Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/01 23:11:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR504638.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_SRR504638 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR504638_1.fastq.gz SRR504638_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Jan 01 23:11:53 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR504638.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	395,619,616
Mapped reads	369,241,814 / 93.33%
Unmapped reads	26,377,802 / 6.67%
Mapped paired reads	369,241,814 / 93.33%
Mapped reads, first in pair	185,998,458 / 47.01%
Mapped reads, second in pair	183,243,356 / 46.32%
Mapped reads, both in pair	364,044,040 / 92.02%
Mapped reads, singletons	5,197,774 / 1.31%
Secondary alignments	0
Supplementary alignments	2,277,263 / 0.58%
Read min/max/mean length	30 / 100 / 100.24
Duplicated reads (estimated)	96,719,223 / 24.45%
Duplication rate	23.28%
Clipped reads	77,710,083 / 19.64%

2.2. ACGT Content

Number/percentage of A's	9,327,897,010 / 26.51%
Number/percentage of C's	8,073,912,239 / 22.95%
Number/percentage of T's	9,290,012,996 / 26.4%
Number/percentage of G's	8,339,733,579 / 23.7%
Number/percentage of N's	153,493,817 / 0.44%

GC Percentage	46.65%

2.3. Coverage

Mean	11.3685
Standard Deviation	26.388

2.4. Mapping Quality

Mean Mapping Quality	53.79

2.5. Insert size

Mean	45,528.77
Standard Deviation	2,032,824.05
P25/Median/P75	315 / 349 / 385

2.6. Mismatches and indels

General error rate	1.57%
Mismatches	325,514,355
Insertions	136,644,088
Mapped reads with at least one insertion	33.78%
Deletions	3,941,917
Mapped reads with at least one deletion	1.04%
Homopolymer indels	20.11%

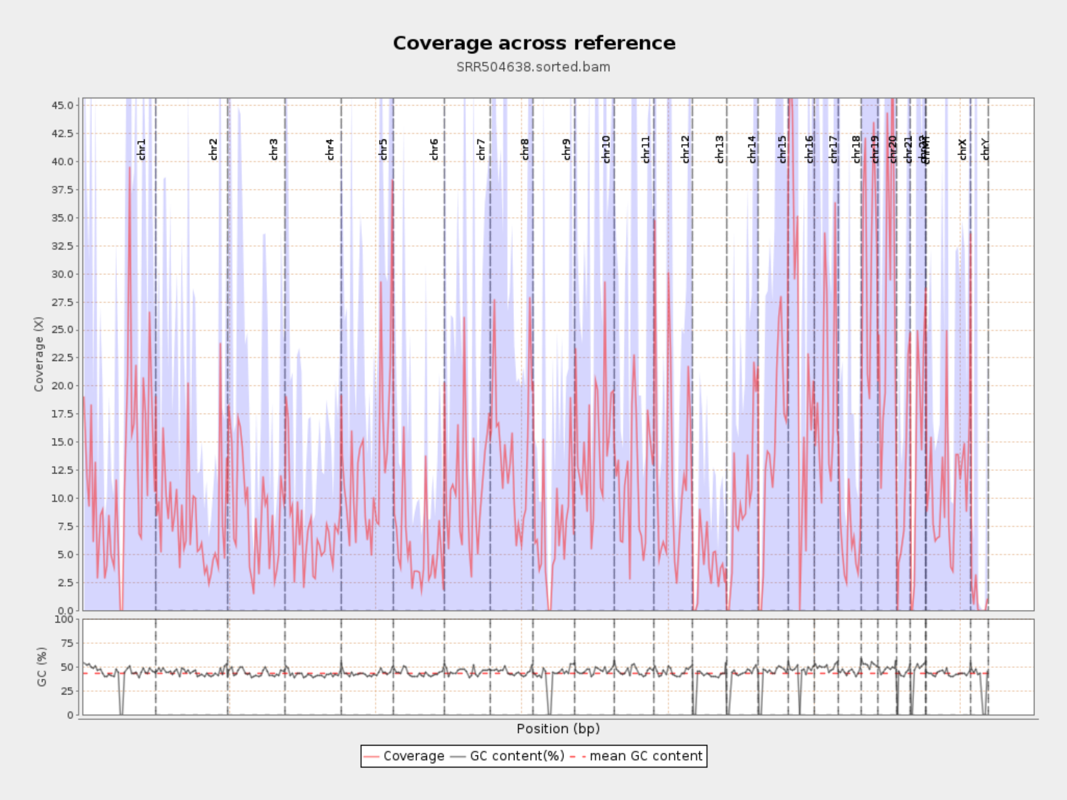
2.7. Chromosome stats

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

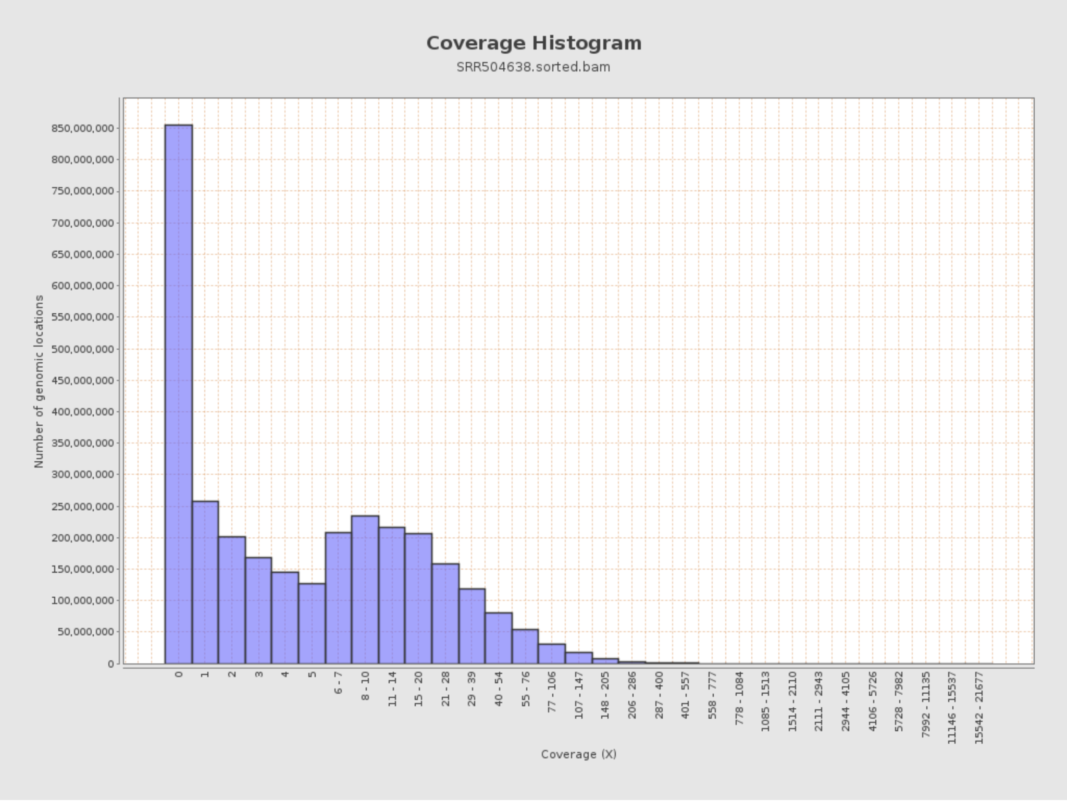
		bases	**coverage**	**deviation**
chr1	249250621	2971072308	11.92	24.8289
chr2	243199373	1959770069	8.0583	16.8097
chr3	198022430	1733819109	8.7557	17.5012
chr4	191154276	1346896984	7.0461	12.5179
chr5	180915260	2377979132	13.1442	22.287
chr6	171115067	921550266	5.3856	12.1325
chr7	159138663	1802438341	11.3262	19.0873
chr8	146364022	2044483306	13.9685	37.2462
chr9	141213431	969773880	6.8674	15.4871
chr10	135534747	2032213483	14.994	25.1833
chr11	135006516	1558319825	11.5426	21.559
chr12	133851895	1685359942	12.5912	25.9799
chr13	115169878	453684185	3.9393	7.5947
chr14	107349540	1061571982	9.8889	18.1486
chr15	102531392	1435435329	14	26.4471
chr16	90354753	2099629641	23.2376	37.4838
chr17	81195210	1570447081	19.3416	34.0674
chr18	78077248	475078447	6.0847	53.7503
chr19	59128983	1852219774	31.3251	64.6721
chr20	63025520	1775572952	28.1723	40.2753
chr21	48129895	534580000	11.107	21.7443
chr22	51304566	725595648	14.1429	30.1676
chrMT	16571	421412	25.4307	22.3613
chrX	155270560	1756551961	11.3128	20.5107

chrY	59373566	49042792	0.826	29.8718

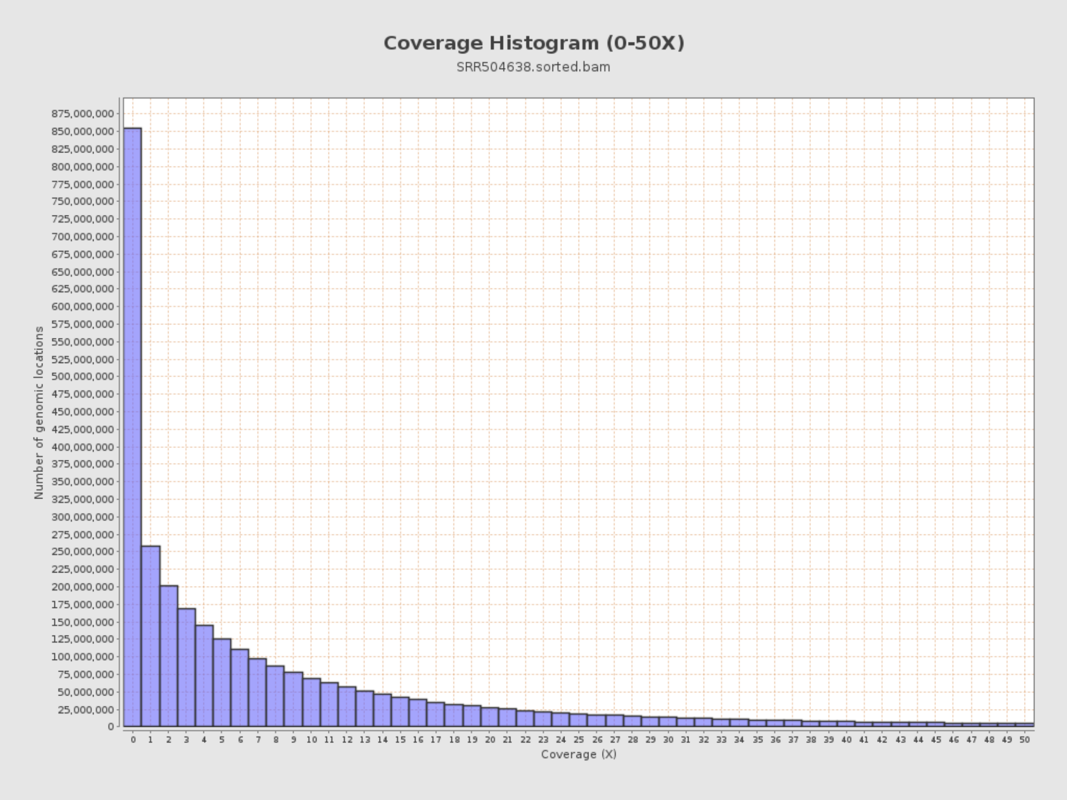
3. Results : Coverage across reference



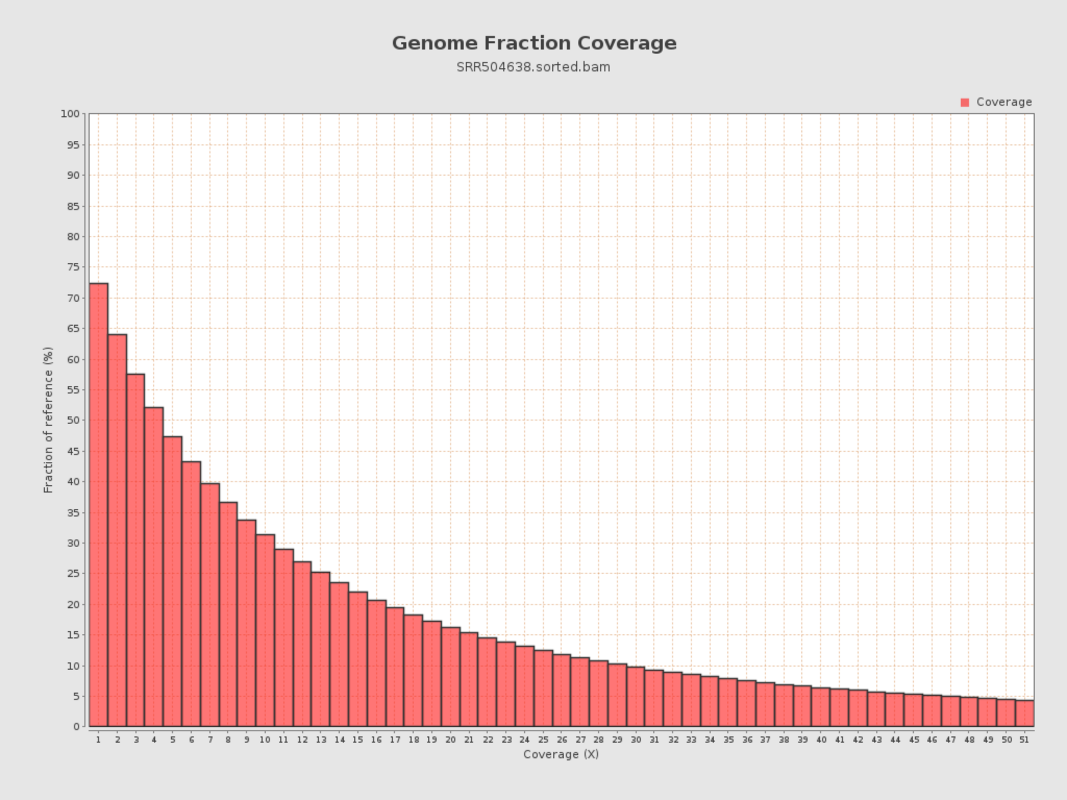
4. Results : Coverage Histogram



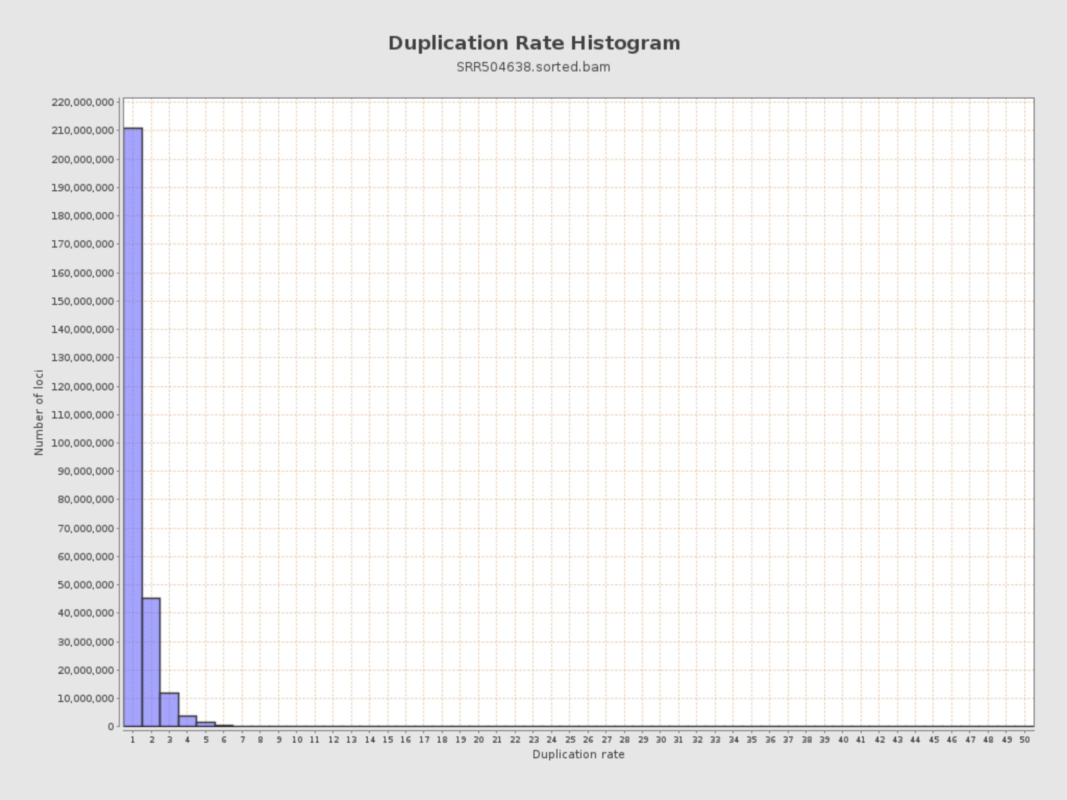
5. Results : Coverage Histogram (0-50X)



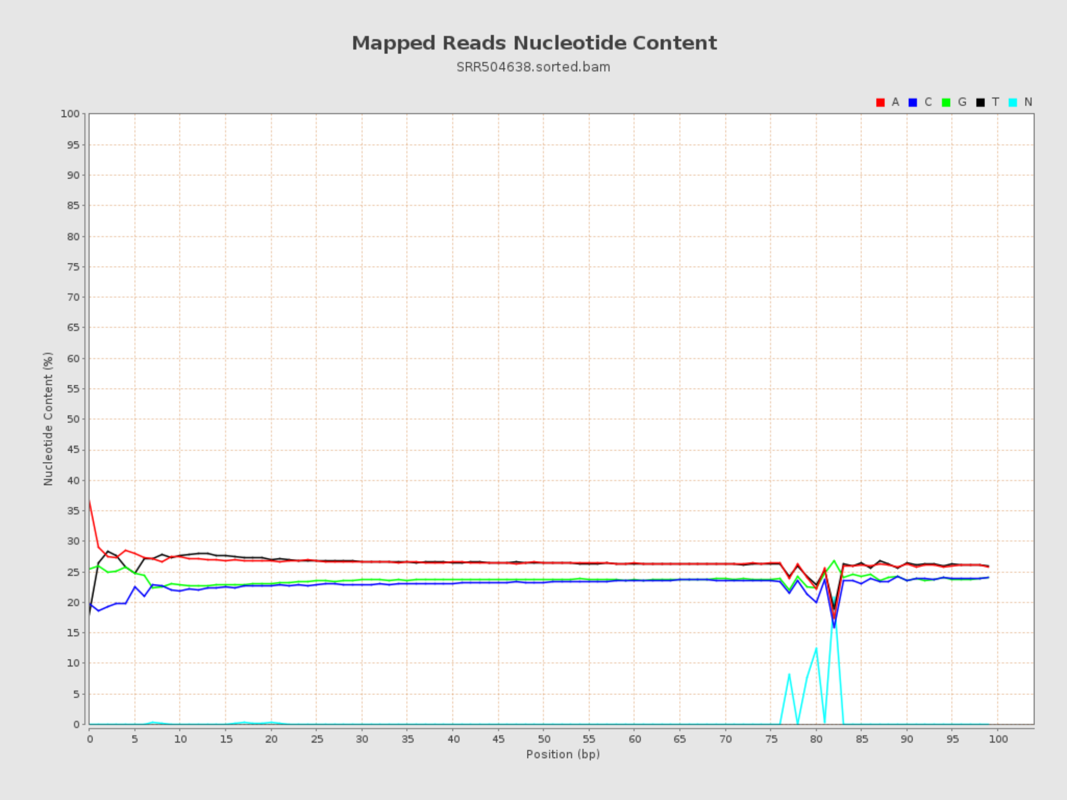
6. Results : Genome Fraction Coverage



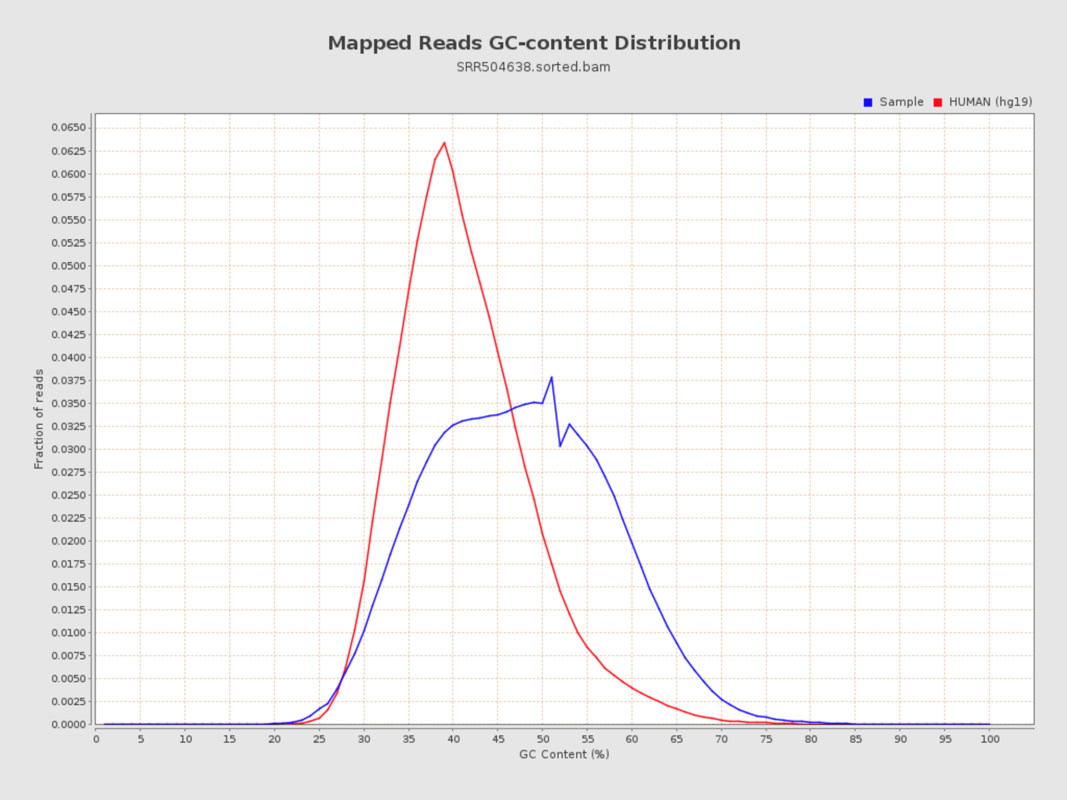
7. Results : Duplication Rate Histogram



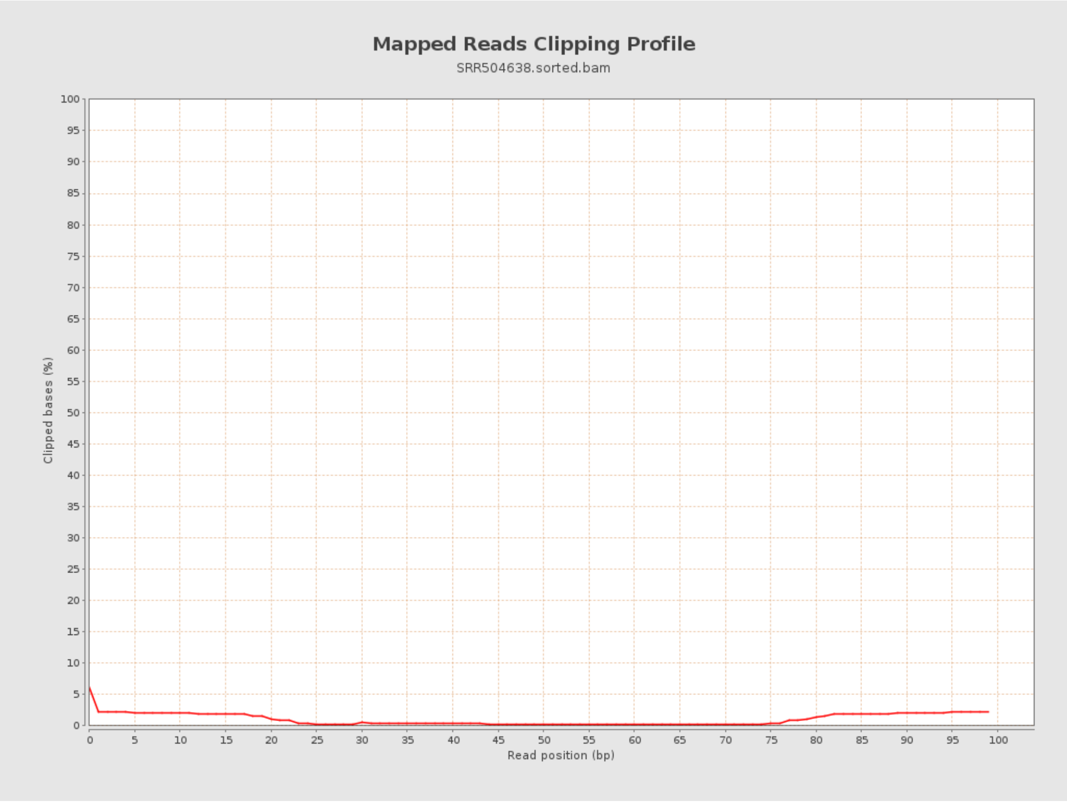
8. Results : Mapped Reads Nucleotide Content



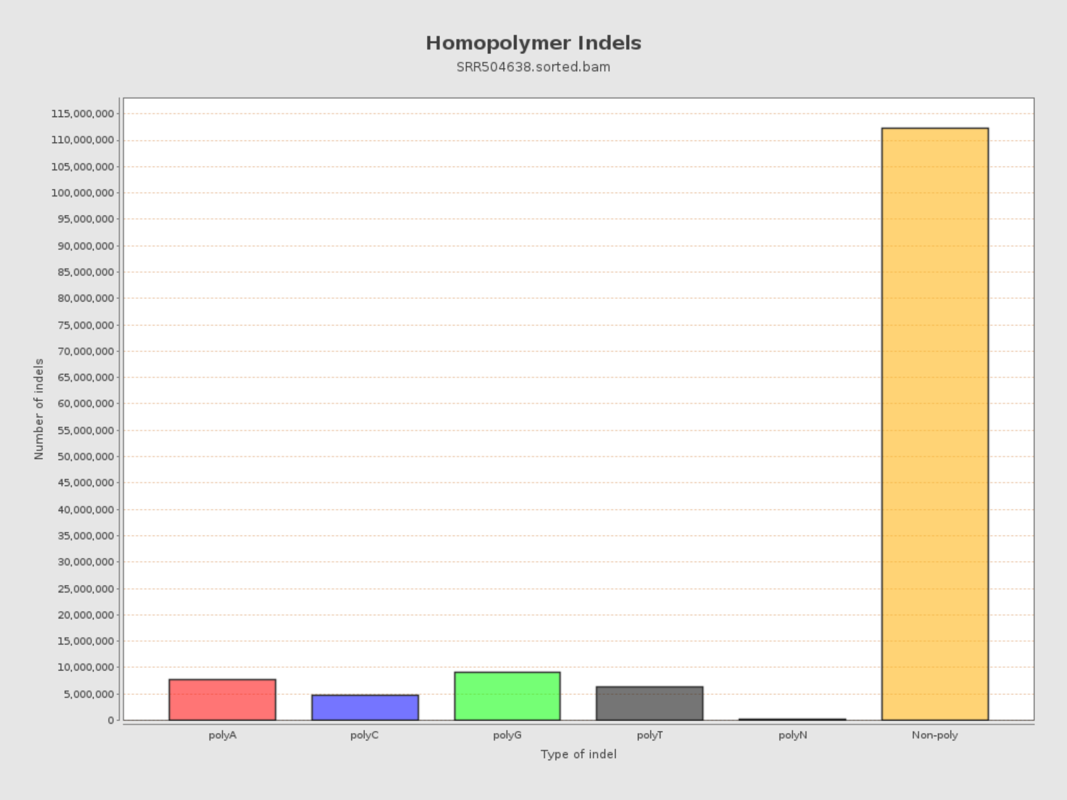
9. Results : Mapped Reads GC-content Distribution



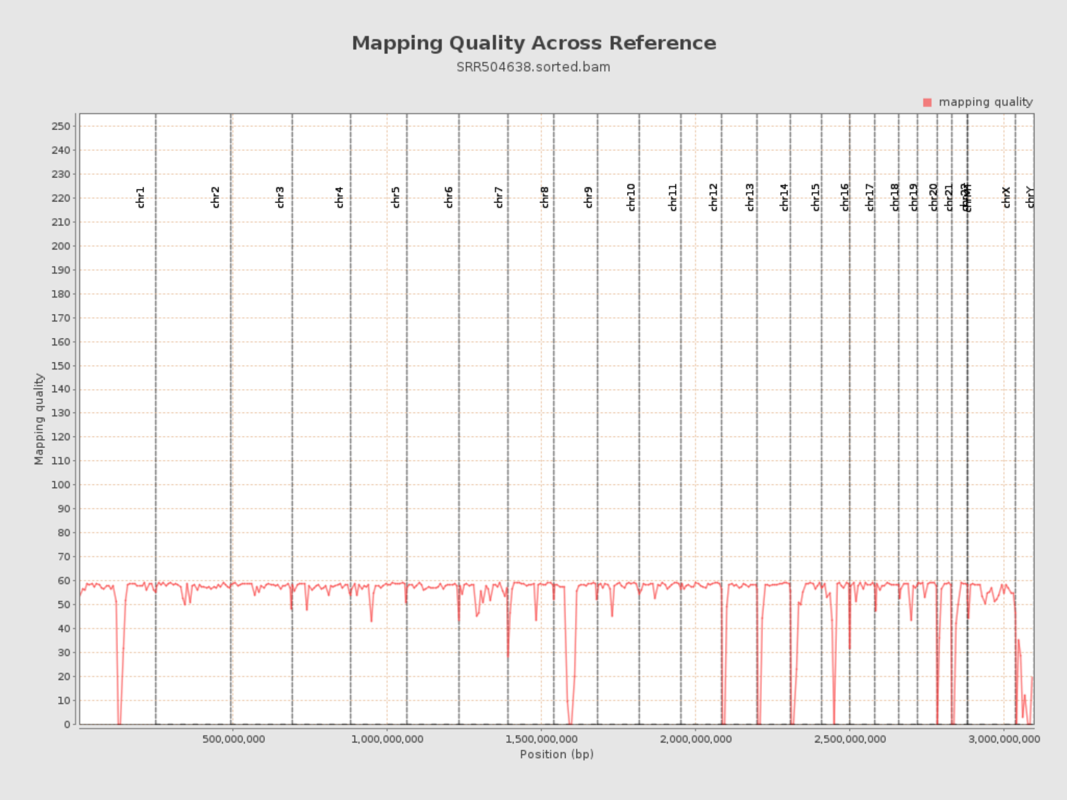
10. Results : Mapped Reads Clipping Profile



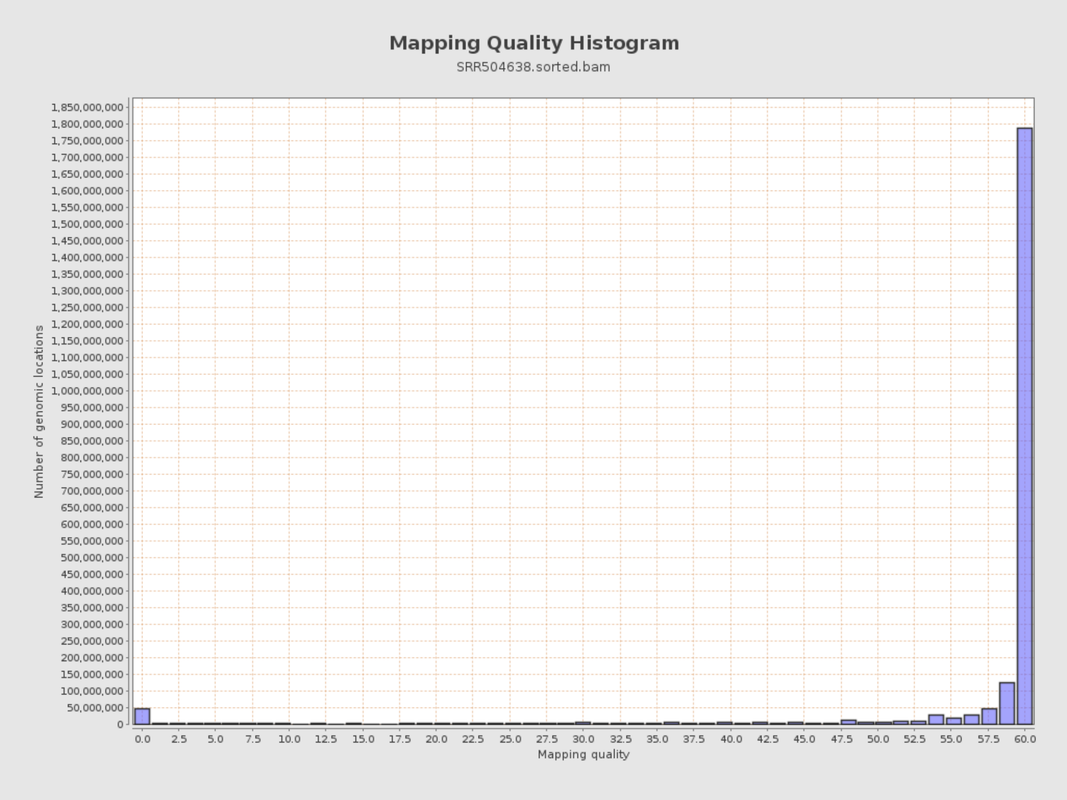
11. Results : Homopolymer Indels



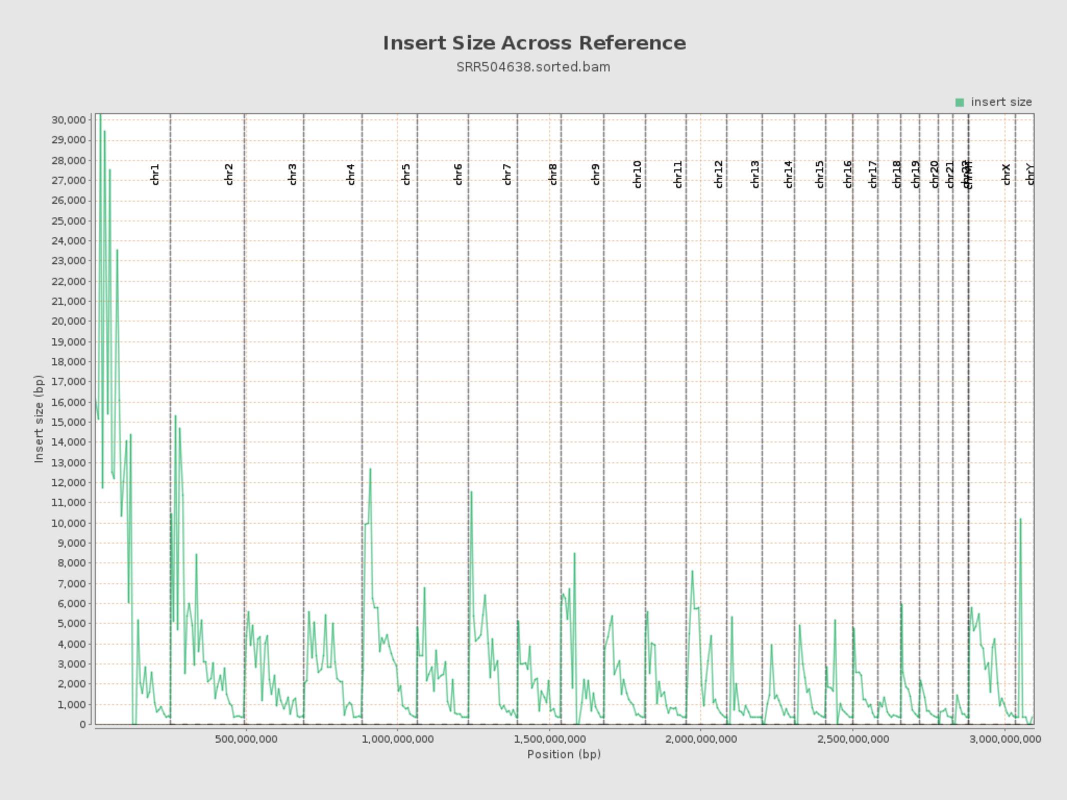
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram