Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/01 17:51:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR504637.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_SRR504637 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR504637_1.fastq.gz SRR504637_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Jan 01 17:51:52 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR504637.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	421,641,610
Mapped reads	393,541,396 / 93.34%
Unmapped reads	28,100,214 / 6.66%
Mapped paired reads	393,541,396 / 93.34%
Mapped reads, first in pair	198,047,545 / 46.97%
Mapped reads, second in pair	195,493,851 / 46.36%
Mapped reads, both in pair	388,434,190 / 92.12%
Mapped reads, singletons	5,107,206 / 1.21%
Secondary alignments	0
Supplementary alignments	2,348,294 / 0.56%
Read min/max/mean length	30 / 100 / 100.23
Duplicated reads (estimated)	107,029,805 / 25.38%
Duplication rate	24.14%
Clipped reads	87,545,066 / 20.76%

2.2. ACGT Content

Number/percentage of A's	9,782,232,720 / 26.37%
Number/percentage of C's	8,471,201,784 / 22.83%
Number/percentage of T's	9,764,496,625 / 26.32%
Number/percentage of G's	8,760,279,296 / 23.61%
Number/percentage of N's	320,436,737 / 0.86%

GC Percentage	46.45%

2.3. Coverage

Mean	11.9866
Standard Deviation	27.7926

2.4. Mapping Quality

Mean Mapping Quality	53.74

2.5. Insert size

Mean	45,773.84
Standard Deviation	2,034,781.83
P25/Median/P75	315 / 349 / 385

2.6. Mismatches and indels

General error rate	2.23%
Mismatches	363,070,794
Insertions	141,455,694
Mapped reads with at least one insertion	33.3%
Deletions	3,790,175
Mapped reads with at least one deletion	0.94%
Homopolymer indels	28.98%

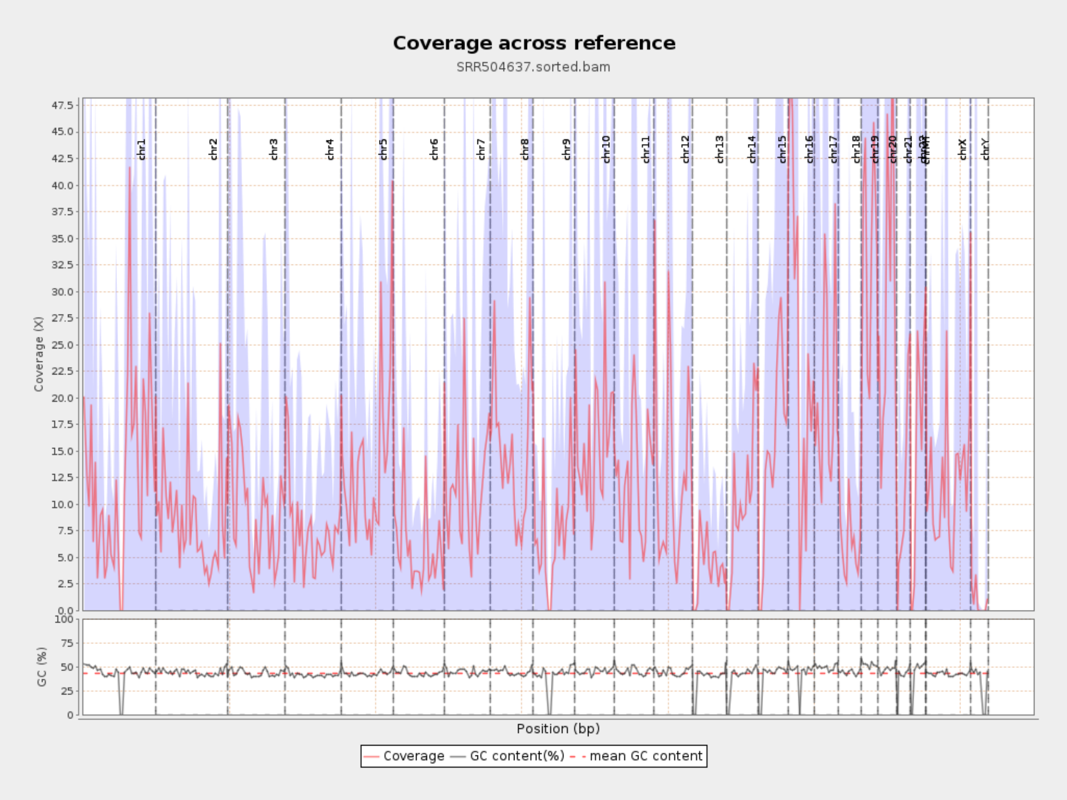
2.7. Chromosome stats

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

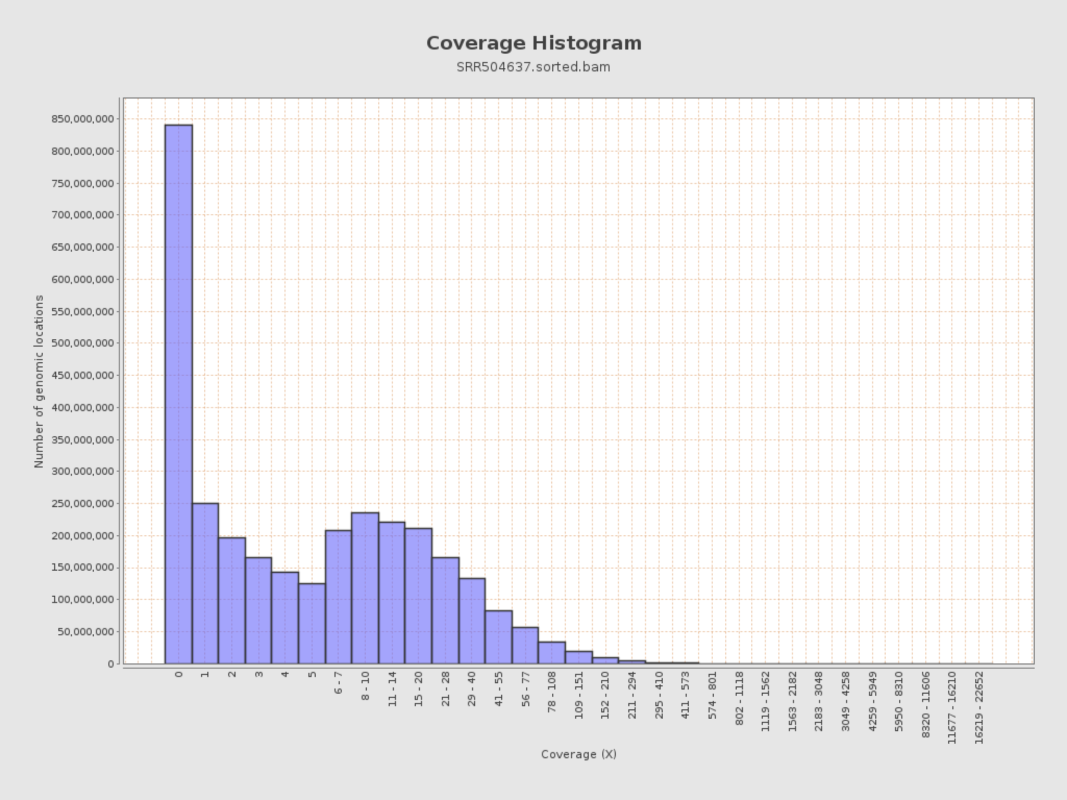
		bases	coverage	deviation
chr1	249250621	3133414684	12.5713	26.1818
chr2	243199373	2065945259	8.4949	17.7304
chr3	198022430	1825933027	9.2208	18.4136
chr4	191154276	1420282542	7.43	13.2064
chr5	180915260	2507700471	13.8612	23.4515
chr6	171115067	973395231	5.6885	12.8161
chr7	159138663	1901217317	11.9469	20.1292
chr8	146364022	2154573902	14.7207	39.2841
chr9	141213431	1022871001	7.2434	16.3223
chr10	135534747	2141254162	15.7986	26.4767
chr11	135006516	1644089254	12.1779	22.7559
chr12	133851895	1777936676	13.2829	27.5768
chr13	115169878	477847343	4.1491	7.9599
chr14	107349540	1118519943	10.4194	19.1117
chr15	102531392	1512524739	14.7518	27.9054
chr16	90354753	2214303861	24.5068	39.5177
chr17	81195210	1655203076	20.3855	35.8717
chr18	78077248	500345801	6.4083	55.8273
chr19	59128983	1956204505	33.0837	68.4523
chr20	63025520	1870675371	29.6812	42.4349
chr21	48129895	563135103	11.7003	22.9358
chr22	51304566	765661016	14.9238	31.8762
chrMT	16571	443850	26.7847	21.0875
chrX	155270560	1851828429	11.9265	21.623

chrY	59373566	51659584	0.8701	31.4065

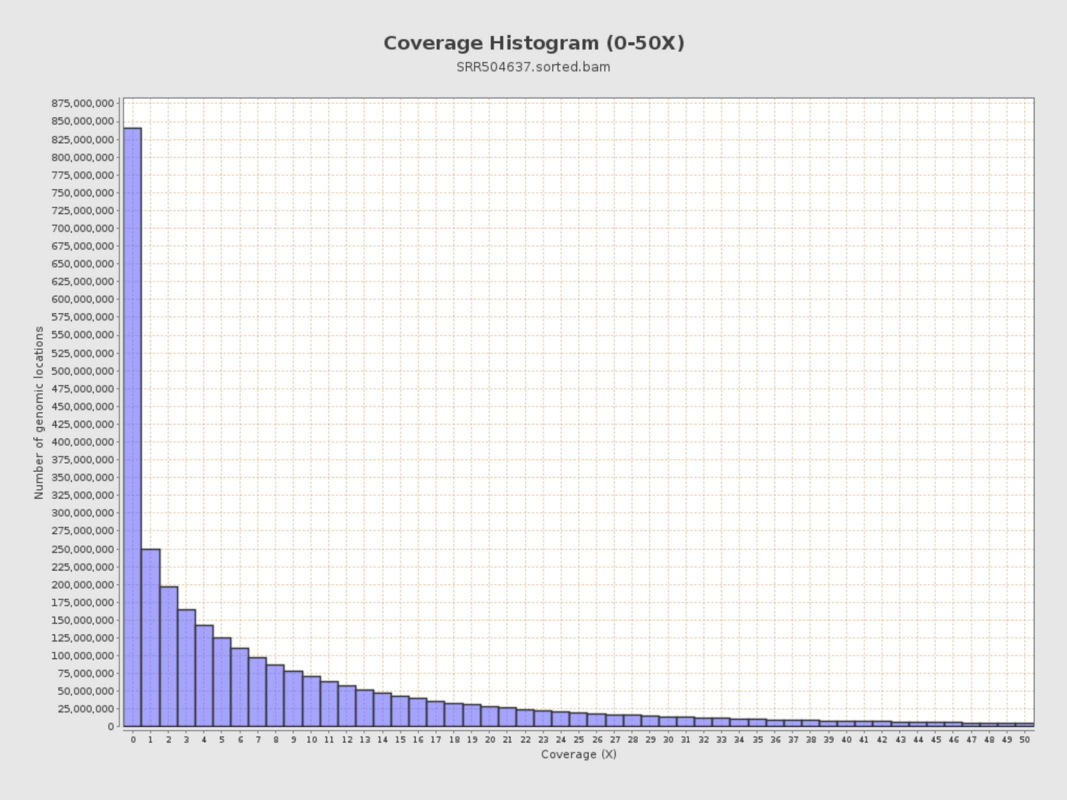
3. Results : Coverage across reference



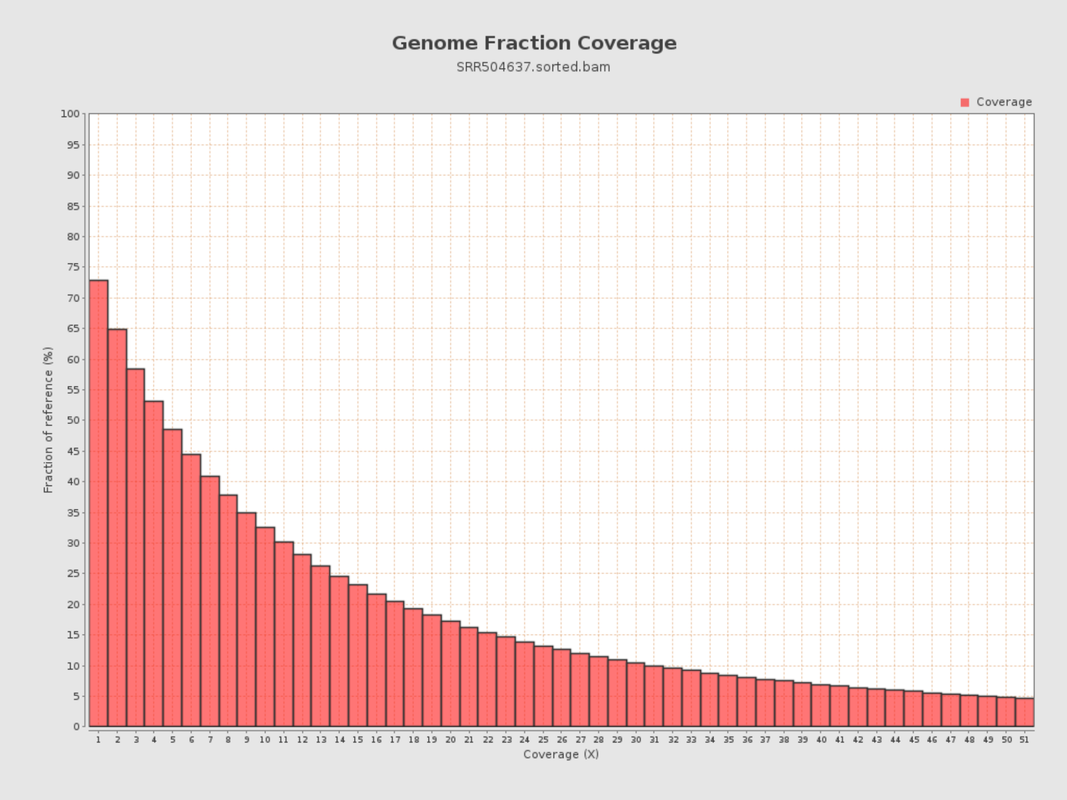
4. Results : Coverage Histogram



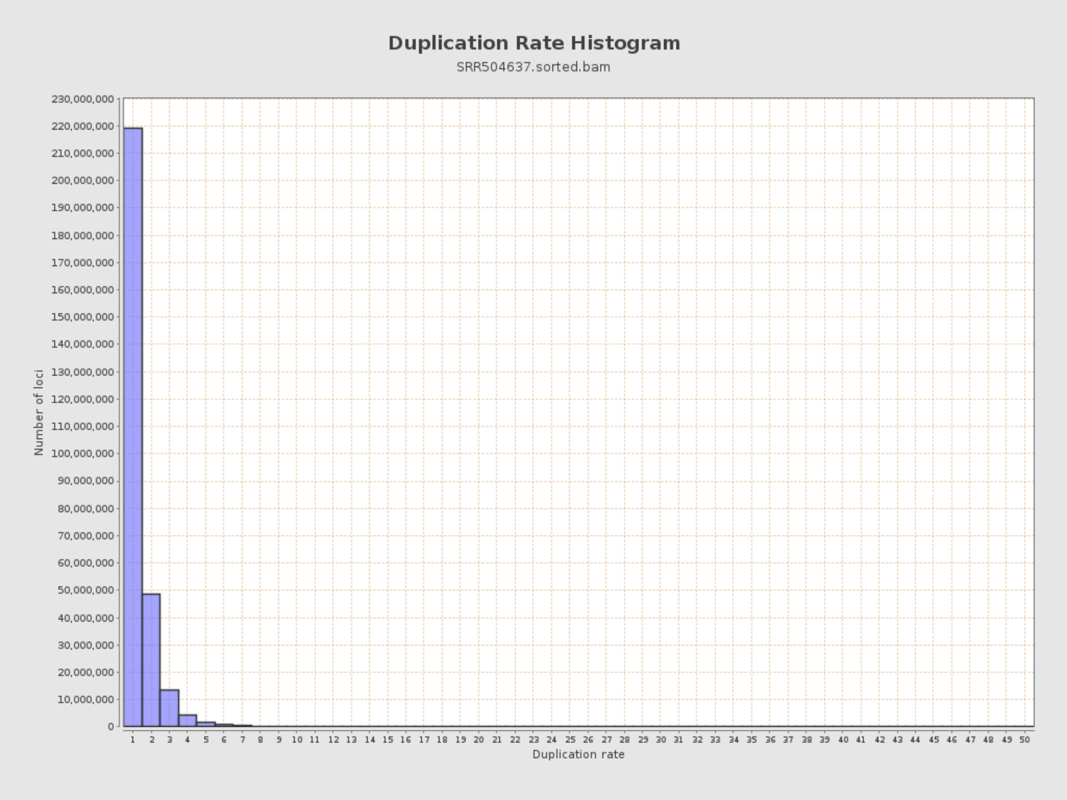
5. Results : Coverage Histogram (0-50X)



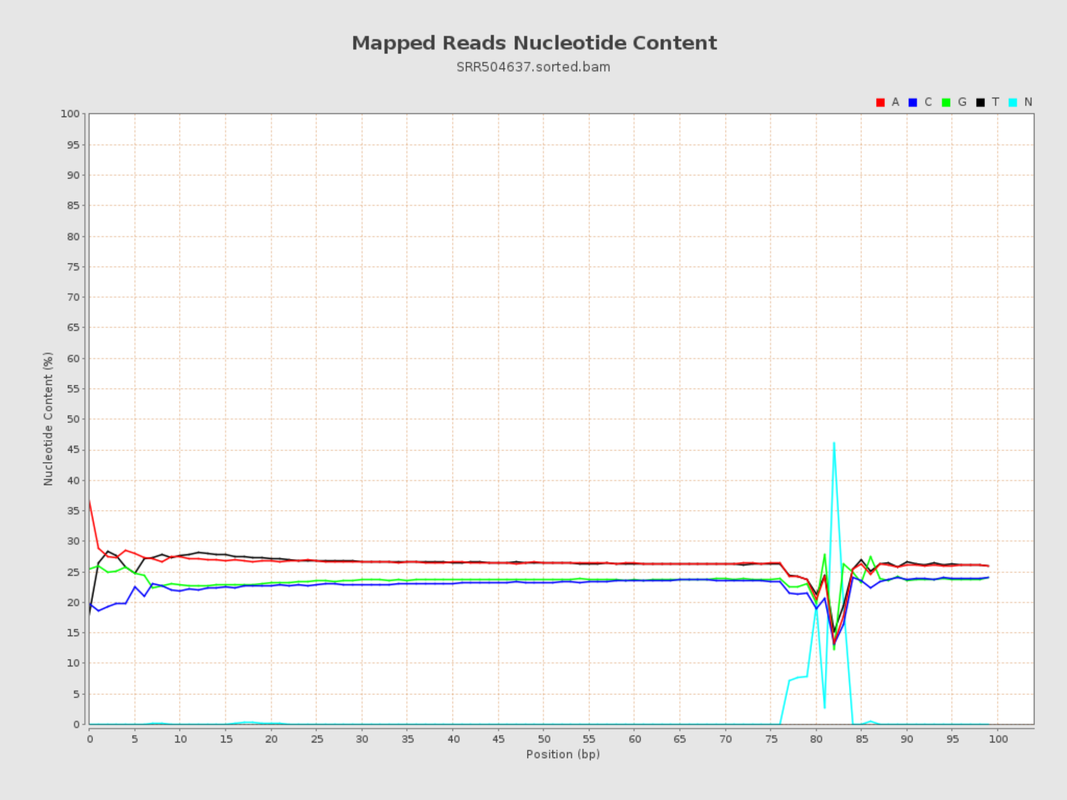
6. Results : Genome Fraction Coverage



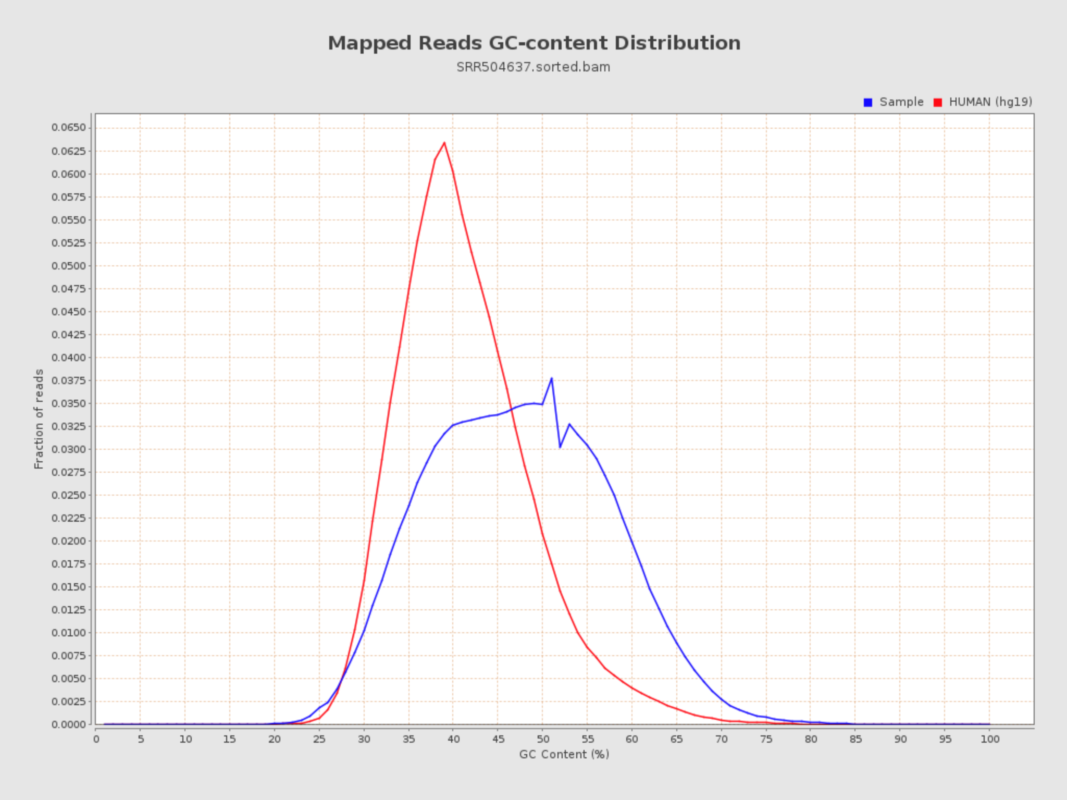
7. Results : Duplication Rate Histogram



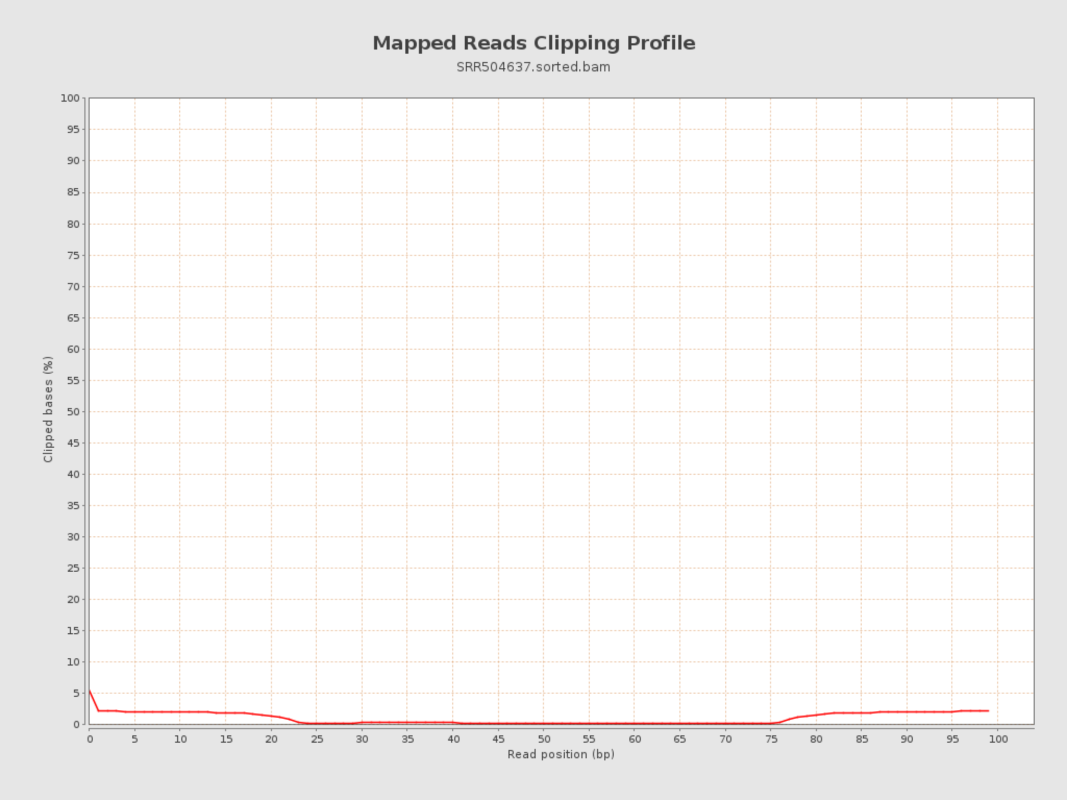
8. Results : Mapped Reads Nucleotide Content



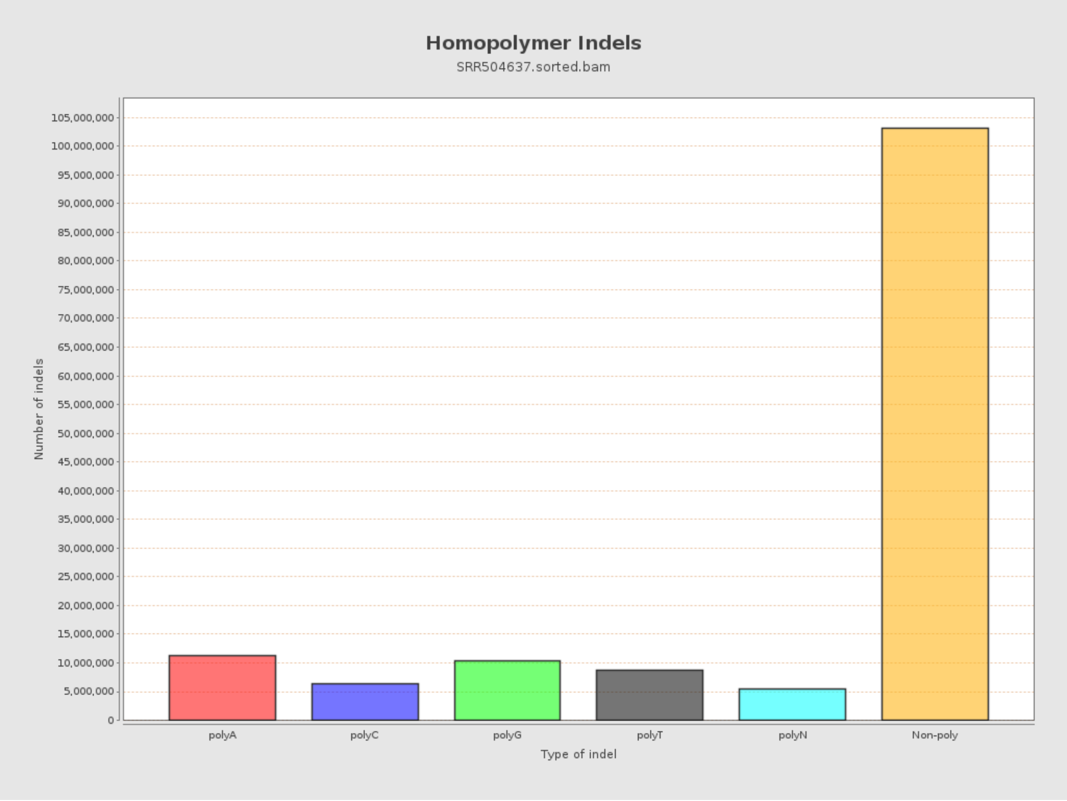
9. Results : Mapped Reads GC-content Distribution



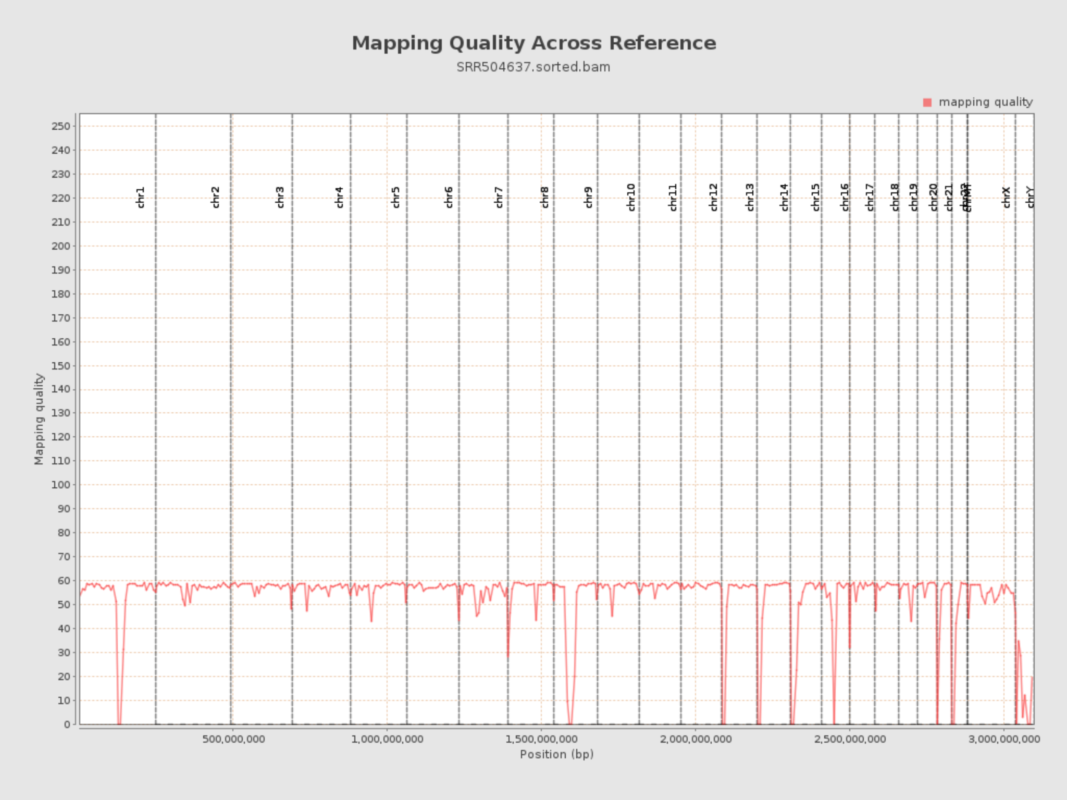
10. Results : Mapped Reads Clipping Profile



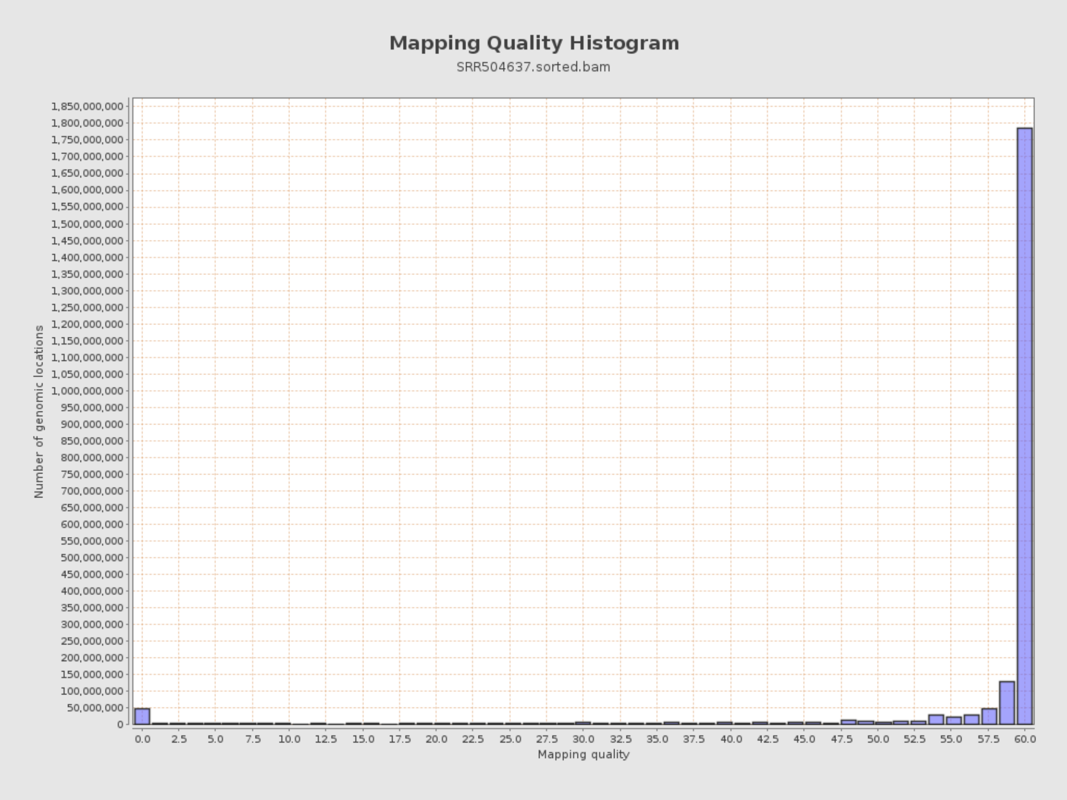
11. Results : Homopolymer Indels



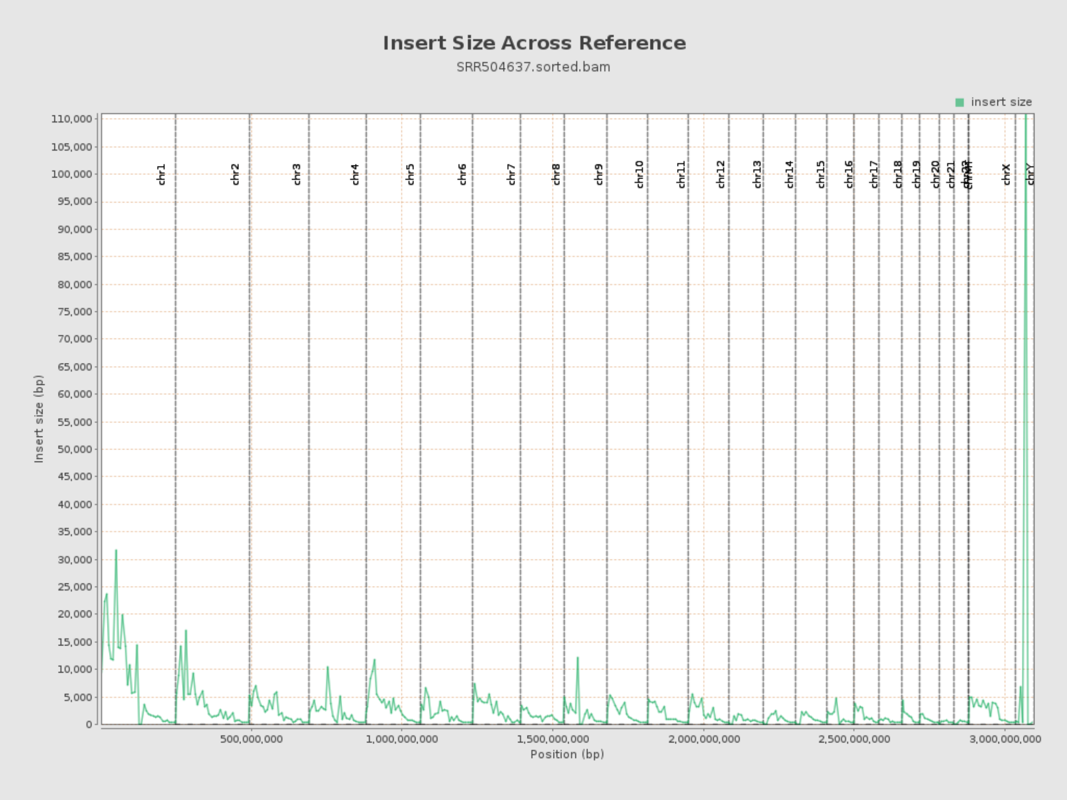
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram