Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/12 11:12:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618274.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_SRR618274 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618274_1.fastq.gz SRR618274_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Oct 12 11:12:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618274.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	741,419,584
Mapped reads	691,077,122 / 93.21%
Unmapped reads	50,342,462 / 6.79%
Mapped paired reads	691,077,122 / 93.21%
Mapped reads, first in pair	347,935,873 / 46.93%
Mapped reads, second in pair	343,141,249 / 46.28%
Mapped reads, both in pair	670,989,710 / 90.5%
Mapped reads, singletons	20,087,412 / 2.71%
Secondary alignments	0
Supplementary alignments	9,020,488 / 1.22%
Read min/max/mean length	30 / 101 / 101.49
Duplicated reads (estimated)	326,082,966 / 43.98%
Duplication rate	27.03%
Clipped reads	304,014,420 / 41%

2.2. ACGT Content

Number/percentage of A's	17,720,704,858 / 29.04%
Number/percentage of C's	11,373,010,581 / 18.64%
Number/percentage of T's	18,264,992,948 / 29.93%
Number/percentage of G's	13,647,092,974 / 22.36%
Number/percentage of N's	21,840,254 / 0.04%

GC Percentage	41%

2.3. Coverage

Mean	19.725
Standard Deviation	240.6525

2.4. Mapping Quality

Mean Mapping Quality	51.48

2.5. Insert size

Mean	184,720.58
Standard Deviation	4,130,291.04
P25/Median/P75	147 / 185 / 236

2.6. Mismatches and indels

General error rate	1.26%
Mismatches	753,680,348
Insertions	8,983,498
Mapped reads with at least one insertion	1.27%
Deletions	20,966,954
Mapped reads with at least one deletion	2.97%
Homopolymer indels	47.11%

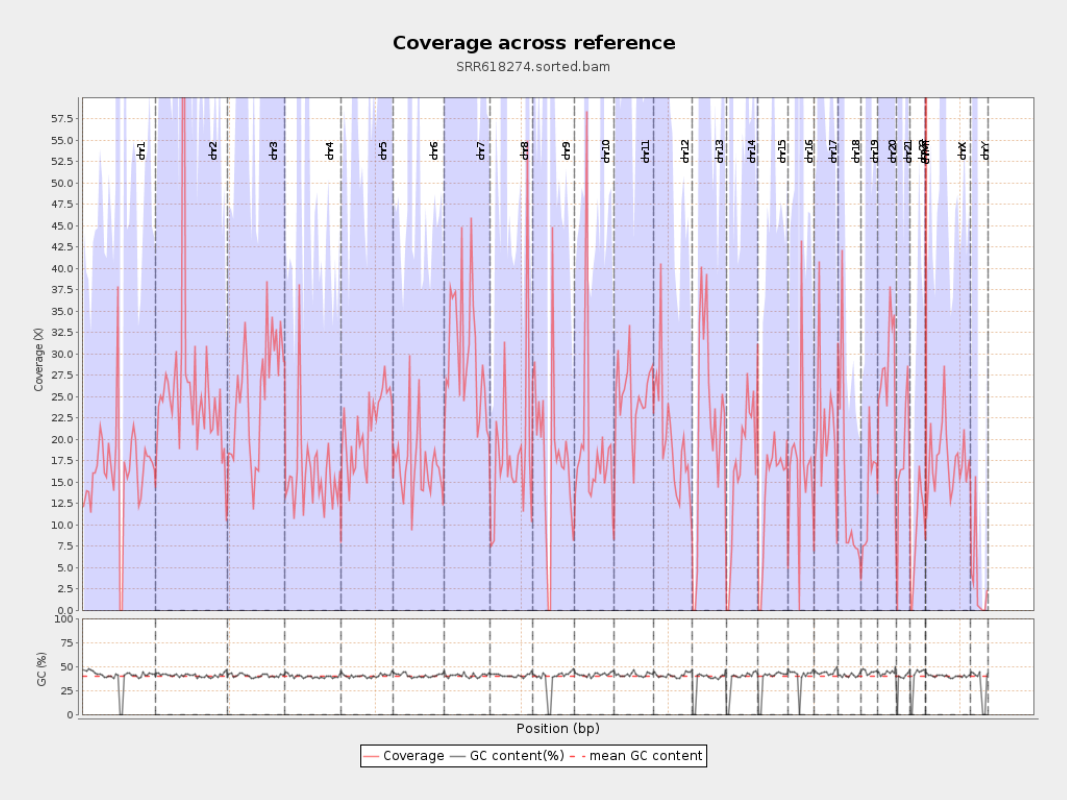
2.7. Chromosome stats

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

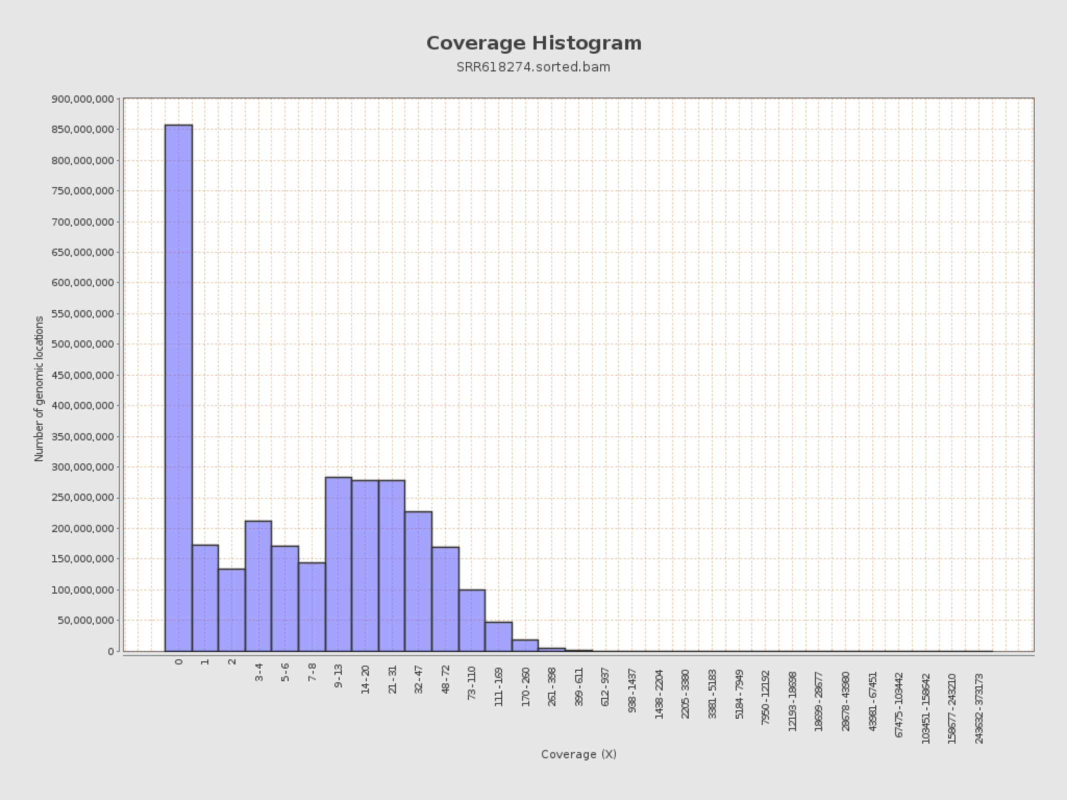
		bases	coverage	deviation
chr1	249250621	4064067672	16.3051	279.2602
chr2	243199373	6368336480	26.1857	366.1592
chr3	198022430	4993492059	25.2168	41.9218
chr4	191154276	3080214636	16.1138	131.6298
chr5	180915260	3854231320	21.3041	42.5304
chr6	171115067	2928278672	17.1129	139.8413
chr7	159138663	4740383359	29.7878	354.0762
chr8	146364022	2724201008	18.6125	120.3233
chr9	141213431	2548436391	18.0467	508.1498
chr10	135534747	2566356645	18.935	302.422
chr11	135006516	3366157088	24.9333	245.2058
chr12	133851895	2698393554	20.1595	42.6314
chr13	115169878	2525696237	21.9302	38.7102
chr14	107349540	1798511467	16.7538	78.4032
chr15	102531392	1427678882	13.9243	28.943
chr16	90354753	1524232831	16.8694	197.3978
chr17	81195210	1762792571	21.7105	326.4788
chr18	78077248	1149270164	14.7197	502.6373
chr19	59128983	797531827	13.488	173.9527
chr20	63025520	1815221923	28.8014	58.9579
chr21	48129895	846731243	17.5926	78.1908
chr22	51304566	469265271	9.1467	26.9583
chrMT	16571	88615243	5,347.6099	3,072.1055
chrX	155270560	2732457103	17.598	112.907

chrY	59373566	192057373	3.2347	215.9019

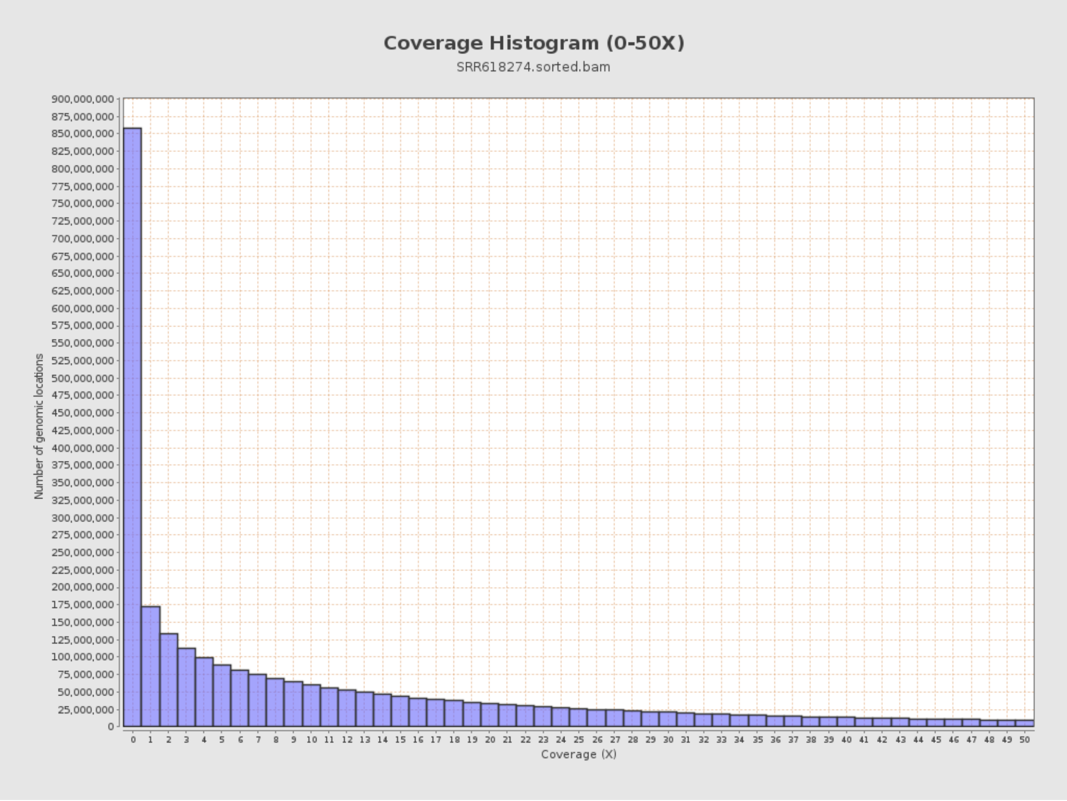
3. Results : Coverage across reference



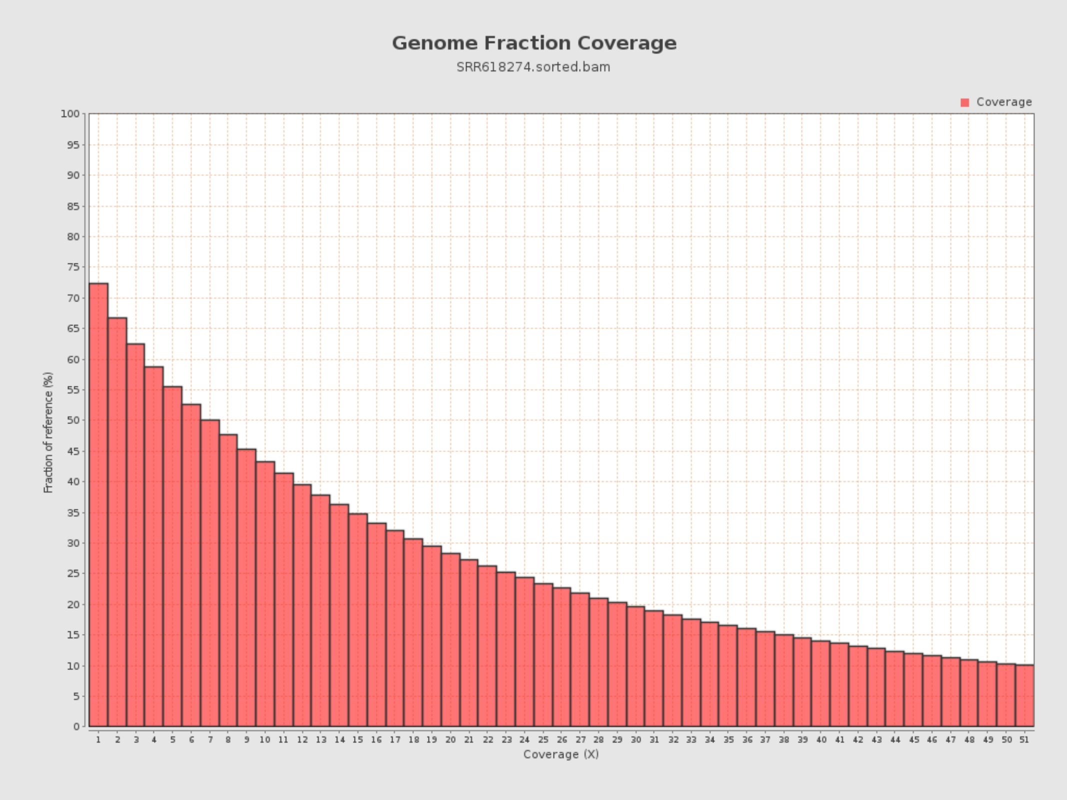
4. Results : Coverage Histogram



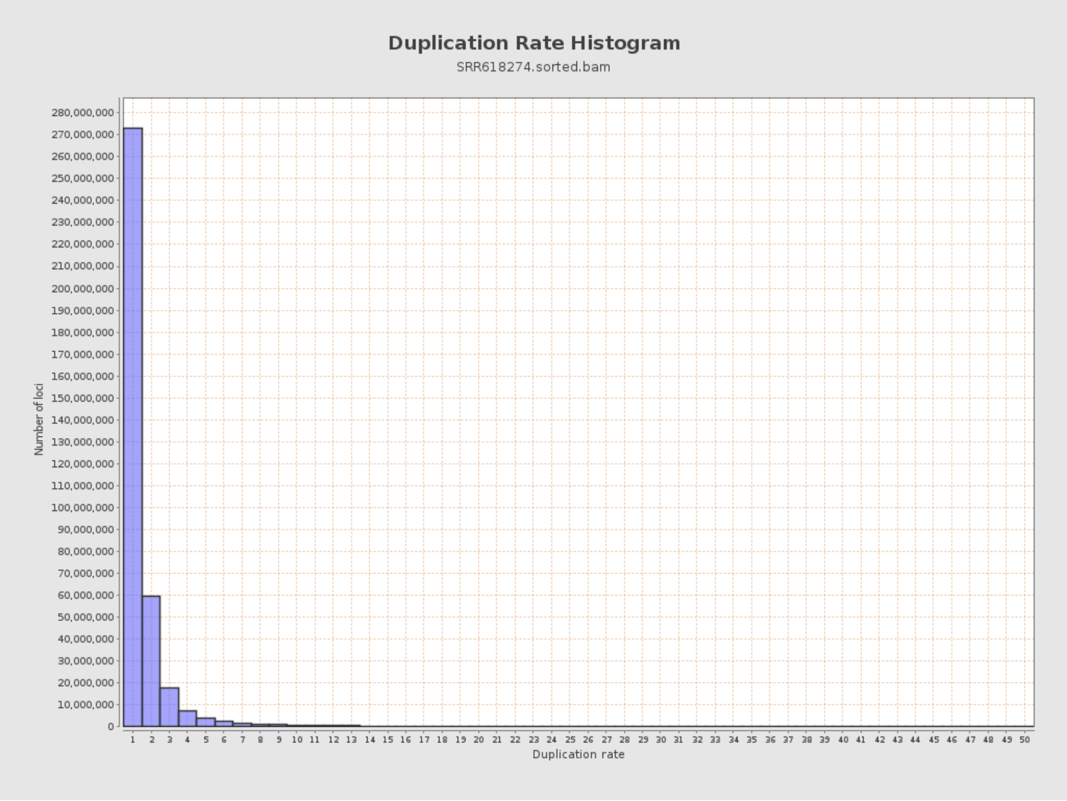
5. Results : Coverage Histogram (0-50X)



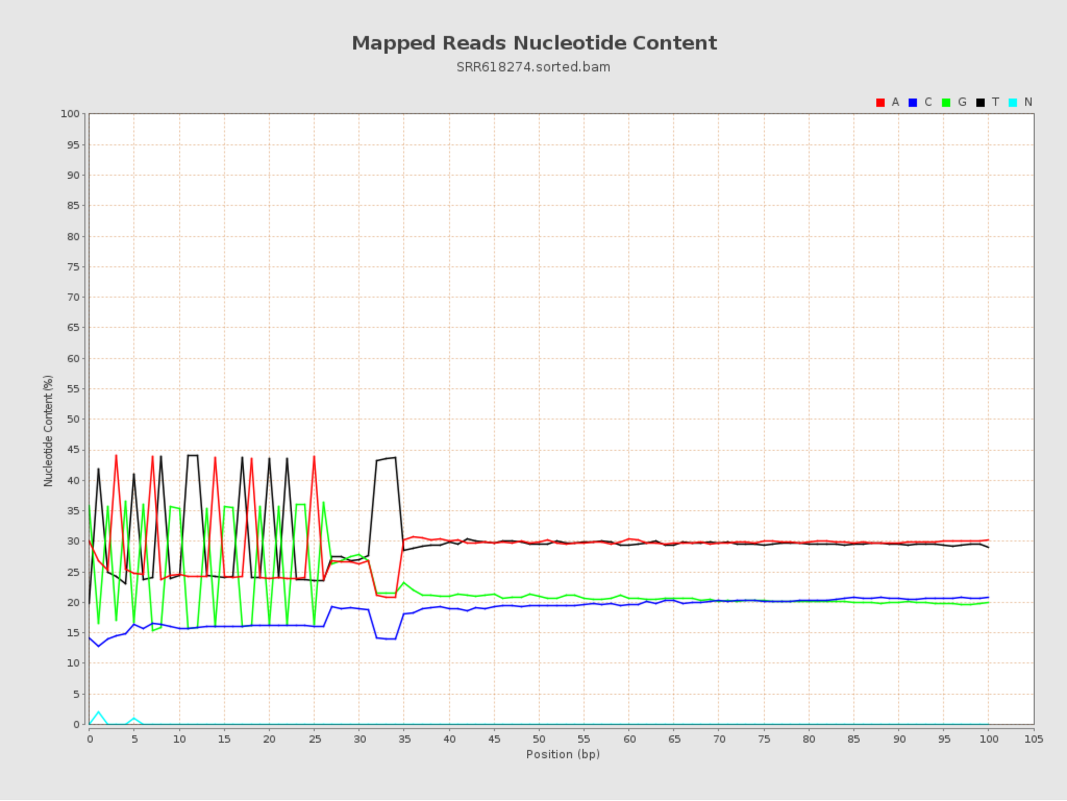
6. Results : Genome Fraction Coverage



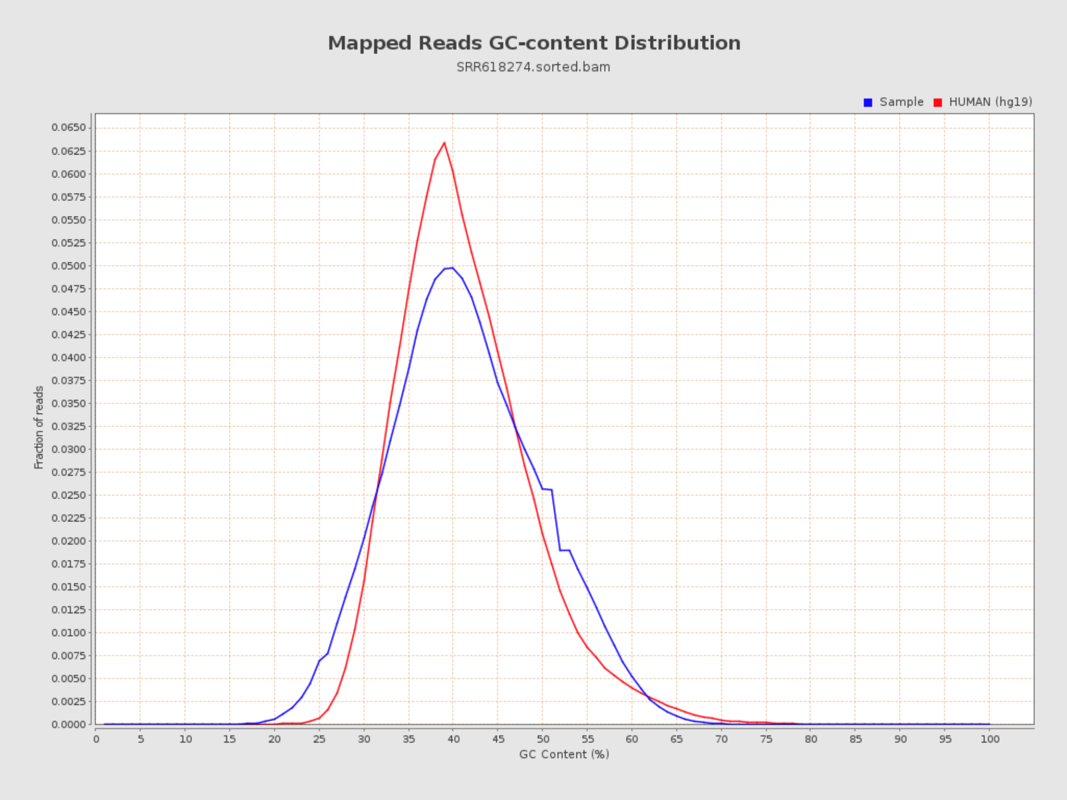
7. Results : Duplication Rate Histogram



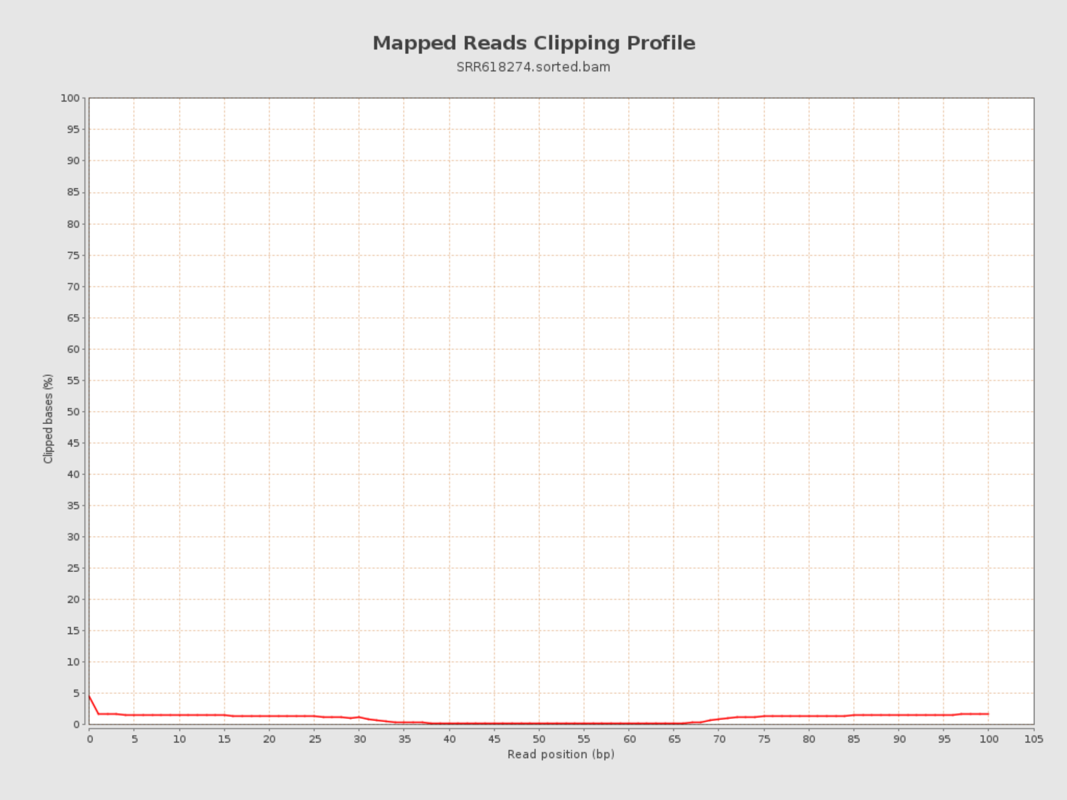
8. Results : Mapped Reads Nucleotide Content



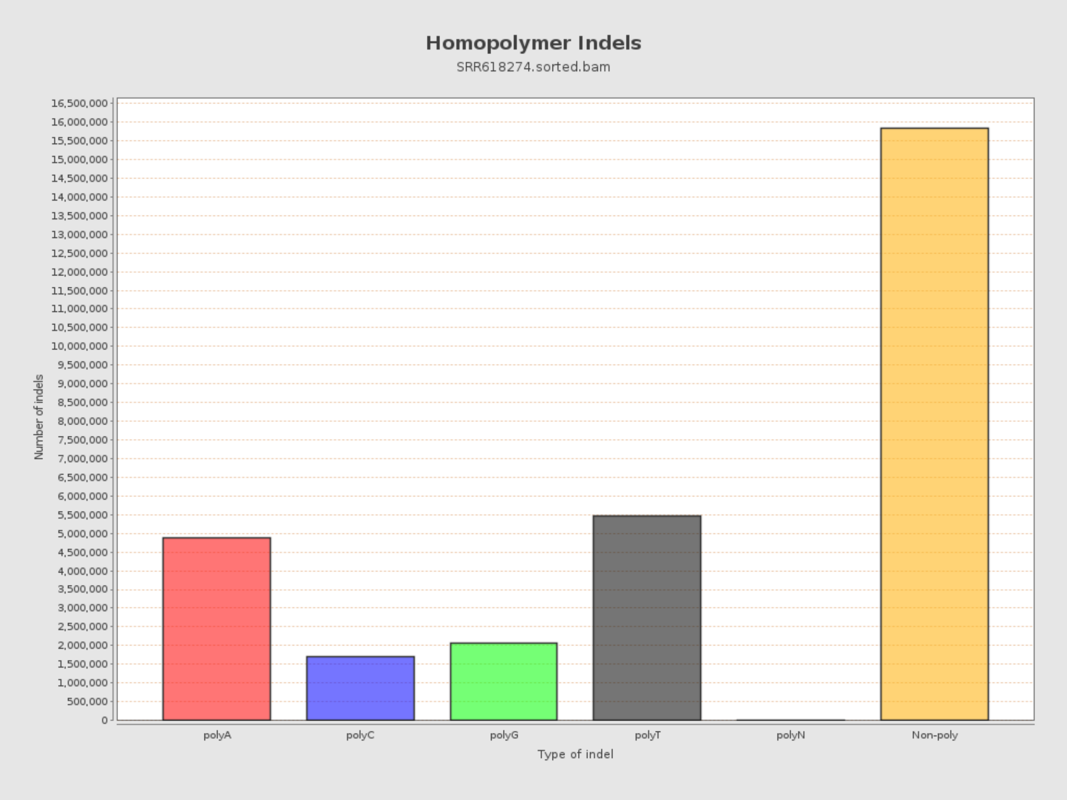
9. Results : Mapped Reads GC-content Distribution



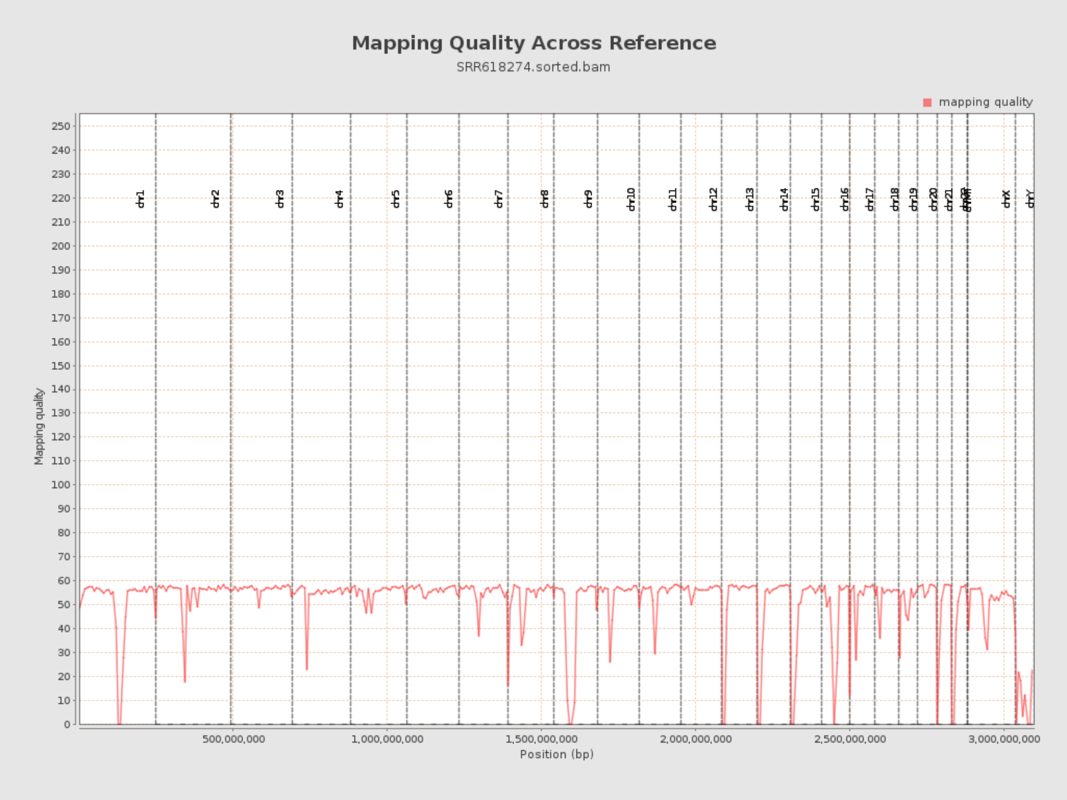
10. Results : Mapped Reads Clipping Profile



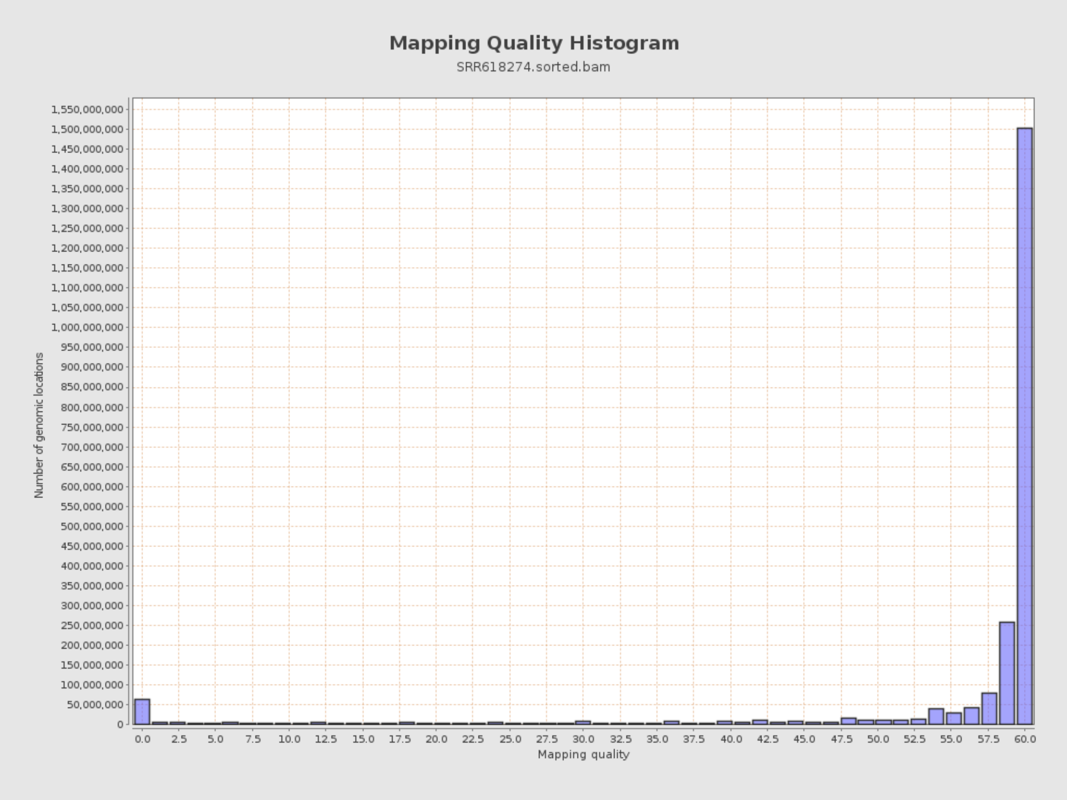
11. Results : Homopolymer Indels



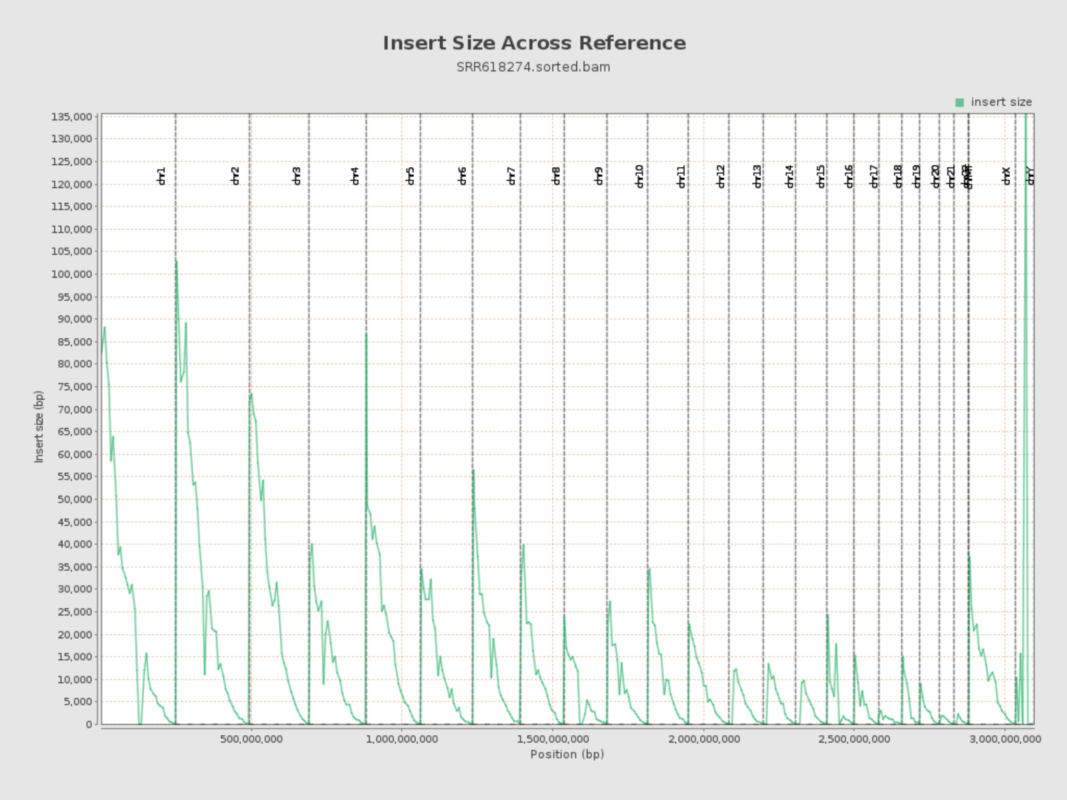
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram