Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/01 04:38:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR504634.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_SRR504634 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR504634_1.fastq.gz SRR504634_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Jan 01 04:38:15 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR504634.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	348,638,182
Mapped reads	302,930,289 / 86.89%
Unmapped reads	45,707,893 / 13.11%
Mapped paired reads	302,930,289 / 86.89%
Mapped reads, first in pair	151,960,395 / 43.59%
Mapped reads, second in pair	150,969,894 / 43.3%
Mapped reads, both in pair	300,568,354 / 86.21%
Mapped reads, singletons	2,361,935 / 0.68%
Secondary alignments	0
Supplementary alignments	3,303,690 / 0.95%
Read min/max/mean length	30 / 100 / 100.39
Duplicated reads (estimated)	94,616,276 / 27.14%
Duplication rate	25.42%
Clipped reads	25,996,215 / 7.46%

2.2. ACGT Content

Number/percentage of A's	7,517,269,528 / 25.16%
Number/percentage of C's	7,321,306,148 / 24.5%
Number/percentage of T's	7,555,255,299 / 25.28%
Number/percentage of G's	7,478,630,703 / 25.03%
Number/percentage of N's	10,843,454 / 0.04%

GC Percentage	49.53%

2.3. Coverage

Mean	9.6555
Standard Deviation	38.0178

2.4. Mapping Quality

Mean Mapping Quality	53.62

2.5. Insert size

Mean	40,155.01
Standard Deviation	1,915,618.44
P25/Median/P75	329 / 367 / 411

2.6. Mismatches and indels

General error rate	0.7%
Mismatches	204,365,850
Insertions	2,411,584
Mapped reads with at least one insertion	0.78%
Deletions	2,884,652
Mapped reads with at least one deletion	0.92%
Homopolymer indels	38.89%

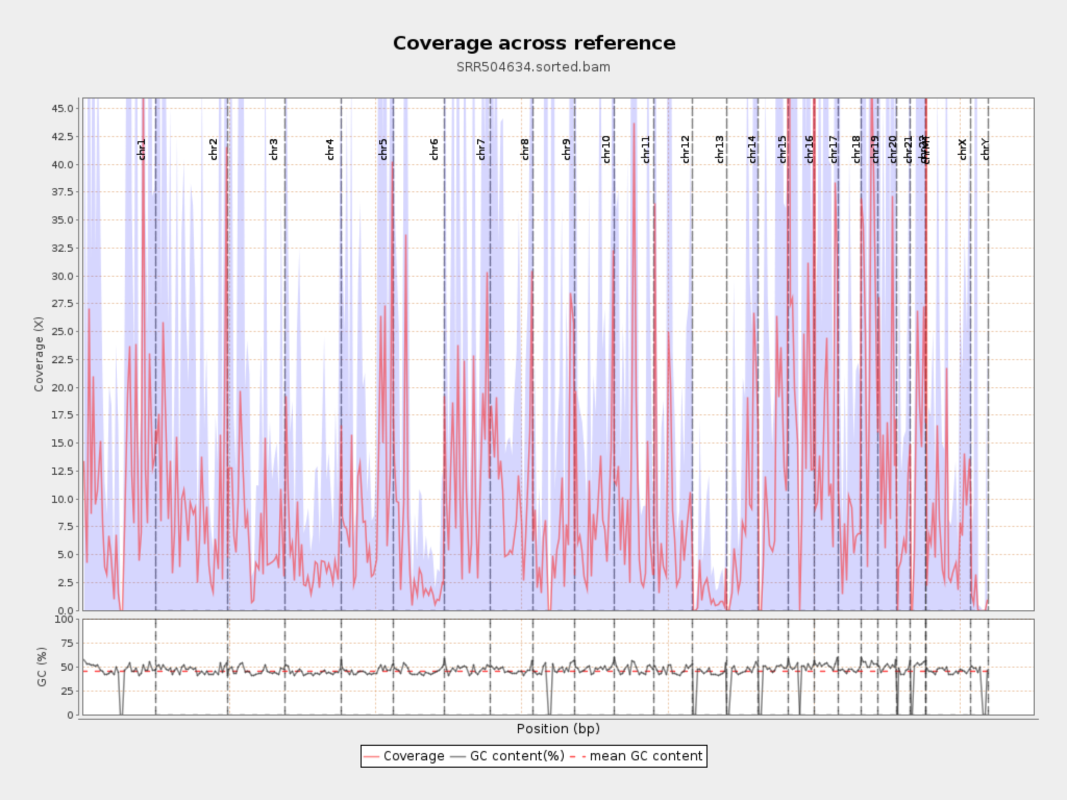
2.7. Chromosome stats

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

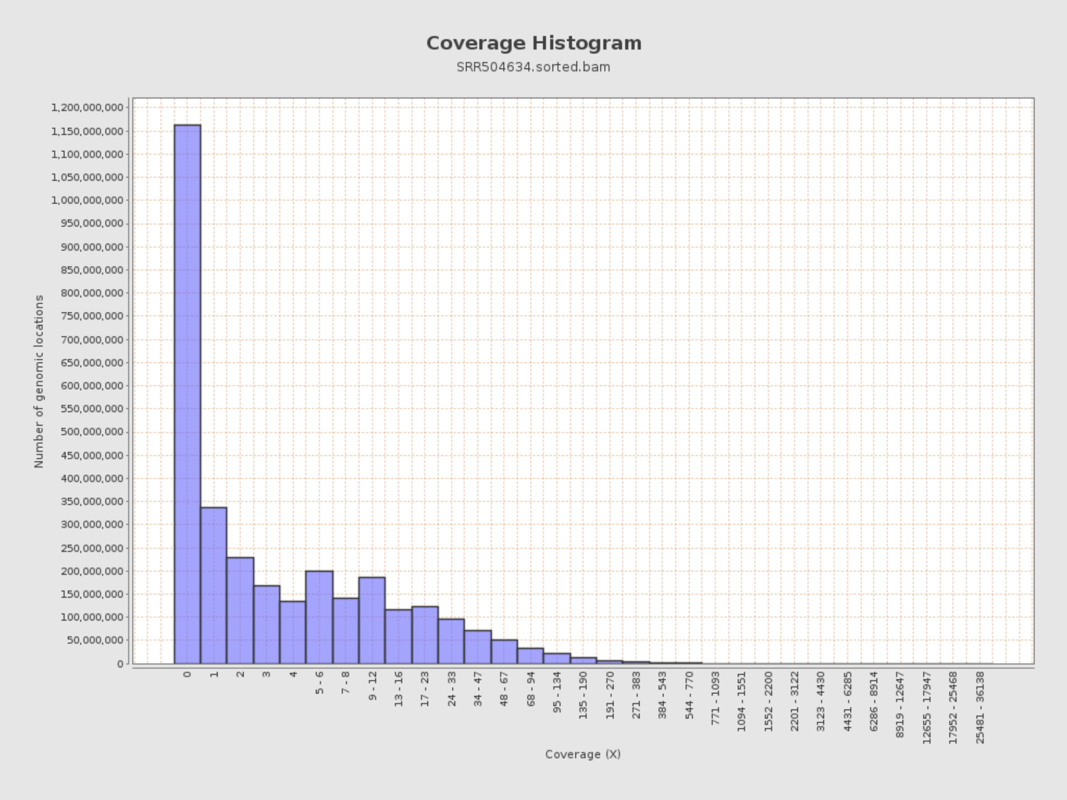
		bases	coverage	deviation
chr1	249250621	2873304878	11.5278	37.3275
chr2	243199373	2424499178	9.9692	29.1951
chr3	198022430	1416719303	7.1543	24.208
chr4	191154276	926313703	4.8459	15.0447
chr5	180915260	2014055469	11.1326	31.478
chr6	171115067	861129011	5.0325	18.4295
chr7	159138663	2057393786	12.9283	33.108
chr8	146364022	1591418298	10.873	28.4008
chr9	141213431	1036285540	7.3384	70.7155
chr10	135534747	1212944181	8.9493	28.4326
chr11	135006516	1397179423	10.349	35.3893
chr12	133851895	1258275727	9.4005	27.8445
chr13	115169878	138198799	1.2	5.5789
chr14	107349540	922110977	8.5898	23.2002
chr15	102531392	1088817235	10.6194	29.7811
chr16	90354753	1934150845	21.4062	53.2576
chr17	81195210	1292270553	15.9156	41.748
chr18	78077248	513229236	6.5734	72.7405
chr19	59128983	1619826690	27.3948	113.0074
chr20	63025520	1020880525	16.1979	48.8789
chr21	48129895	320051438	6.6497	21.6566
chr22	51304566	748409418	14.5876	35.8714
chrMT	16571	2933497	177.0259	68.7869
chrX	155270560	1175620731	7.5714	18.2451

chrY	59373566	44474584	0.7491	33.2527

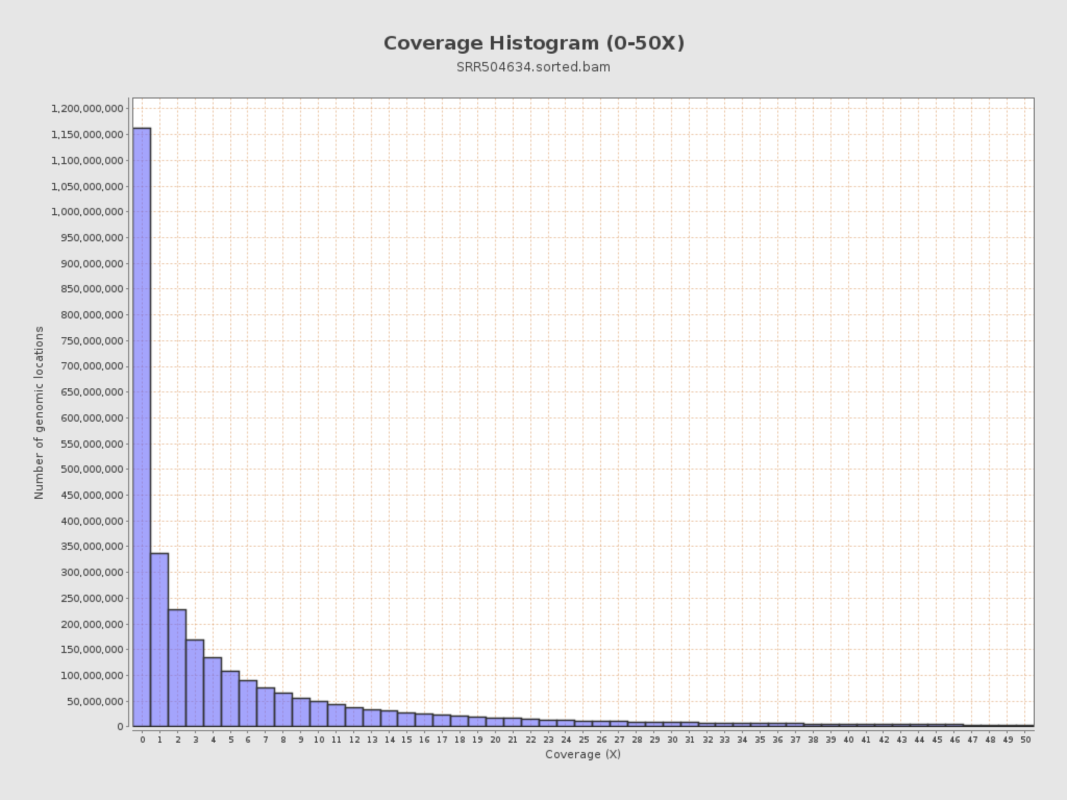
3. Results : Coverage across reference



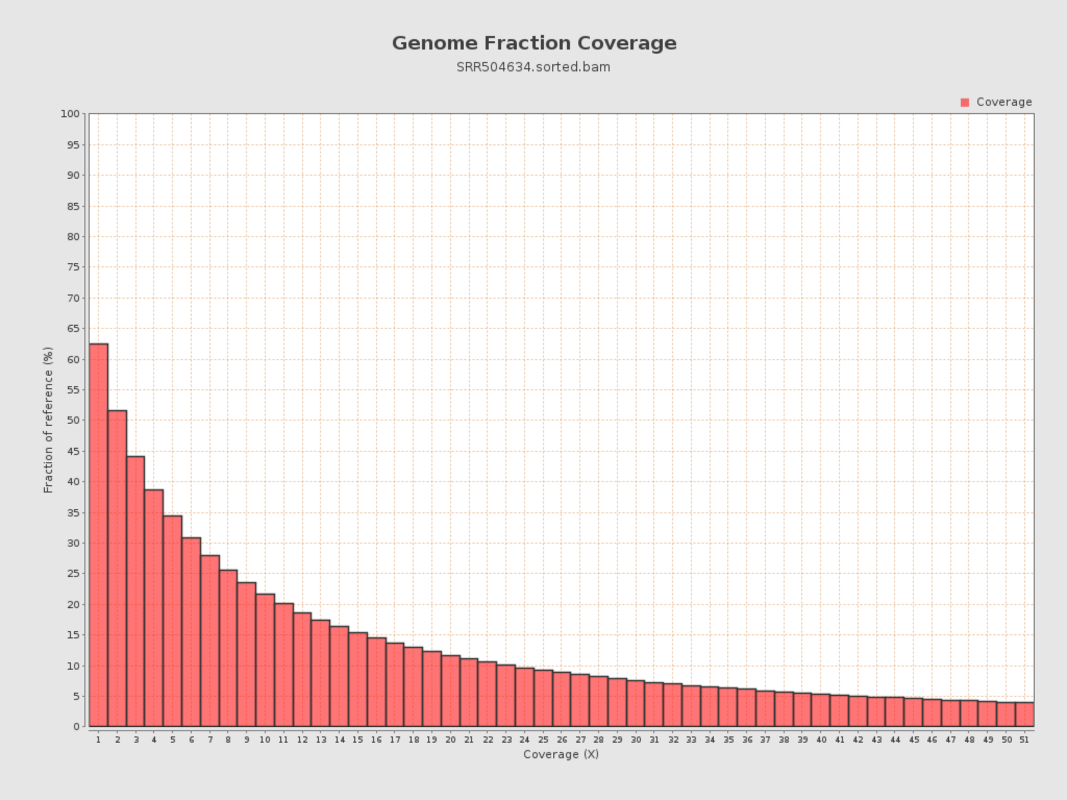
4. Results : Coverage Histogram



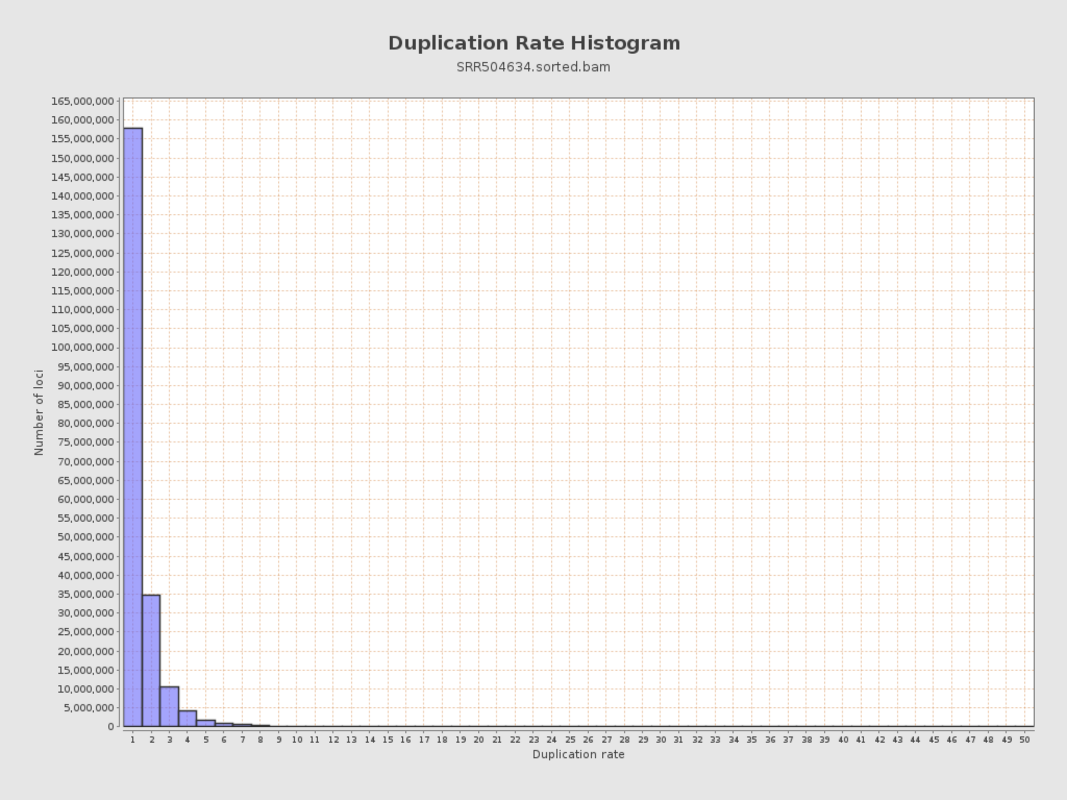
5. Results : Coverage Histogram (0-50X)



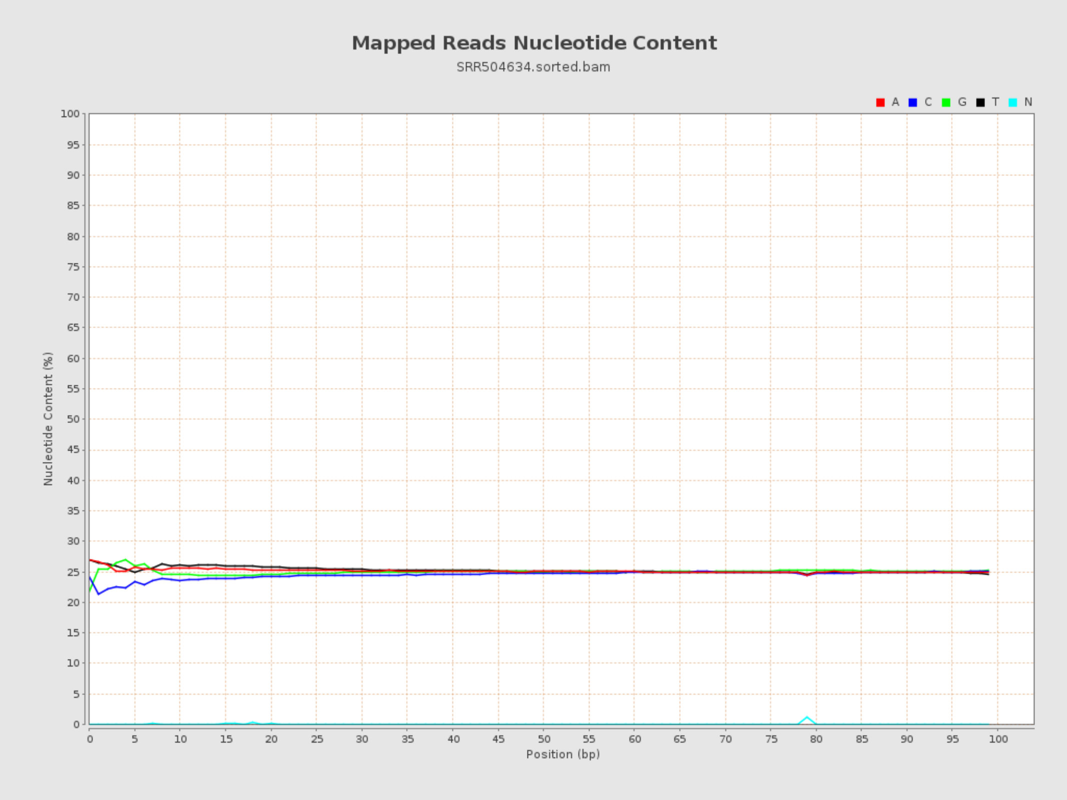
6. Results : Genome Fraction Coverage



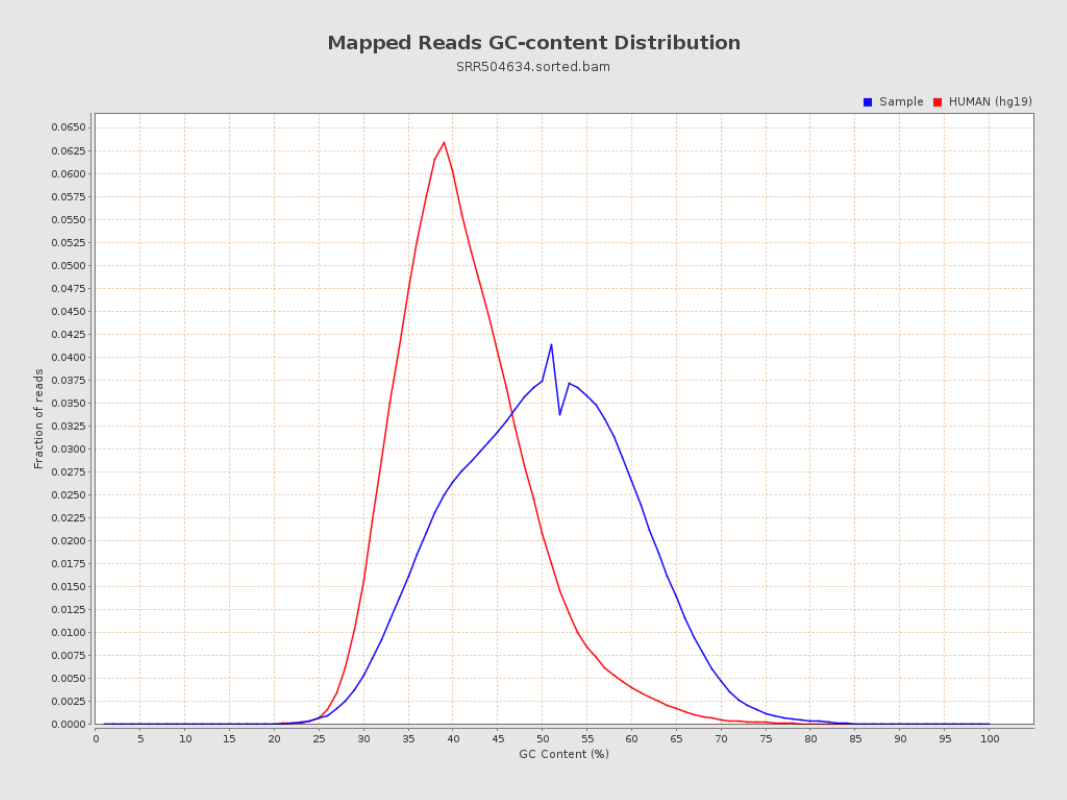
7. Results : Duplication Rate Histogram



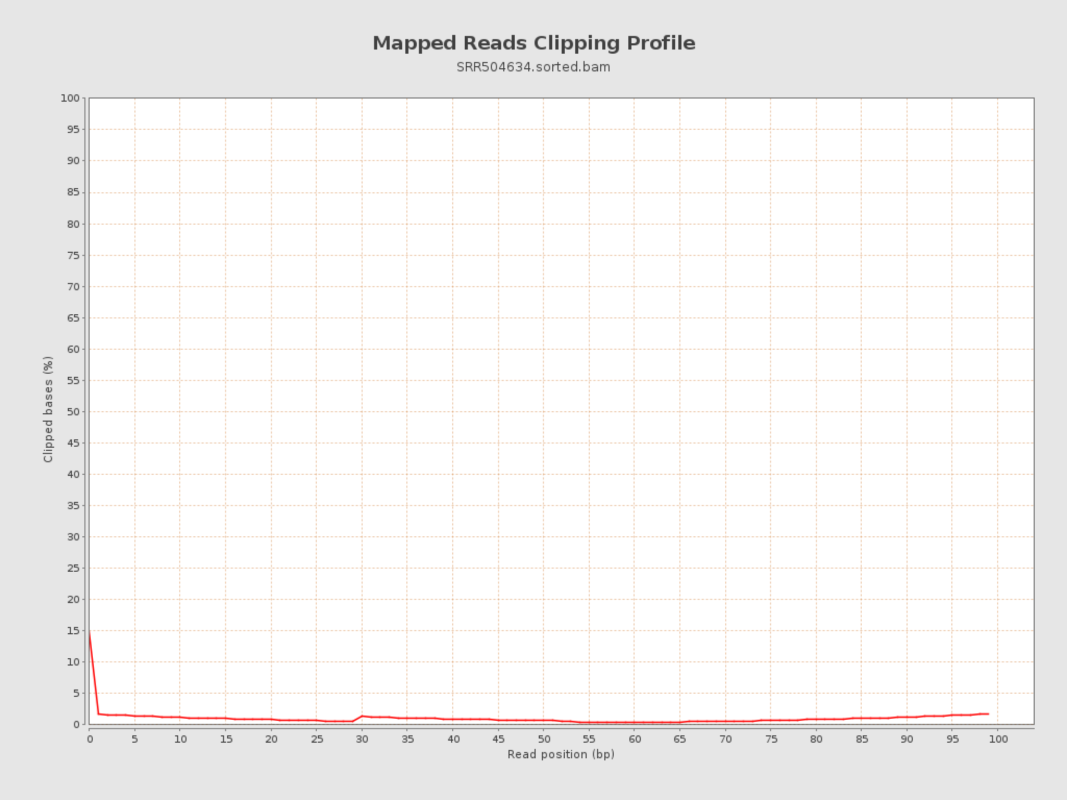
8. Results : Mapped Reads Nucleotide Content



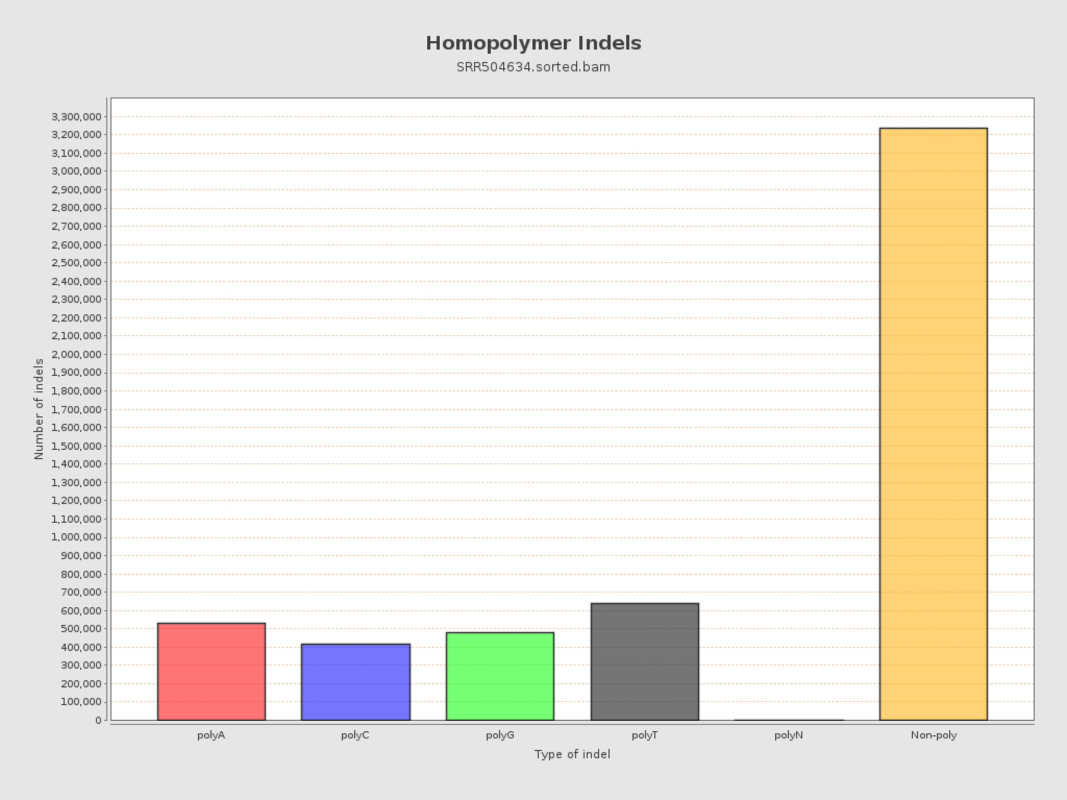
9. Results : Mapped Reads GC-content Distribution



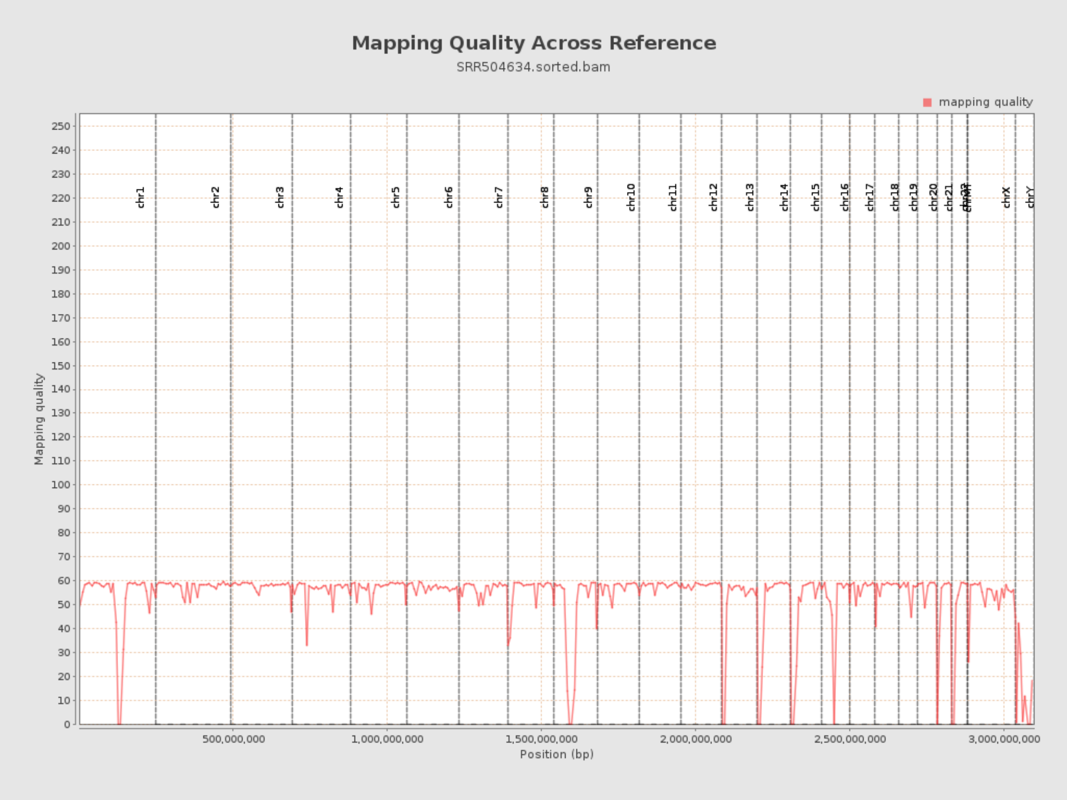
10. Results : Mapped Reads Clipping Profile



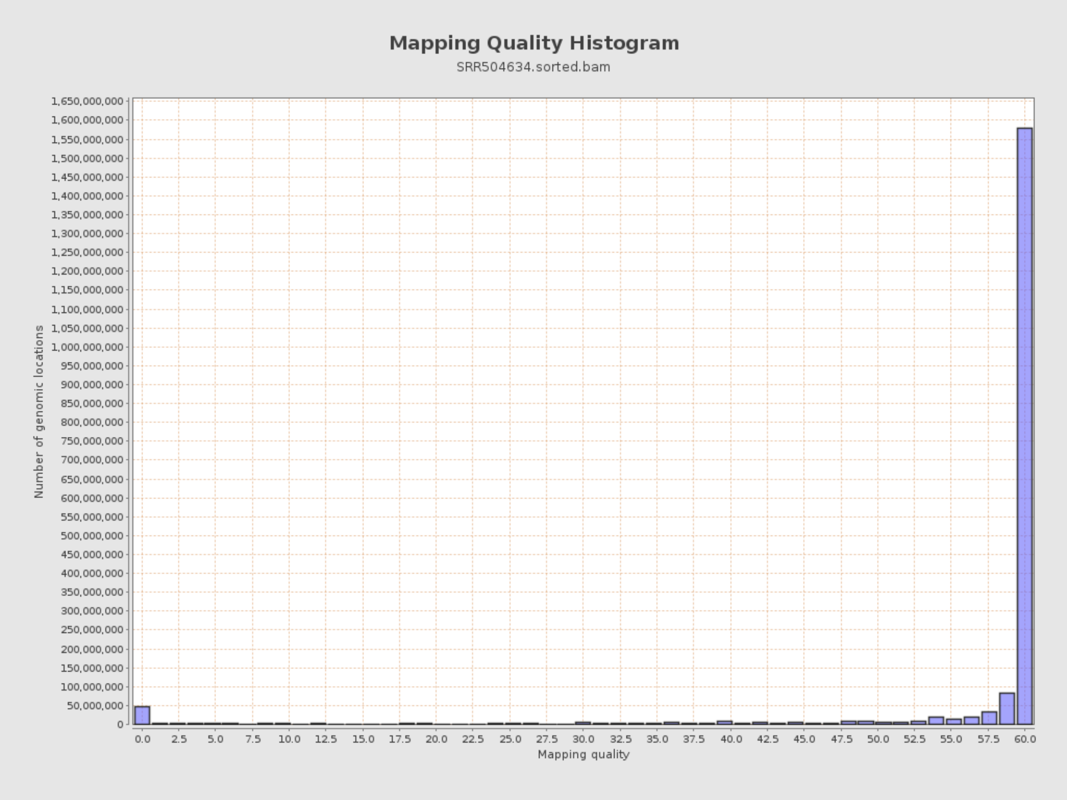
11. Results : Homopolymer Indels



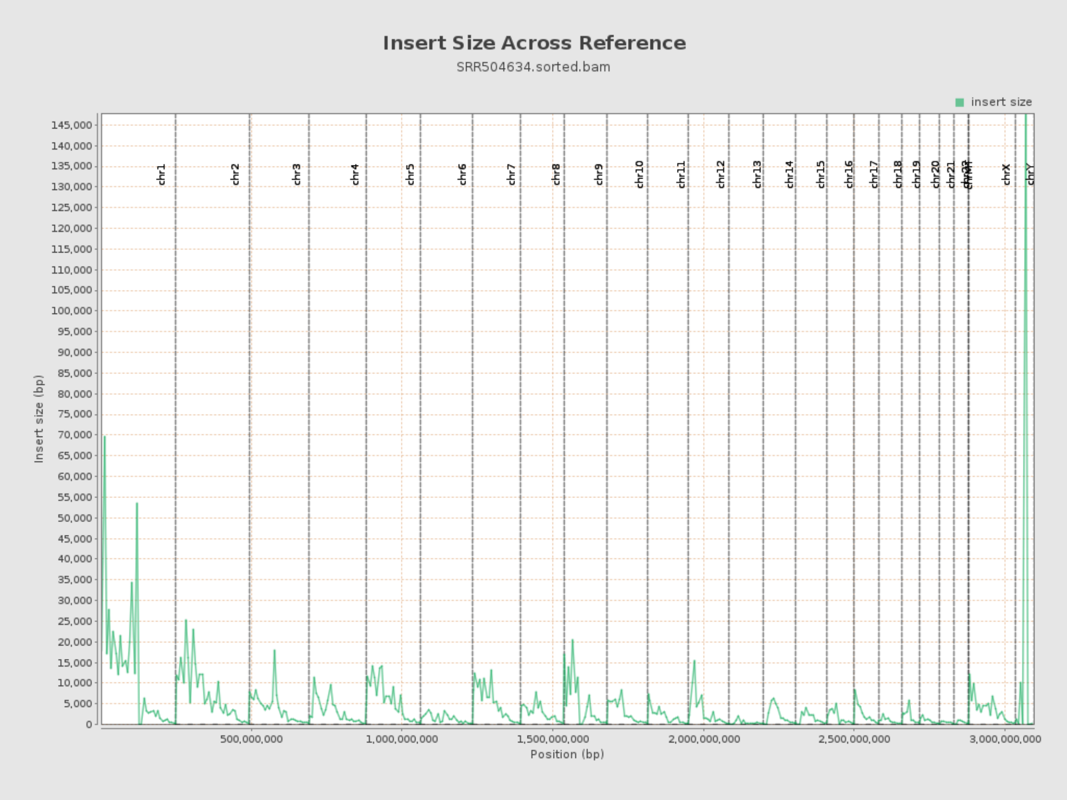
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram