Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 18:09:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234135.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_SRR6234135 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234135.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 18:09:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234135.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,539,183
Mapped reads	752,779 / 48.91%
Unmapped reads	786,404 / 51.09%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,614 / 0.17%
Read min/max/mean length	30 / 76 / 76.06
Duplicated reads (estimated)	49,073 / 3.19%
Duplication rate	5.3%
Clipped reads	555,754 / 36.11%

2.2. ACGT Content

Number/percentage of A's	11,679,121 / 26.39%
Number/percentage of C's	7,025,953 / 15.88%
Number/percentage of T's	14,687,757 / 33.19%
Number/percentage of G's	10,862,079 / 24.54%
Number/percentage of N's	2,963 / 0.01%
GC Percentage	40.42%

2.3. Coverage

Mean	0.0143

Standard Deviation	0.1674

2.4. Mapping Quality

Mean Mapping Quality	44.09

2.5. Mismatches and indels

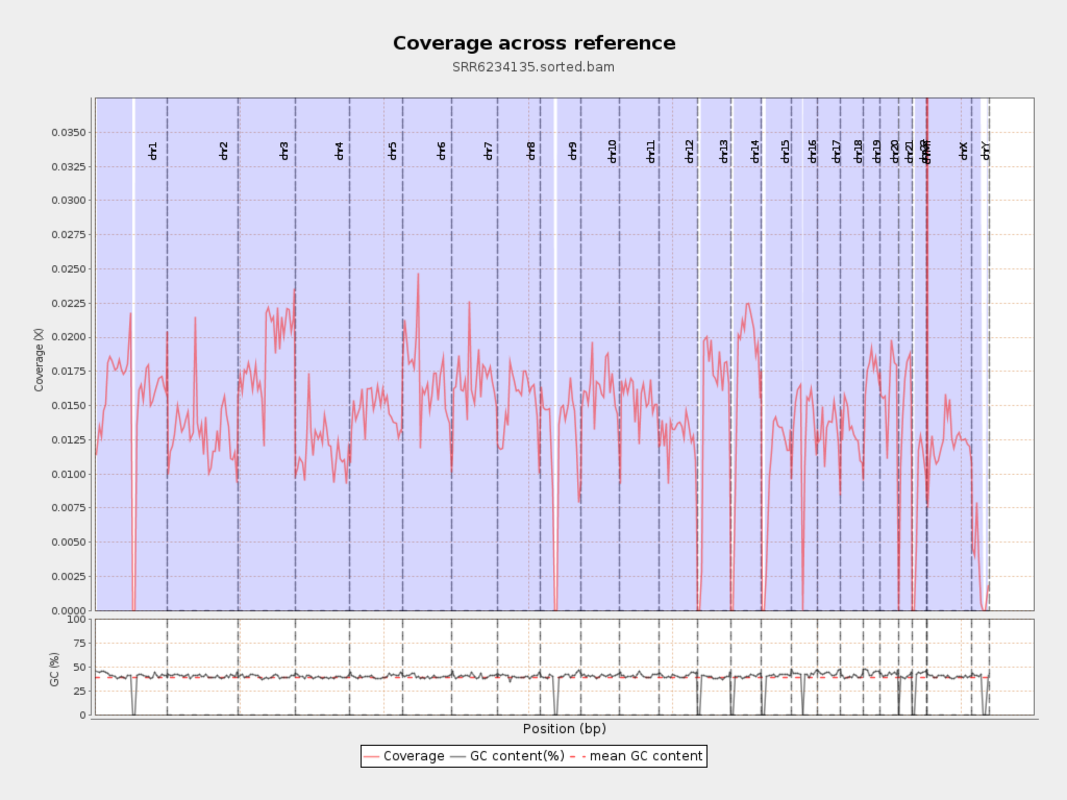
General error rate	1.08%
Mismatches	473,060
Insertions	3,724
Mapped reads with at least one insertion	0.49%
Deletions	17,420
Mapped reads with at least one deletion	2.28%
Homopolymer indels	46.93%

2.6. Chromosome stats

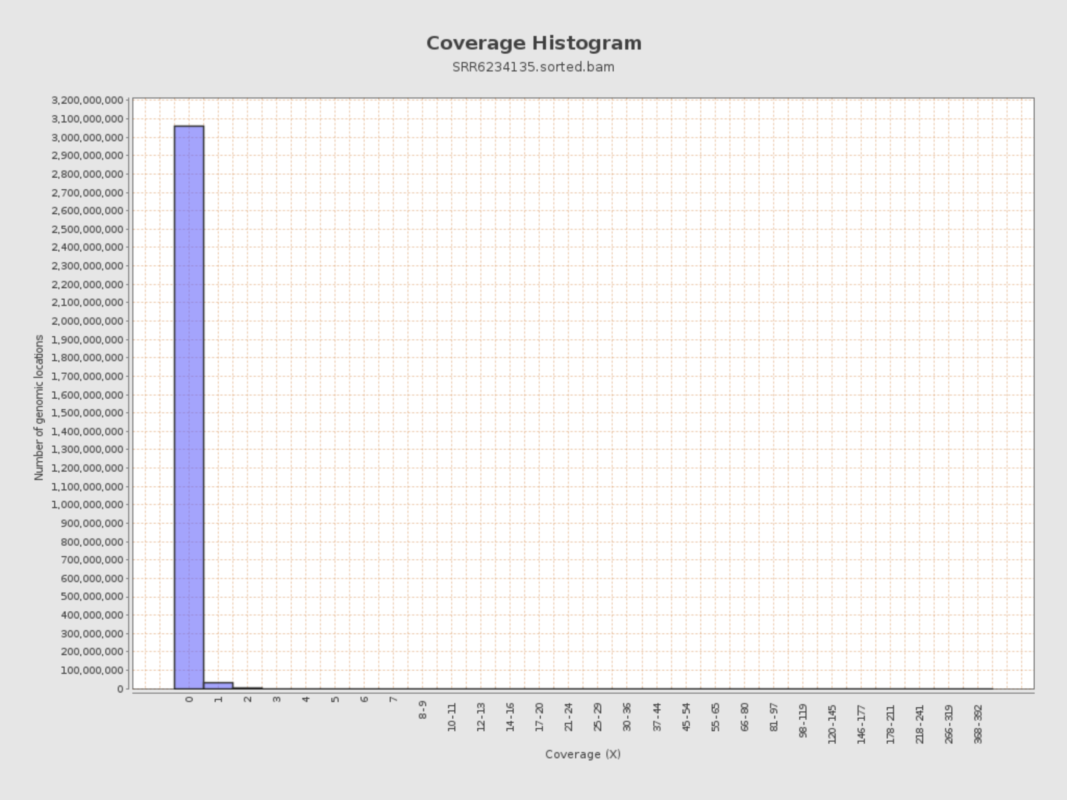
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3862762	0.0155	0.1989
chr2	243199373	3154437	0.013	0.1707
chr3	198022430	3741010	0.0189	0.1642
chr4	191154276	2265938	0.0119	0.1325
chr5	180915260	2666656	0.0147	0.1447
chr6	171115067	2911565	0.017	0.1713
chr7	159138663	2667513	0.0168	0.2099

chr8	146364022	2231988	0.0152	0.2693
chr9	141213431	1753146	0.0124	0.1458
chr10	135534747	2180086	0.0161	0.1607
chr11	135006516	2089628	0.0155	0.1707
chr12	133851895	1714360	0.0128	0.1335
chr13	115169878	1721106	0.0149	0.1475
chr14	107349540	1804957	0.0168	0.1549
chr15	102531392	1033568	0.0101	0.118
chr16	90354753	1175179	0.013	0.1354
chr17	81195210	1060426	0.0131	0.1376
chr18	78077248	1024806	0.0131	0.231
chr19	59128983	1020450	0.0173	0.1711
chr20	63025520	999420	0.0159	0.1509
chr21	48129895	685364	0.0142	0.1404
chr22	51304566	410104	0.008	0.1056
chrMT	16571	33491	2.0211	2.4766
chrX	155270560	1917882	0.0124	0.1354
chrY	59373566	162782	0.0027	0.0632

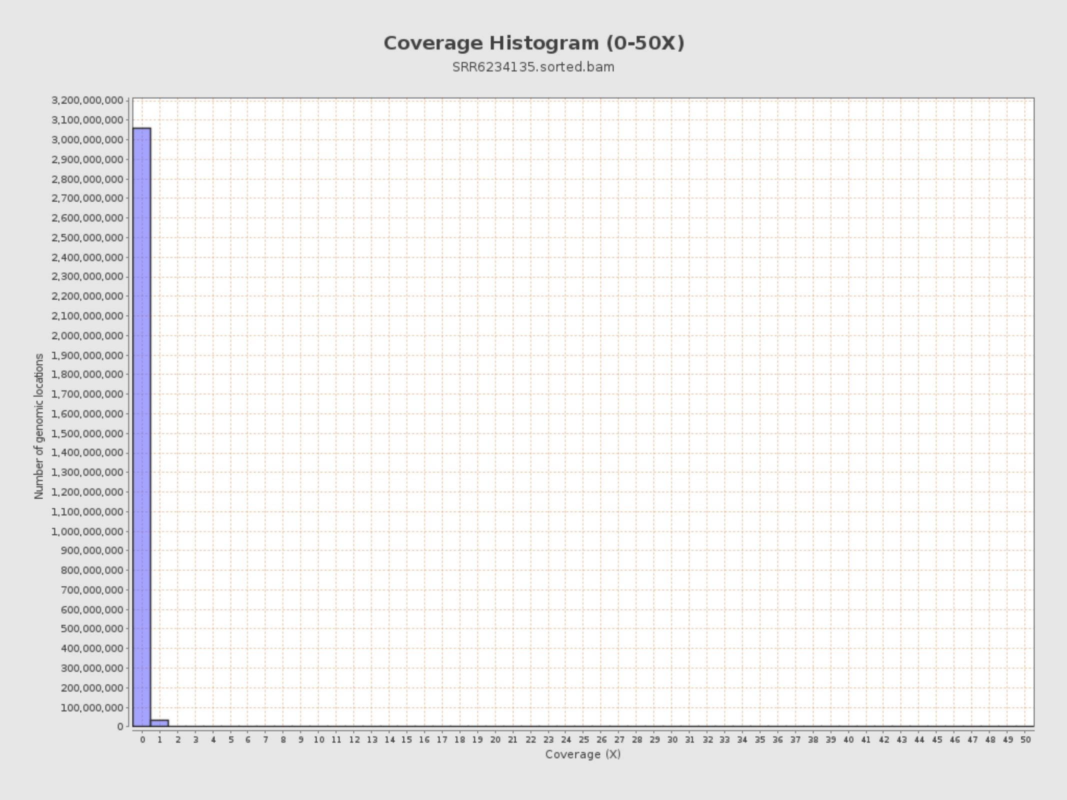
3. Results : Coverage across reference



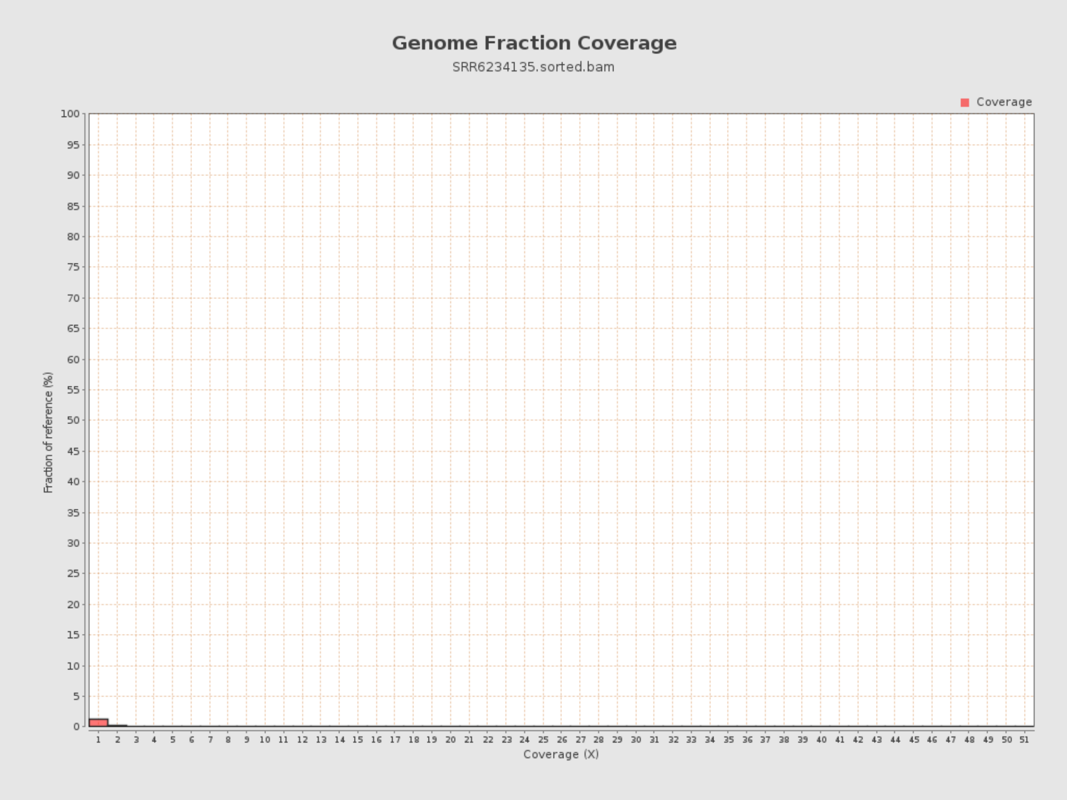
4. Results : Coverage Histogram



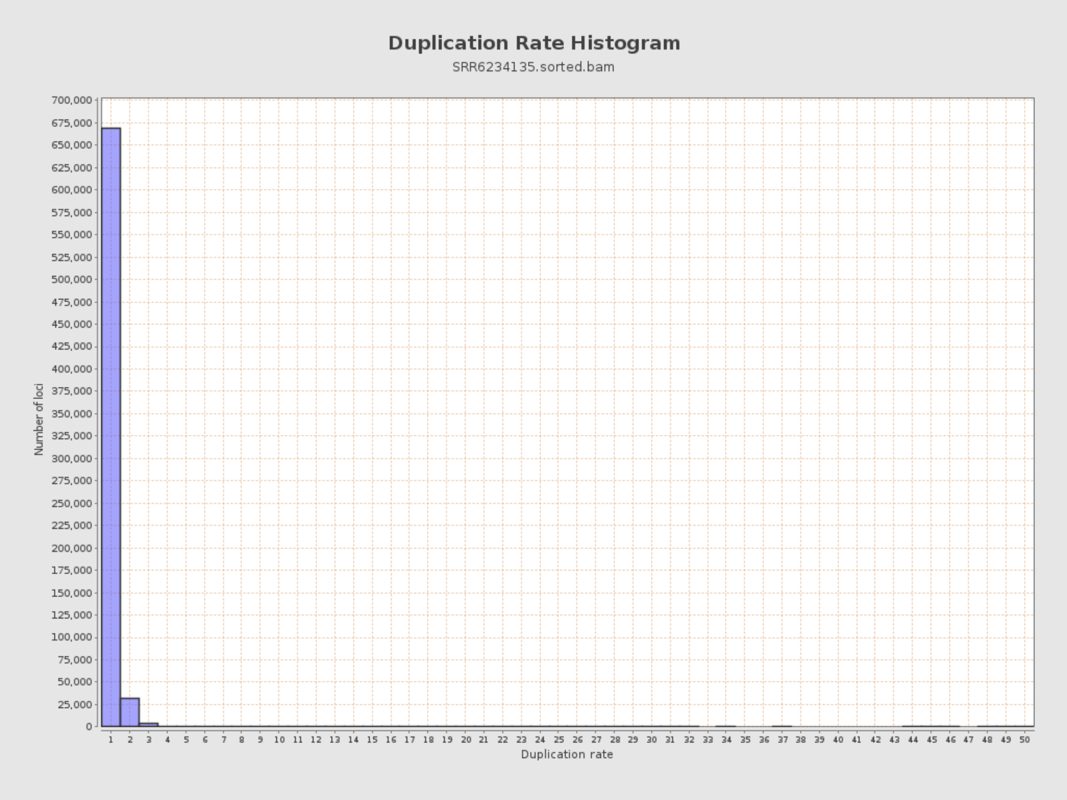
5. Results : Coverage Histogram (0-50X)



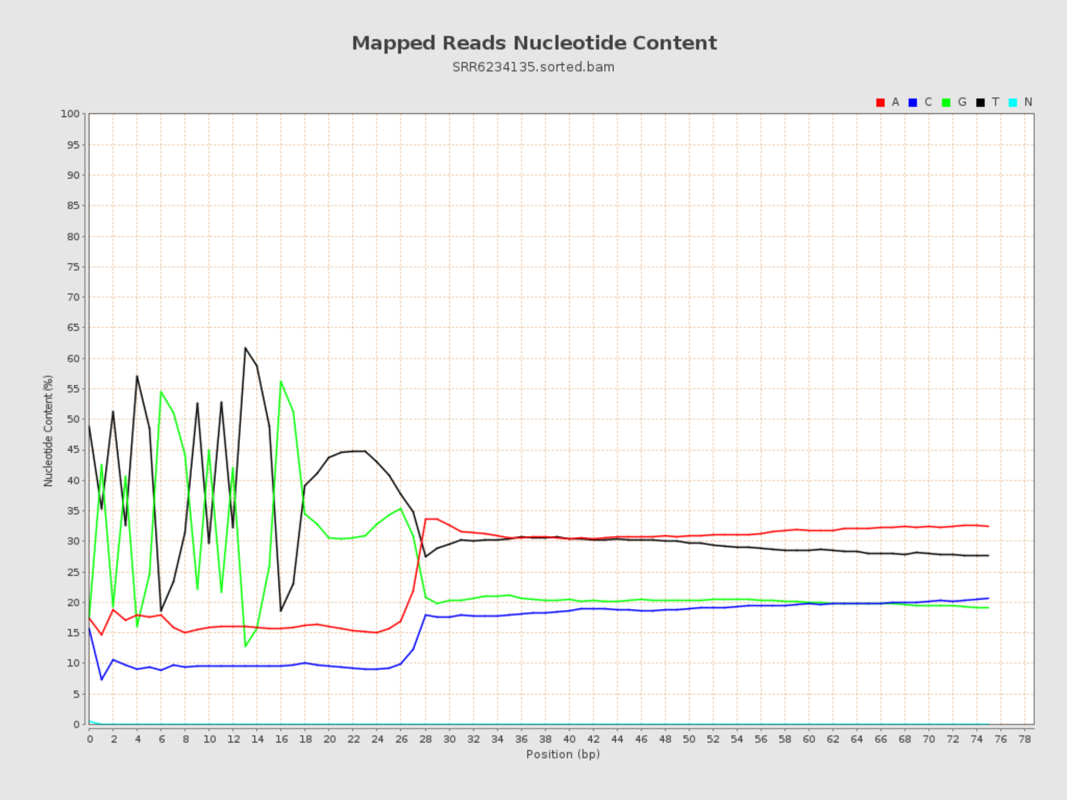
6. Results : Genome Fraction Coverage



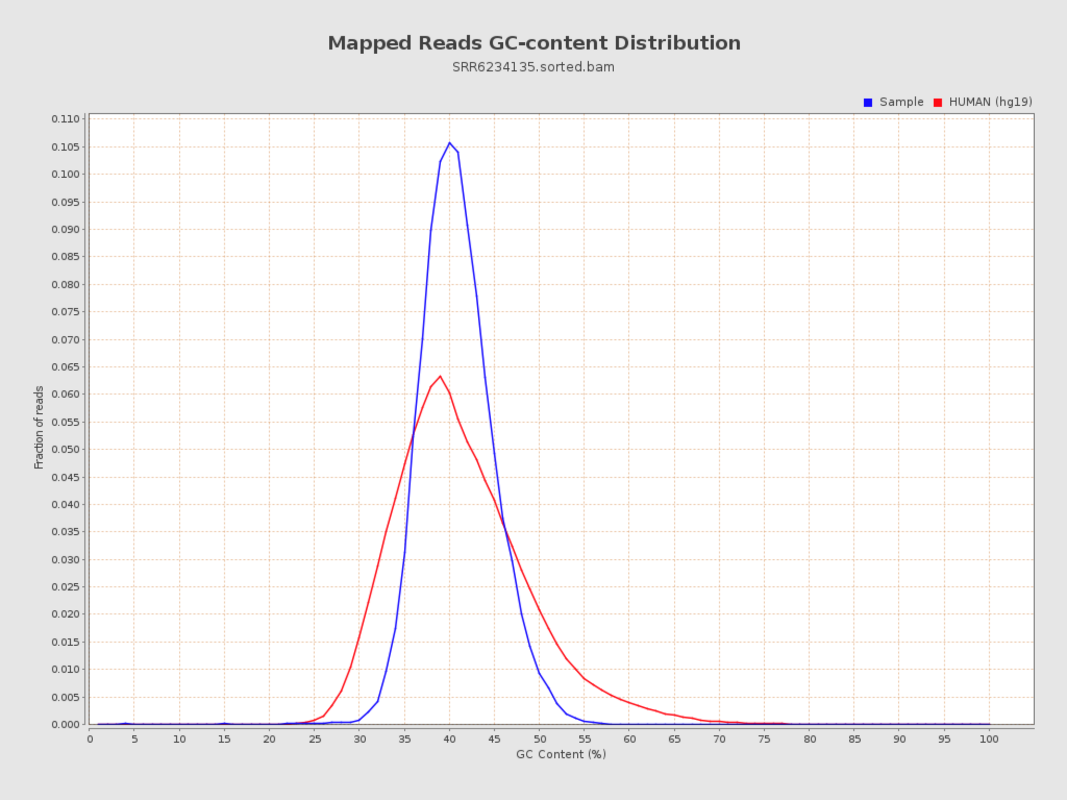
7. Results : Duplication Rate Histogram



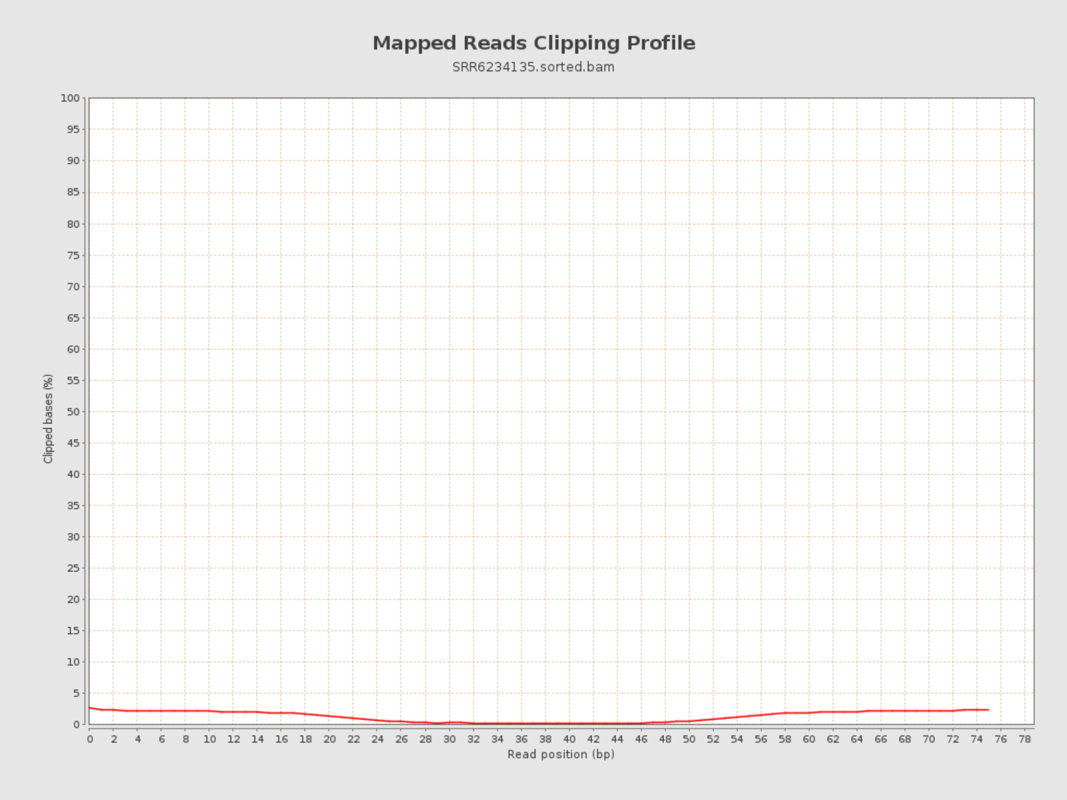
8. Results : Mapped Reads Nucleotide Content



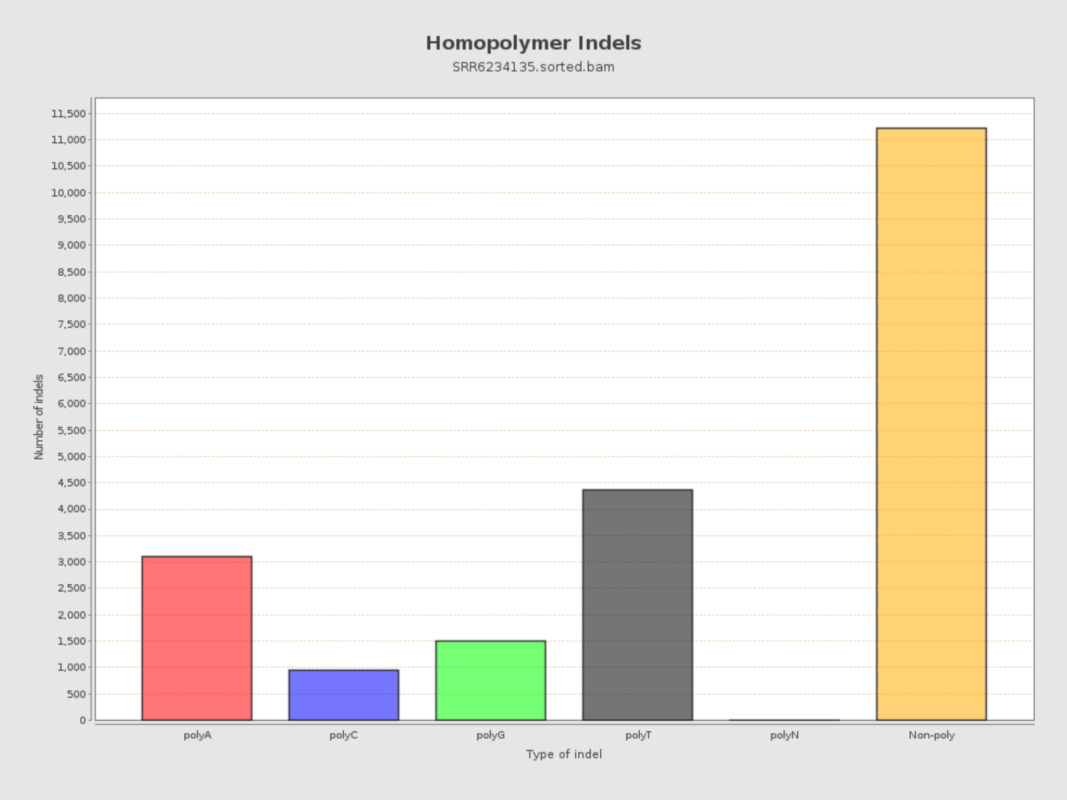
9. Results : Mapped Reads GC-content Distribution



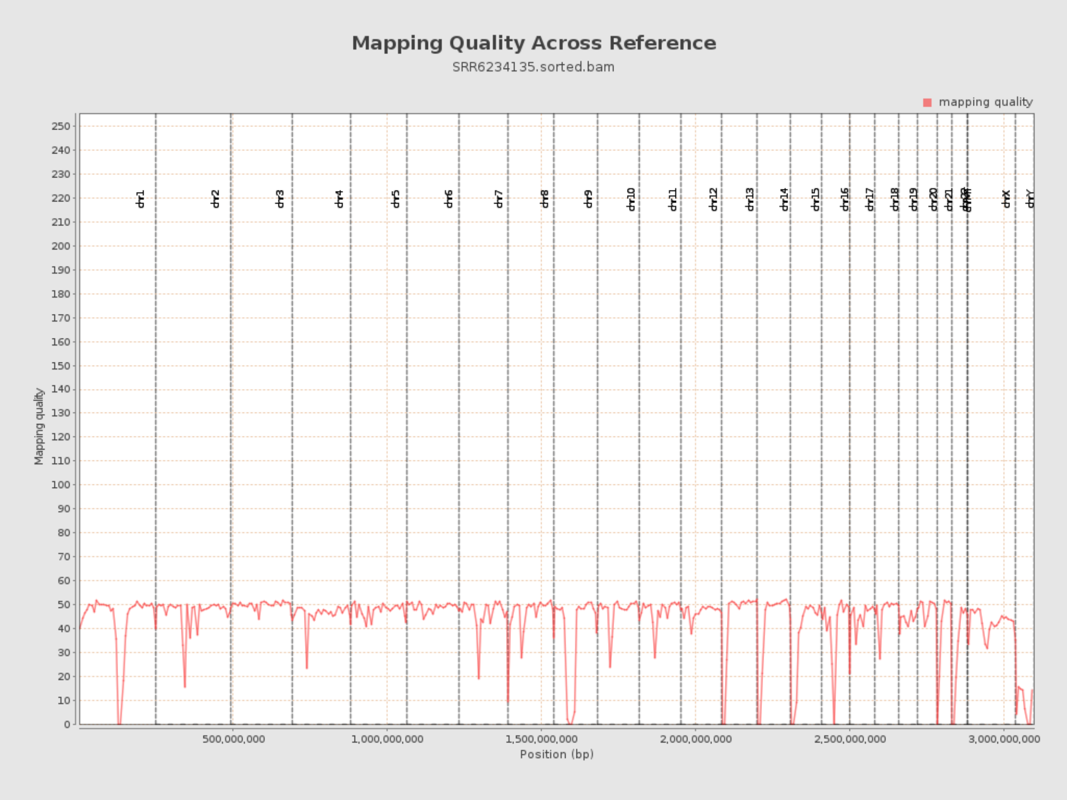
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram