Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/01 08:40:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR504635.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_SRR504635 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR504635_1.fastq.gz SRR504635_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Jan 01 08:40:19 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR504635.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	344,664,866
Mapped reads	299,387,913 / 86.86%
Unmapped reads	45,276,953 / 13.14%
Mapped paired reads	299,387,913 / 86.86%
Mapped reads, first in pair	150,163,904 / 43.57%
Mapped reads, second in pair	149,224,009 / 43.3%
Mapped reads, both in pair	297,046,124 / 86.18%
Mapped reads, singletons	2,341,789 / 0.68%
Secondary alignments	0
Supplementary alignments	3,257,577 / 0.95%
Read min/max/mean length	30 / 100 / 100.39
Duplicated reads (estimated)	93,084,441 / 27.01%
Duplication rate	25.31%
Clipped reads	25,088,272 / 7.28%

2.2. ACGT Content

Number/percentage of A's	7,417,955,630 / 25.11%
Number/percentage of C's	7,231,693,883 / 24.48%
Number/percentage of T's	7,456,379,582 / 25.24%
Number/percentage of G's	7,402,853,043 / 25.06%
Number/percentage of N's	36,007,441 / 0.12%

GC Percentage	49.53%

2.3. Coverage

Mean	9.5461
Standard Deviation	37.567

2.4. Mapping Quality

Mean Mapping Quality	53.63

2.5. Insert size

Mean	40,489.35
Standard Deviation	1,925,209.04
P25/Median/P75	329 / 366 / 411

2.6. Mismatches and indels

General error rate	0.78%
Mismatches	224,945,572
Insertions	2,207,702
Mapped reads with at least one insertion	0.72%
Deletions	2,815,218
Mapped reads with at least one deletion	0.91%
Homopolymer indels	39.07%

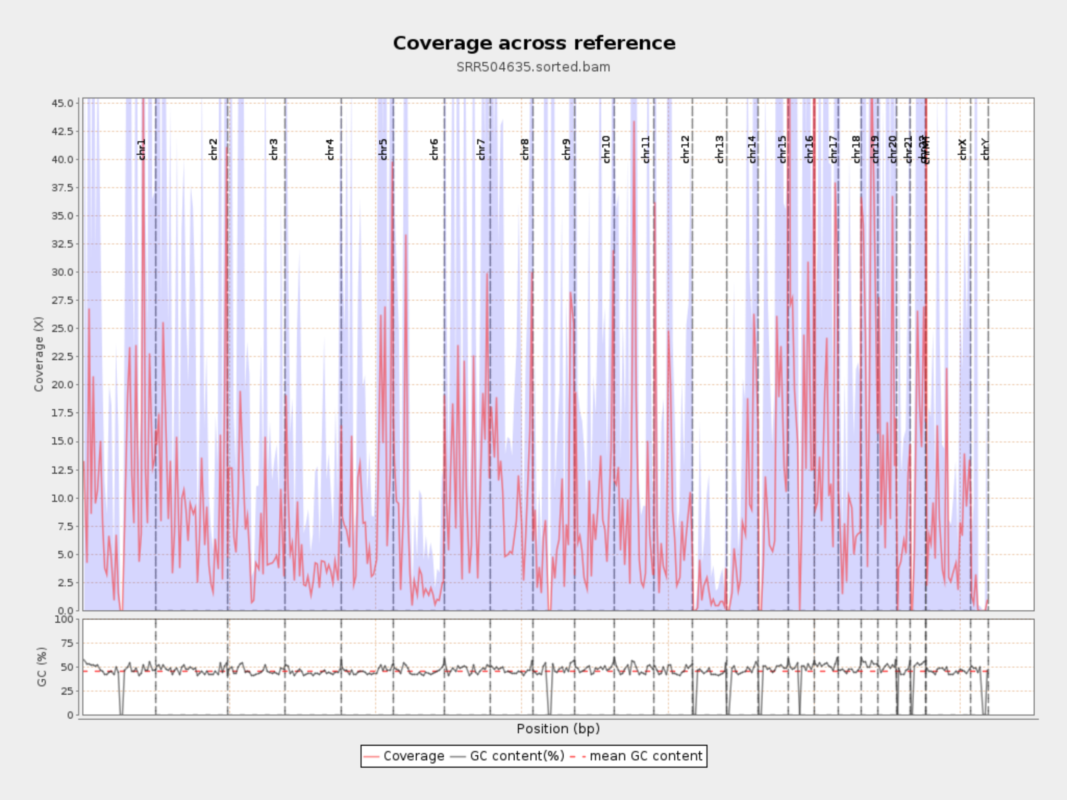
2.7. Chromosome stats

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

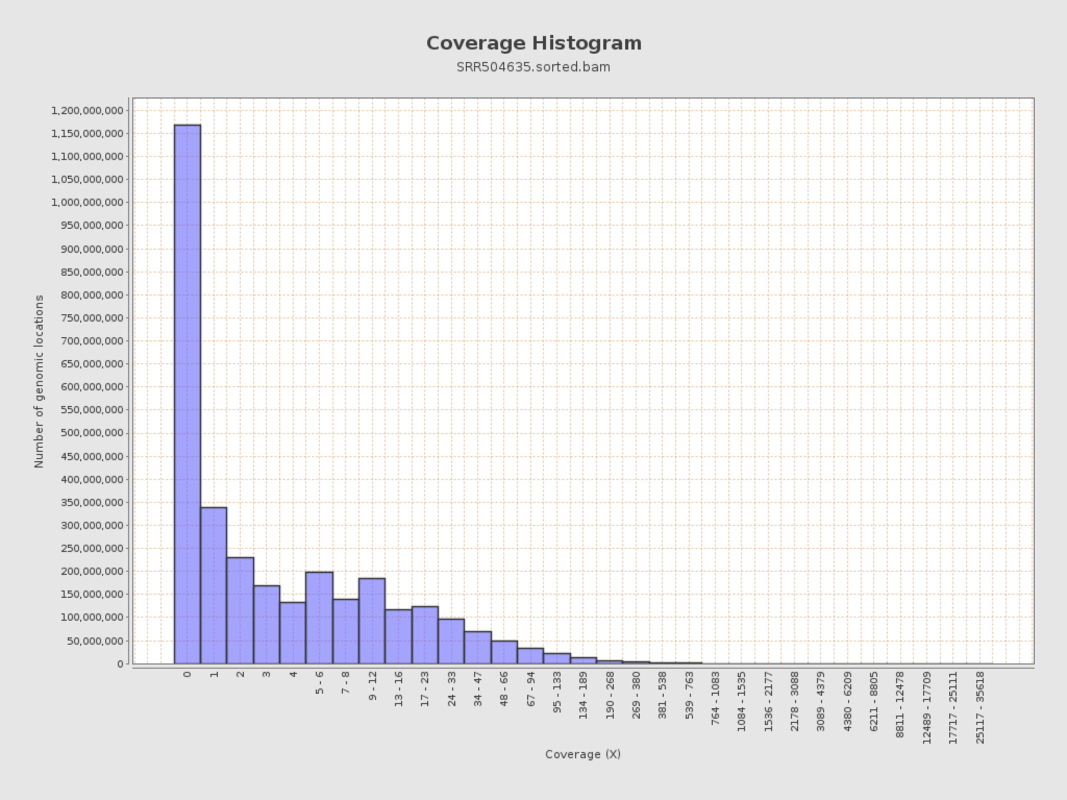
		bases	coverage	deviation
chr1	249250621	2840392581	11.3957	36.9545
chr2	243199373	2397207193	9.857	28.9142
chr3	198022430	1400261283	7.0712	24.0294
chr4	191154276	915099711	4.7872	14.9058
chr5	180915260	1988915384	10.9936	31.1777
chr6	171115067	851026579	4.9734	18.2332
chr7	159138663	2034769124	12.7861	32.826
chr8	146364022	1571637012	10.7379	28.1506
chr9	141213431	1024131019	7.2524	69.5777
chr10	135534747	1199369222	8.8492	28.1953
chr11	135006516	1381316806	10.2315	35.1059
chr12	133851895	1245245990	9.3032	27.7139
chr13	115169878	136513355	1.1853	5.5267
chr14	107349540	911611681	8.492	22.9762
chr15	102531392	1076633262	10.5005	29.5126
chr16	90354753	1913333955	21.1758	52.8313
chr17	81195210	1278022020	15.7401	41.3112
chr18	78077248	507006112	6.4936	70.991
chr19	59128983	1604398925	27.1339	111.8321
chr20	63025520	1009813742	16.0223	48.4547
chr21	48129895	316622907	6.5785	21.3129
chr22	51304566	740682112	14.437	35.5562
chrMT	16571	2865132	172.9004	66.5432
chrX	155270560	1161345121	7.4795	18.042

chrY	59373566	43728500	0.7365	32.6544

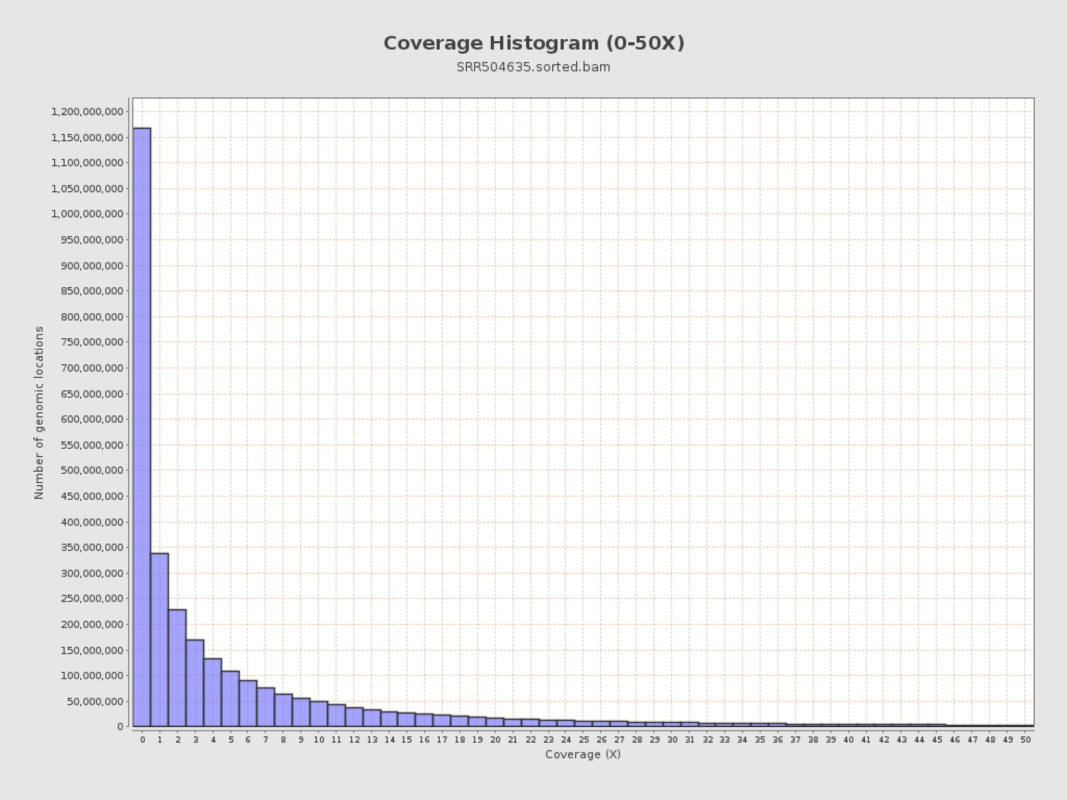
3. Results : Coverage across reference



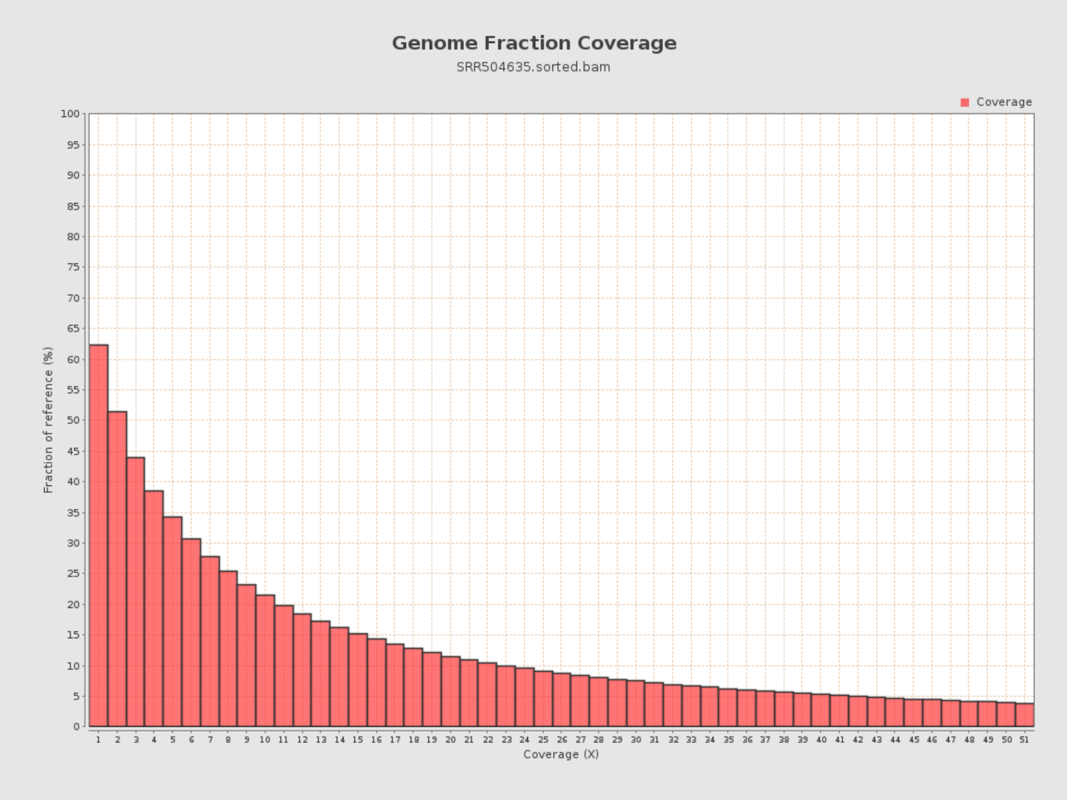
4. Results : Coverage Histogram



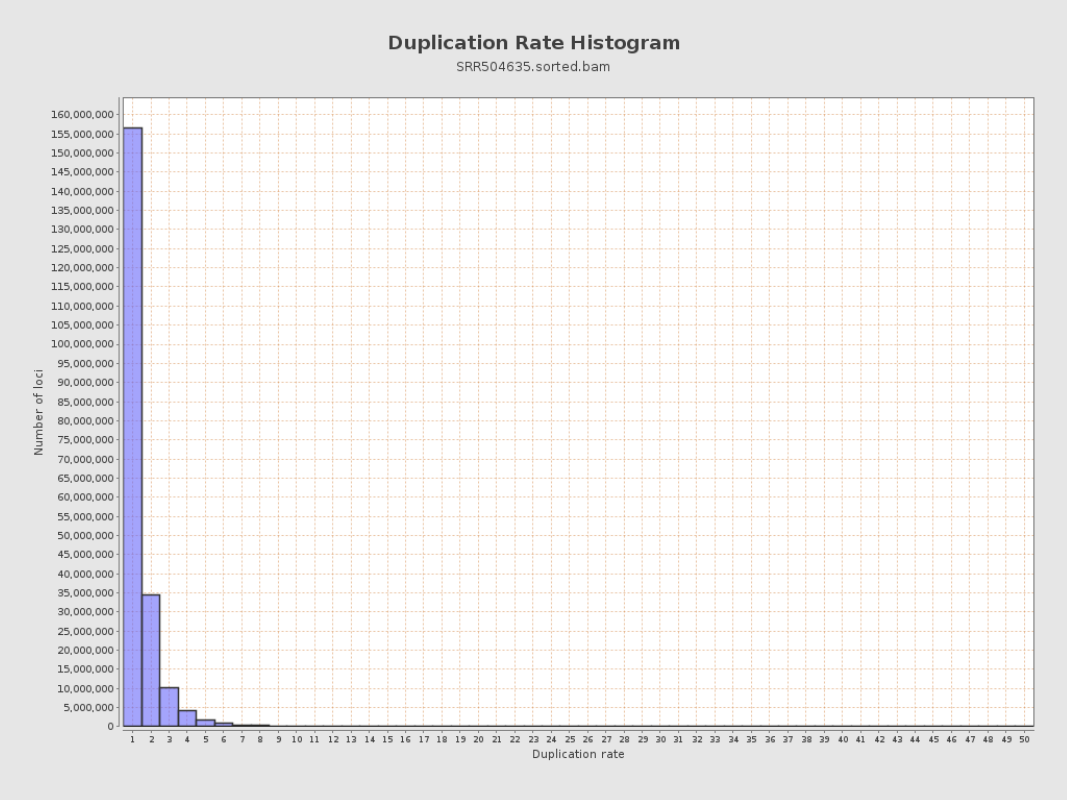
5. Results : Coverage Histogram (0-50X)



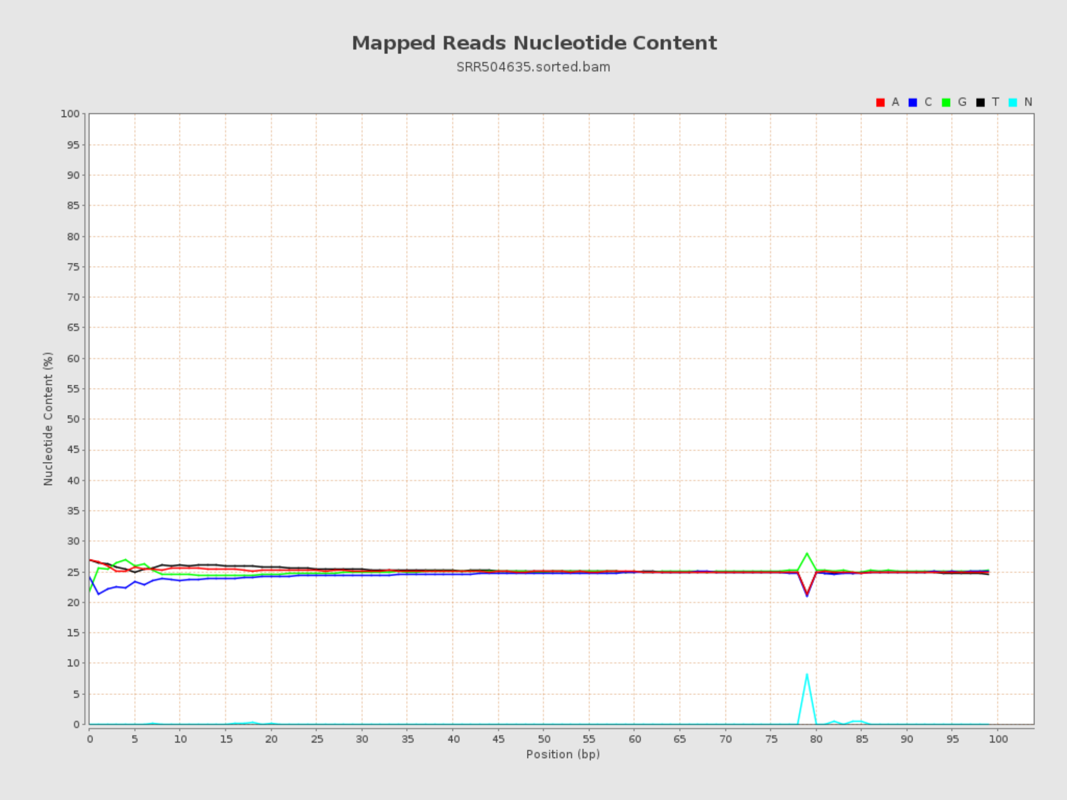
6. Results : Genome Fraction Coverage



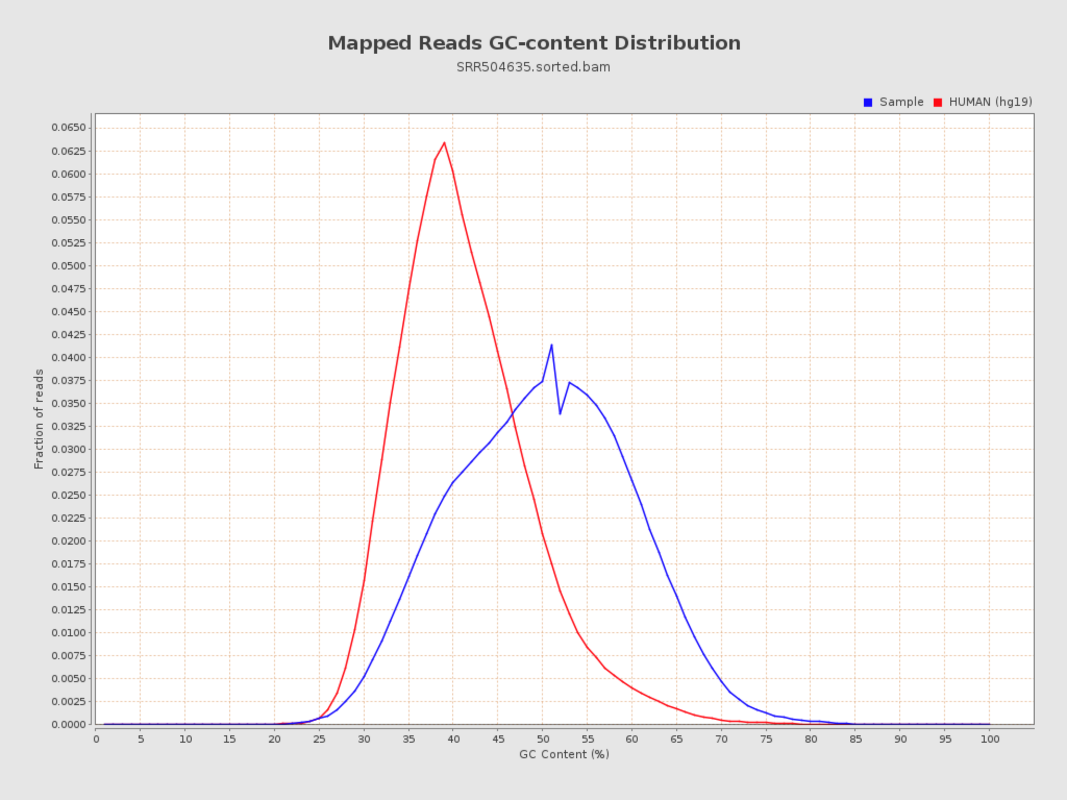
7. Results : Duplication Rate Histogram



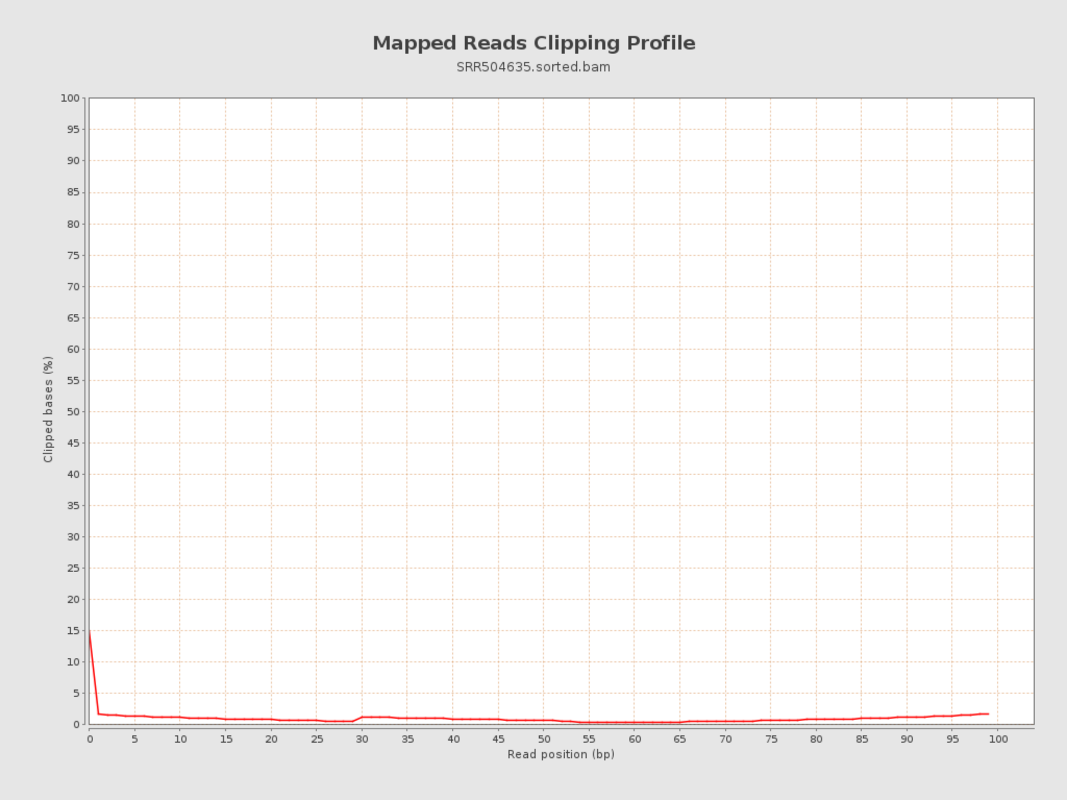
8. Results : Mapped Reads Nucleotide Content



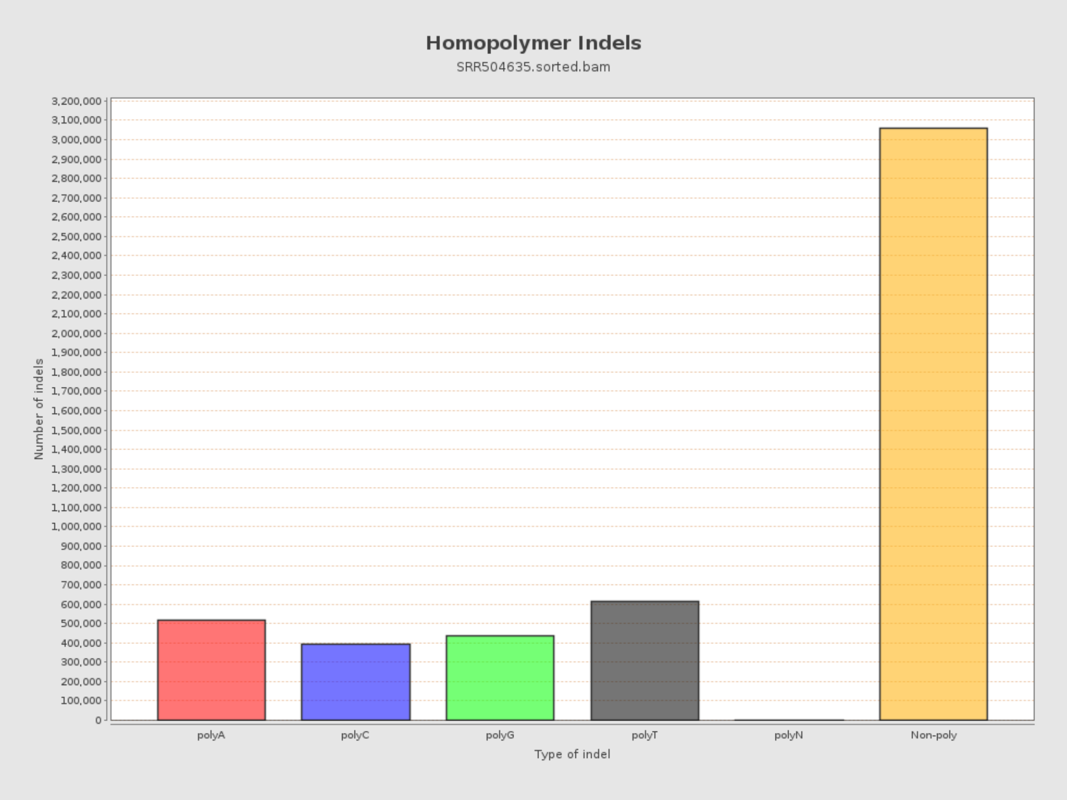
9. Results : Mapped Reads GC-content Distribution



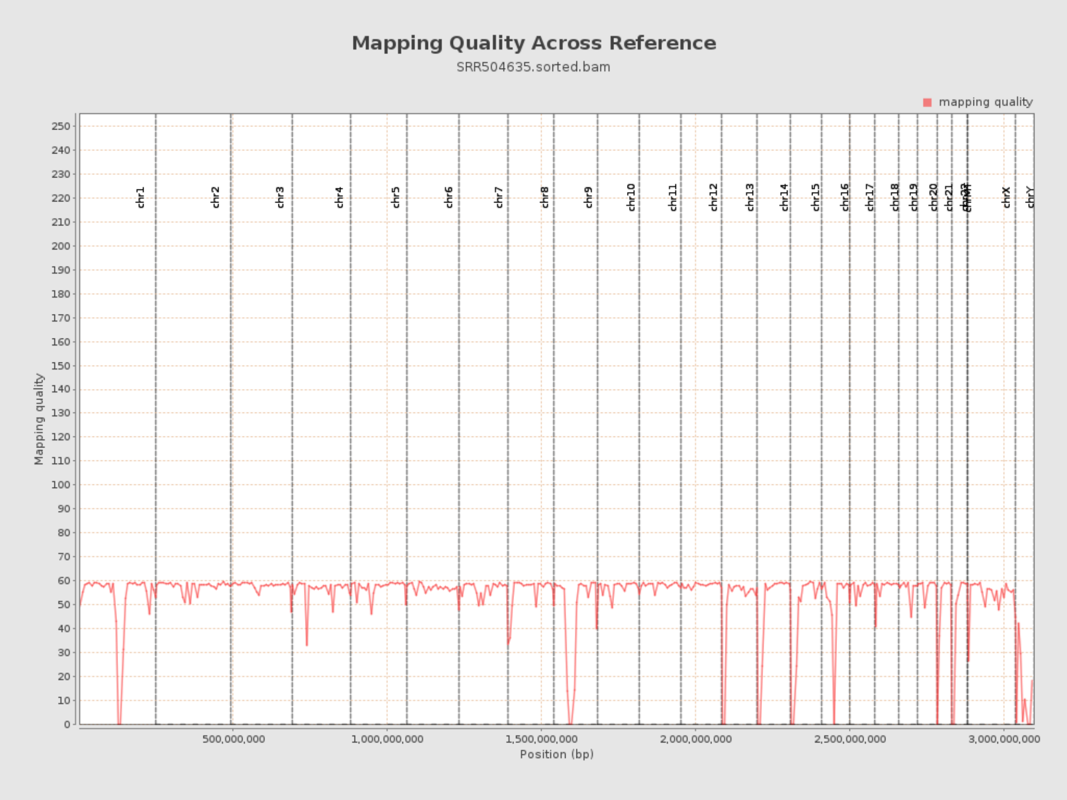
10. Results : Mapped Reads Clipping Profile



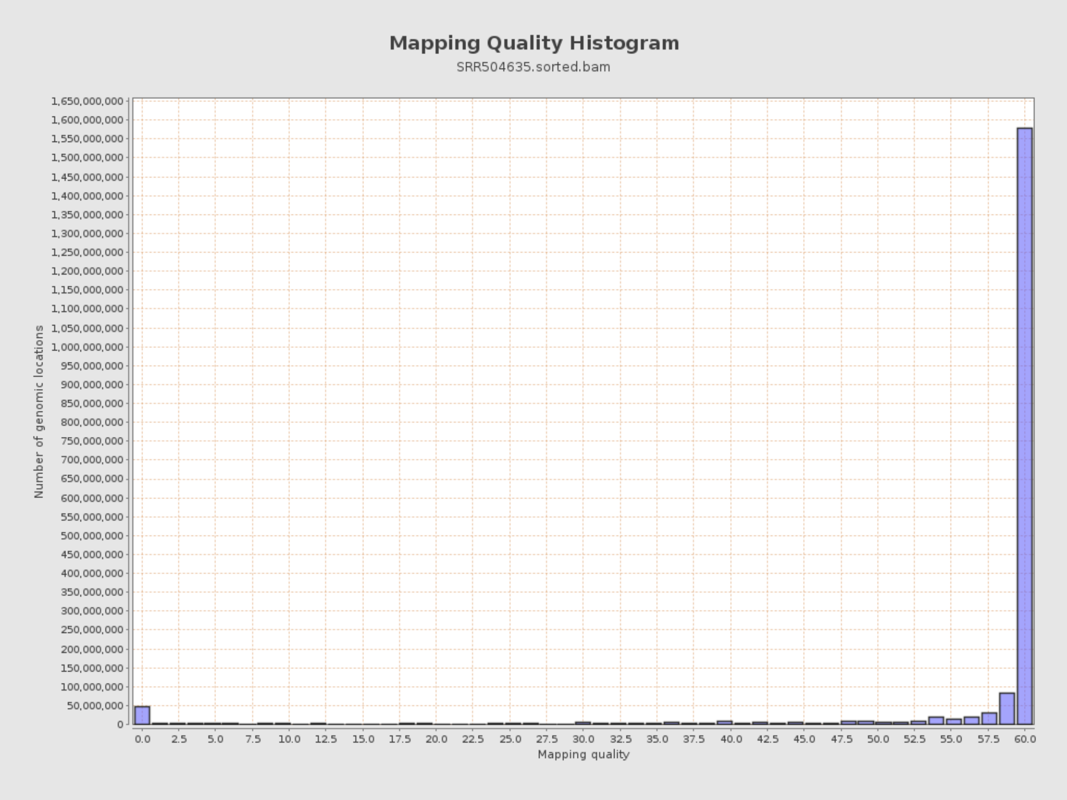
11. Results : Homopolymer Indels



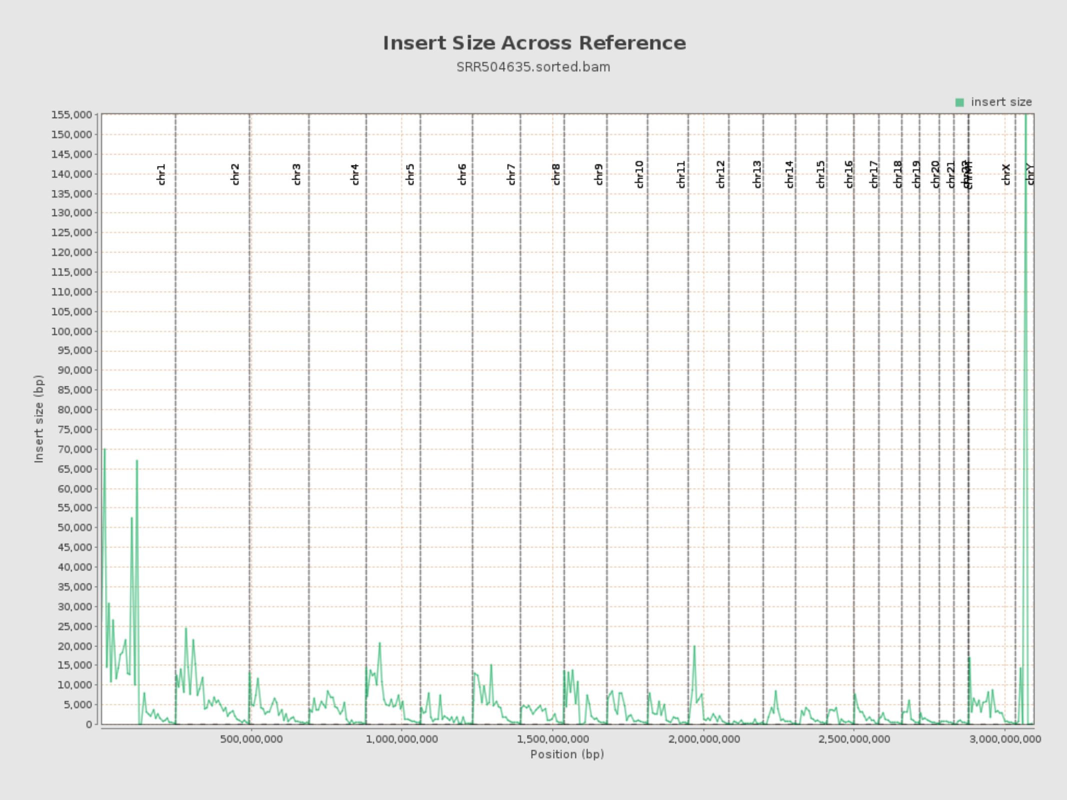
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram