494080722	17.0403	33.5485
chr9	141213431	1061995937	7.5205	27.8714
chr10	135534747	3014830279	22.244	35.5187
chr11	135006516	2659008267	19.6954	35.9636
chr12	133851895	2018921296	15.0832	35.552
chr13	115169878	620762202	5.39	10.9258
chr14	107349540	1280936016	11.9324	23.5192
chr15	102531392	1574211410	15.3535	29.9516
chr16	90354753	2229144940	24.671	41.5493
chr17	81195210	1734157707	21.3579	40.5447
chr18	78077248	691382315	8.8551	98.4099
chr19	59128983	1907094474	32.2531	60.188
chr20	63025520	1365332956	21.6632	35.4042
chr21	48129895	565987188	11.7596	25.3606
chr22	51304566	730121993	14.2311	29.4591
chrMT	16571	200195	12.081	17.2508
chrX	155270560	2642399105	17.018	28.3891

chrY	59373566	83352036	1.4039	48.5556

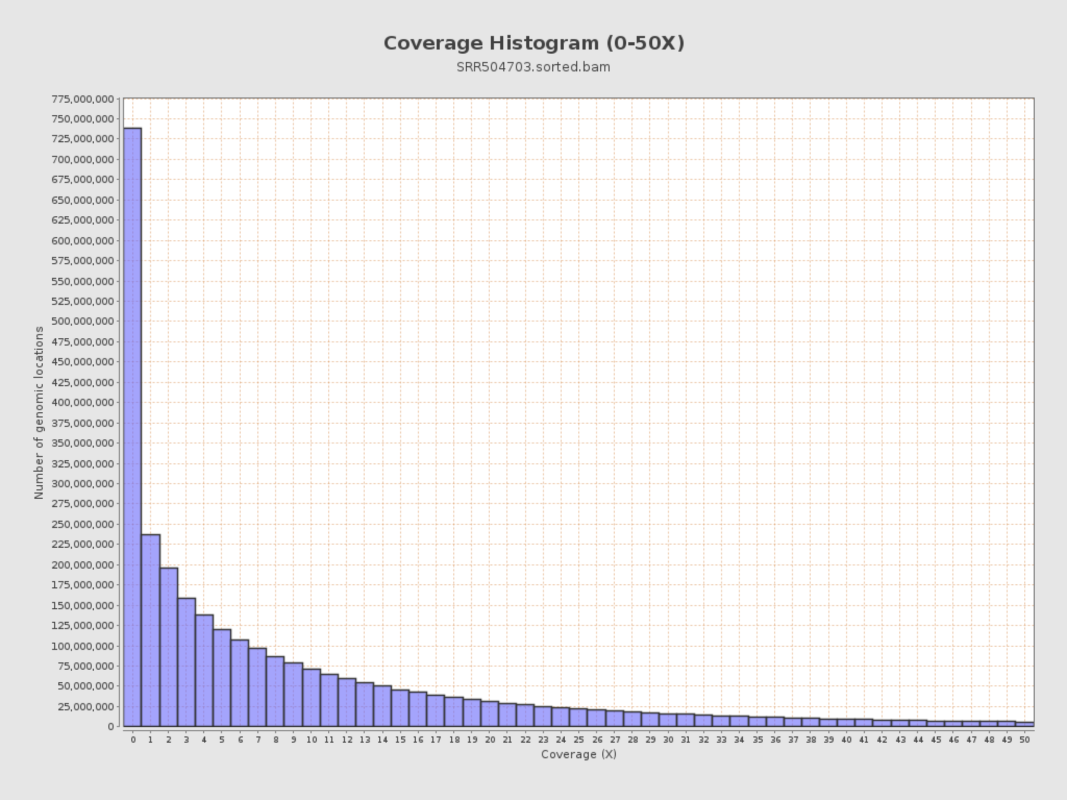
3. Results : Coverage across reference



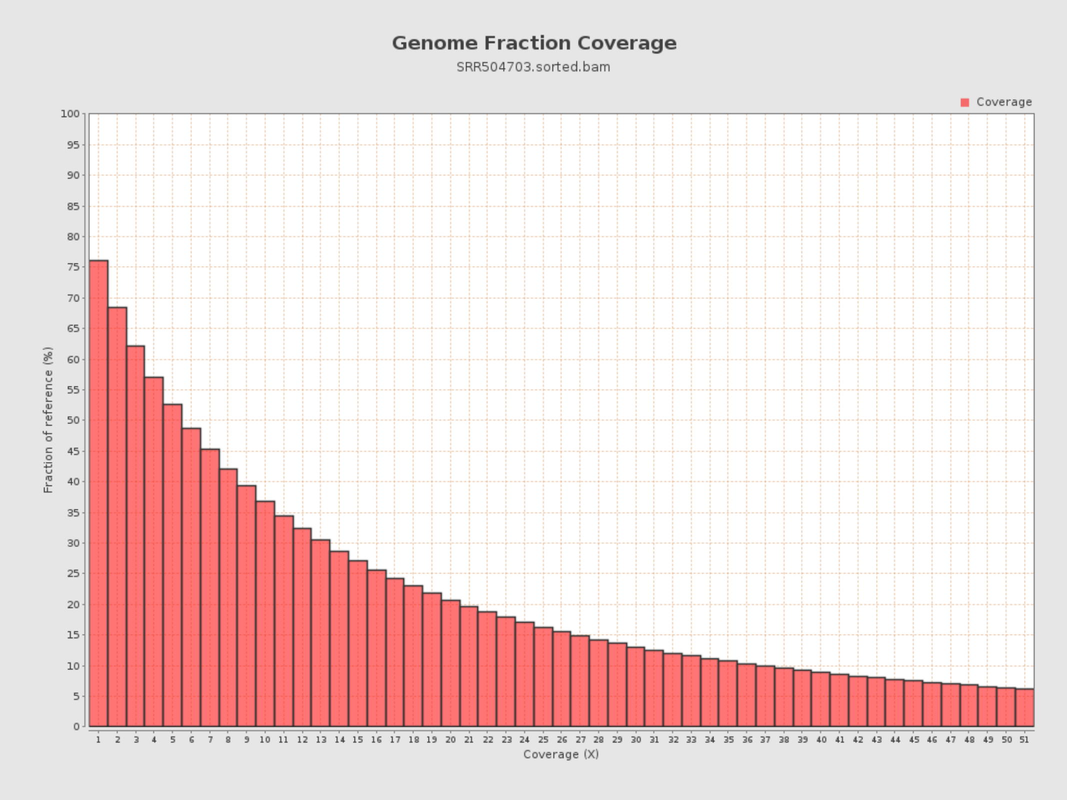
4. Results : Coverage Histogram



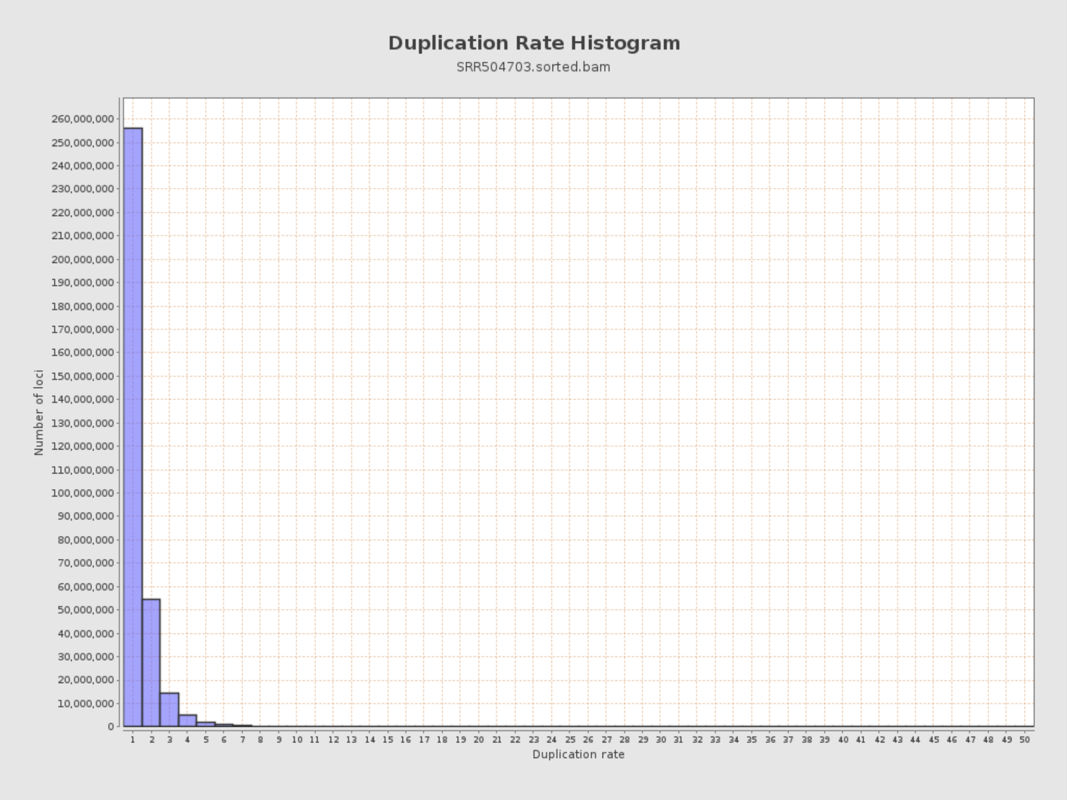
5. Results : Coverage Histogram (0-50X)



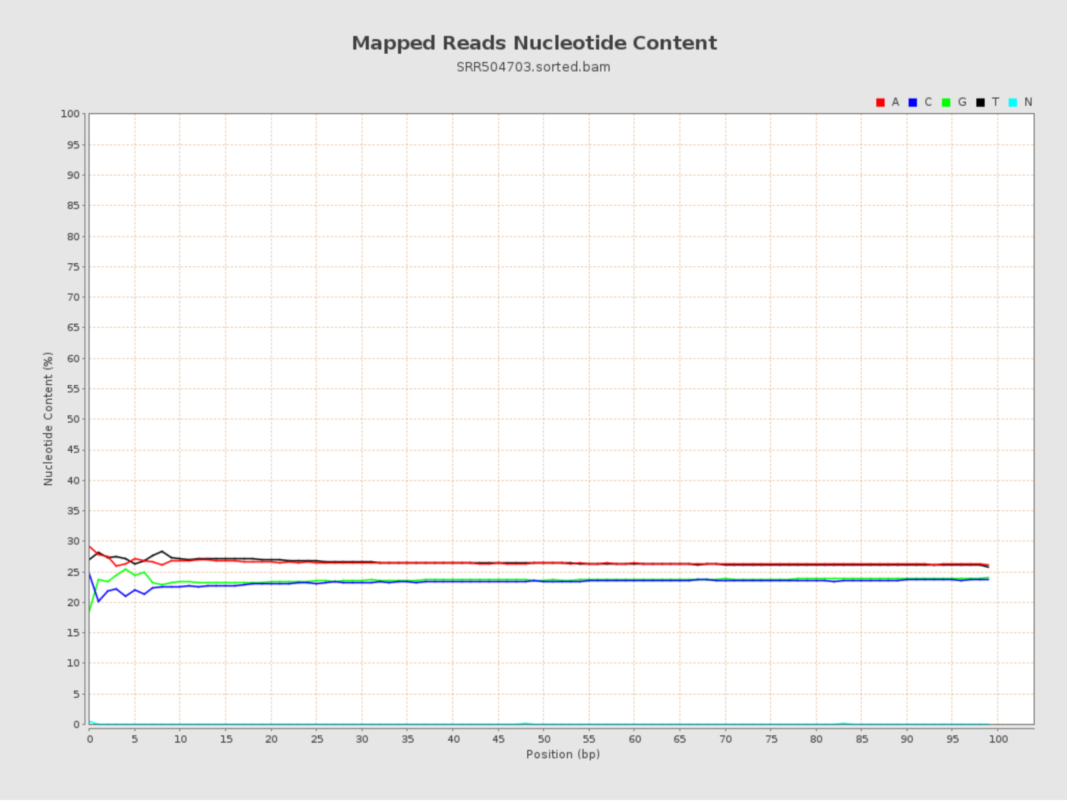
6. Results : Genome Fraction Coverage



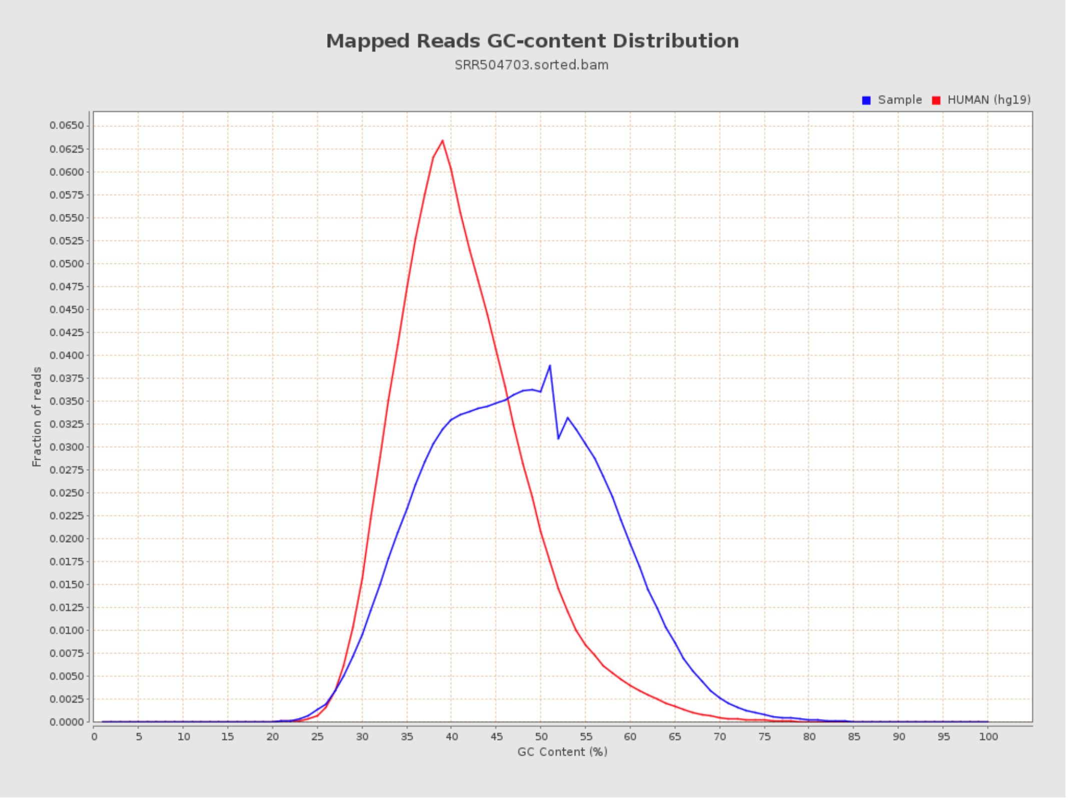
7. Results : Duplication Rate Histogram



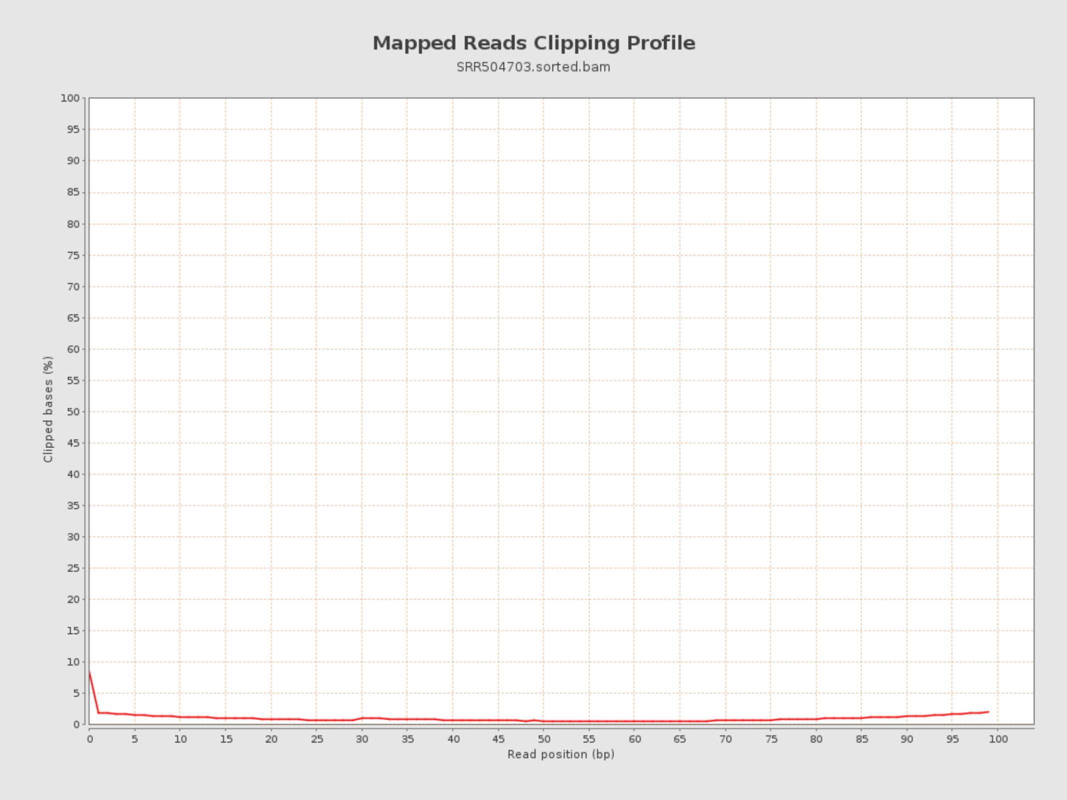
8. Results : Mapped Reads Nucleotide Content



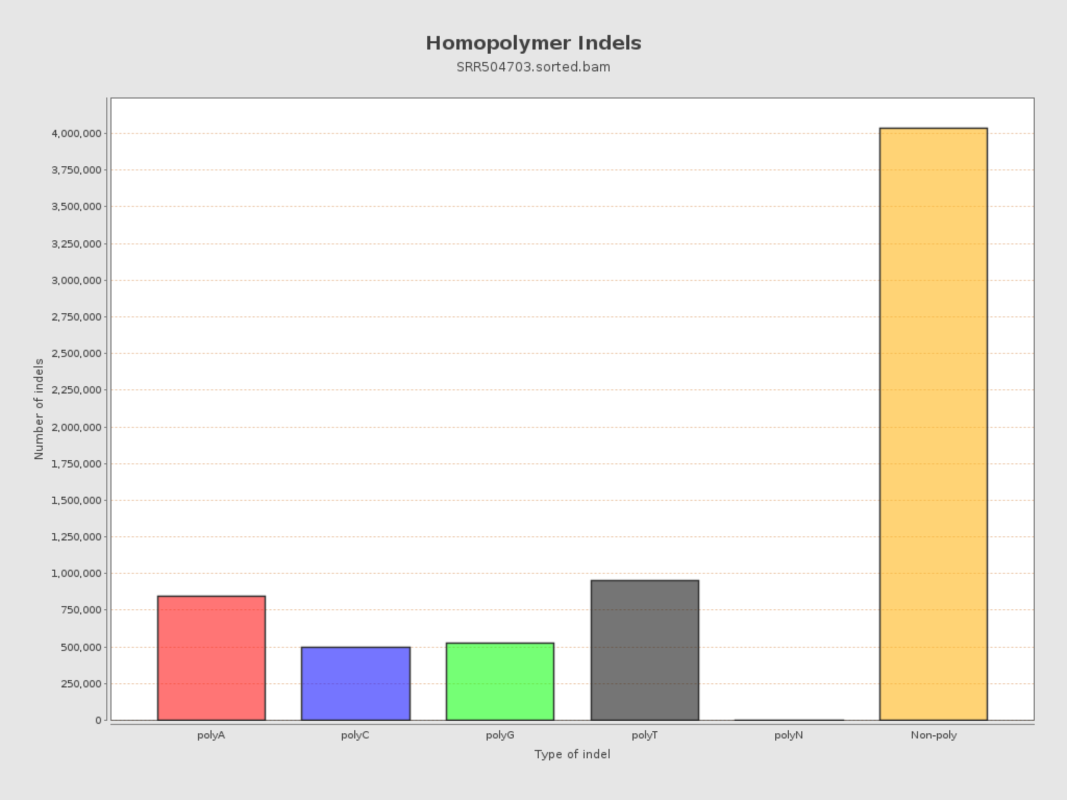
9. Results : Mapped Reads GC-content Distribution



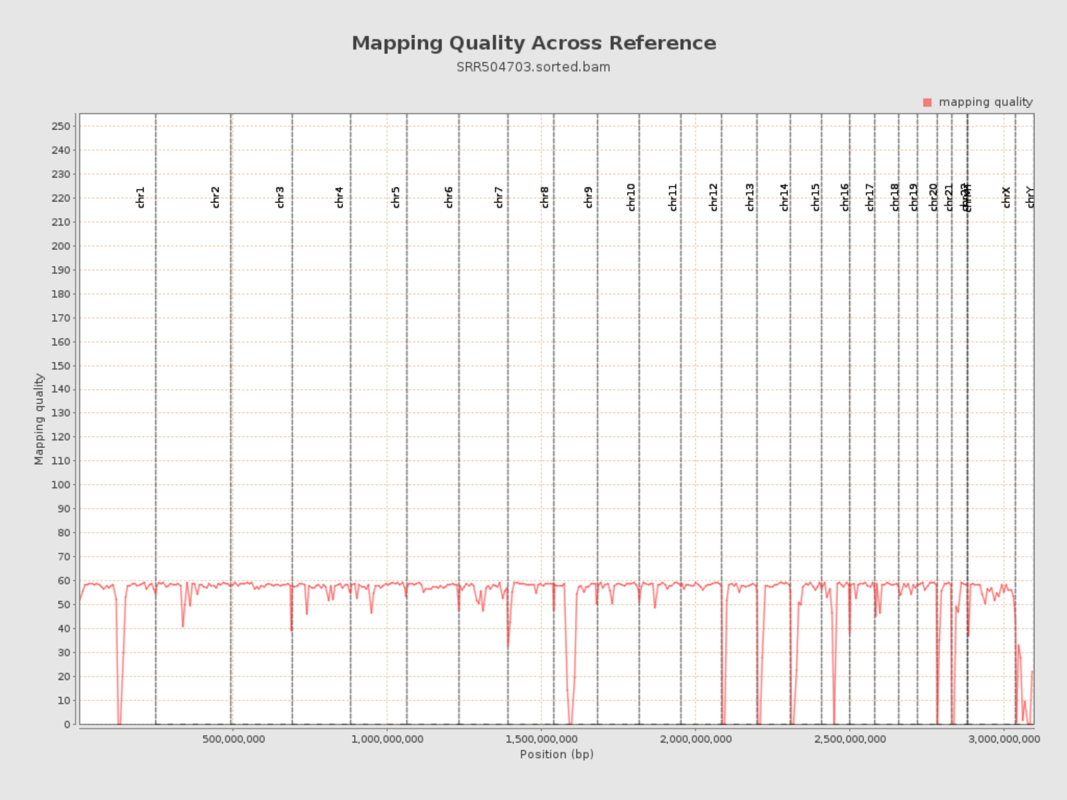
10. Results : Mapped Reads Clipping Profile



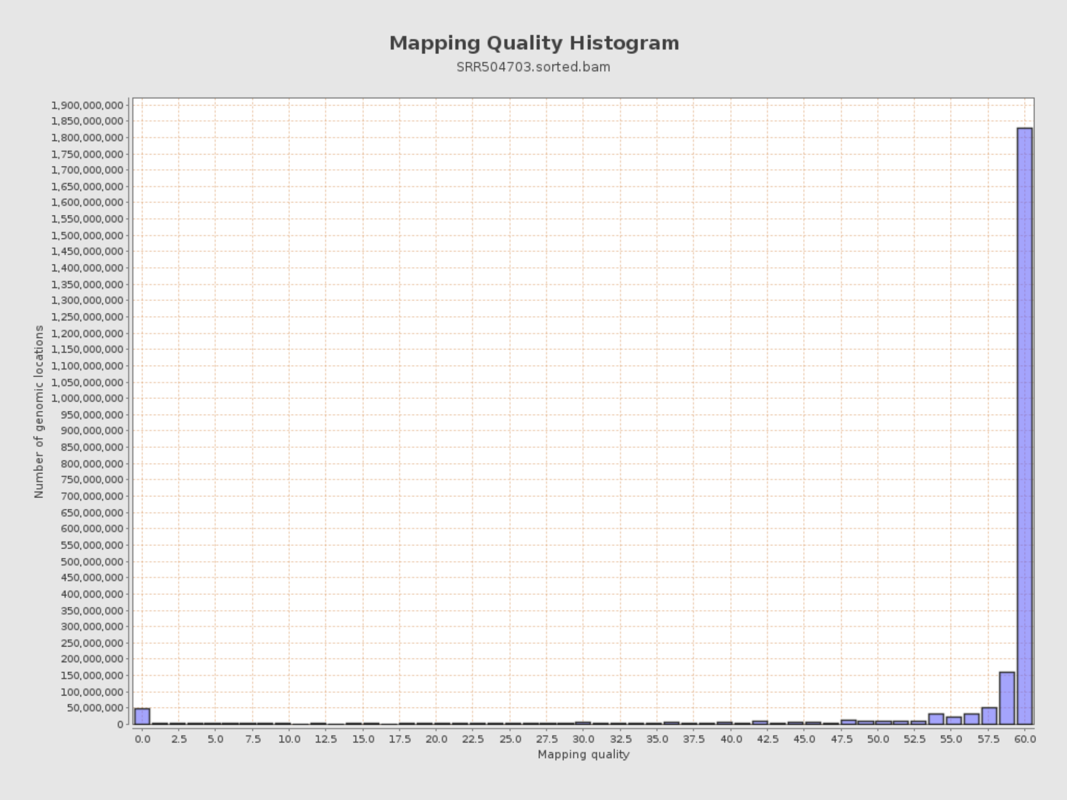
11. Results : Homopolymer Indels



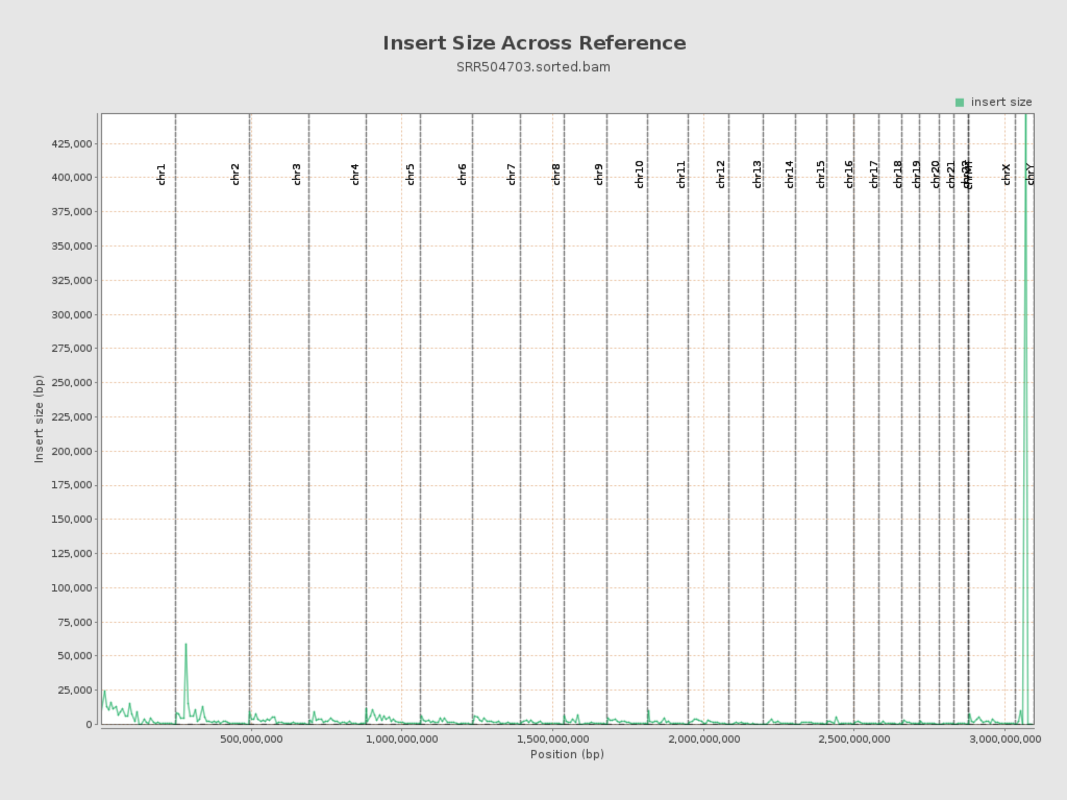
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram