Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 13:17:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234064.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_SRR6234064 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234064.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 13:17:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234064.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,963,882
Mapped reads	3,732,414 / 94.16%
Unmapped reads	231,468 / 5.84%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	38,480 / 0.97%
Read min/max/mean length	30 / 76 / 76.34
Duplicated reads (estimated)	585,989 / 14.78%
Duplication rate	6.18%
Clipped reads	1,309,773 / 33.04%

2.2. ACGT Content

Number/percentage of A's	64,686,083 / 25.16%
Number/percentage of C's	45,388,538 / 17.65%
Number/percentage of T's	70,764,704 / 27.52%
Number/percentage of G's	76,200,045 / 29.64%
Number/percentage of N's	55,716 / 0.02%
GC Percentage	47.29%

2.3. Coverage

Mean	0.0831

Standard Deviation	49.2861

2.4. Mapping Quality

Mean Mapping Quality	44.07

2.5. Mismatches and indels

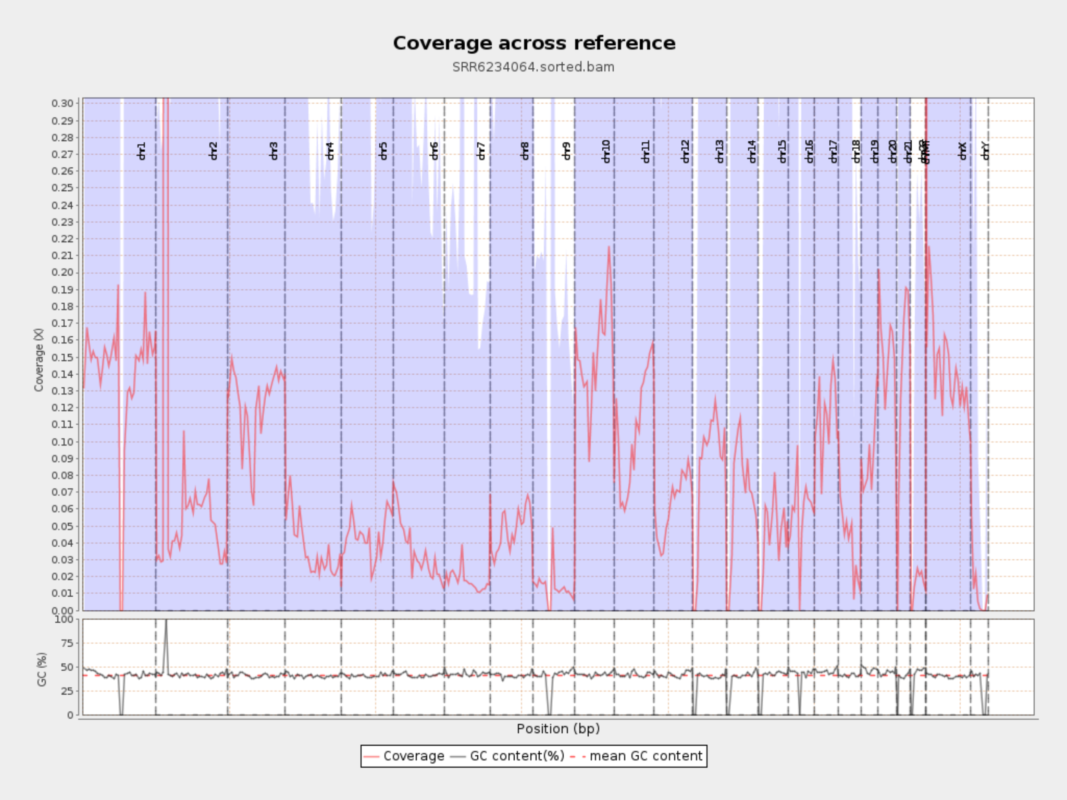
General error rate	0.62%
Mismatches	1,553,554
Insertions	16,109
Mapped reads with at least one insertion	0.43%
Deletions	51,370
Mapped reads with at least one deletion	1.36%
Homopolymer indels	47.48%

2.6. Chromosome stats

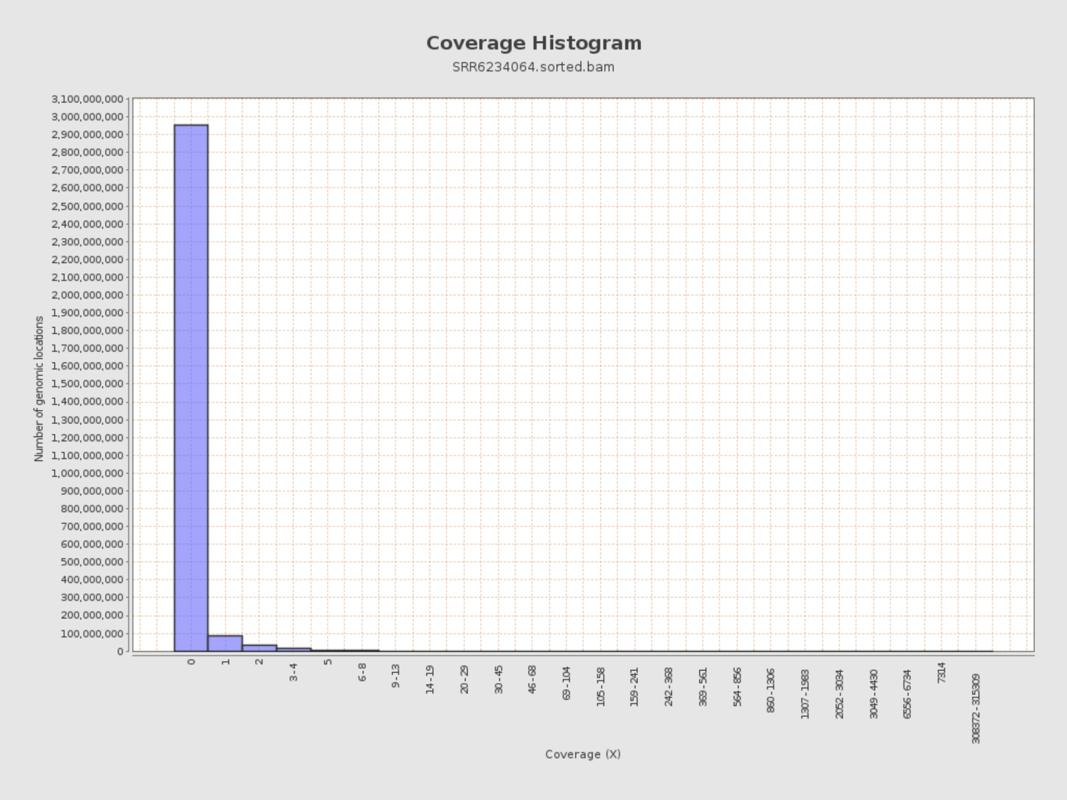
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	34790825	0.1396	1.3369
chr2	243199373	36542063	0.1503	175.8284
chr3	198022430	24173637	0.1221	0.5303
chr4	191154276	7161040	0.0375	0.2976
chr5	180915260	7964618	0.044	0.3163
chr6	171115067	5979051	0.0349	0.3151
chr7	159138663	2811608	0.0177	0.2883

chr8	146364022	7028926	0.048	0.7162
chr9	141213431	1959995	0.0139	0.3545
chr10	135534747	20847649	0.1538	0.7702
chr11	135006516	14380007	0.1065	0.7245
chr12	133851895	8443008	0.0631	0.3788
chr13	115169878	9784684	0.085	0.4415
chr14	107349540	7361262	0.0686	0.5019
chr15	102531392	4451642	0.0434	0.3119
chr16	90354753	5135926	0.0568	0.4041
chr17	81195210	9540025	0.1175	0.6525
chr18	78077248	3282974	0.042	0.8187
chr19	59128983	5355058	0.0906	0.8448
chr20	63025520	9681530	0.1536	0.6292
chr21	48129895	6513375	0.1353	0.5803
chr22	51304566	796517	0.0155	0.1823
chrMT	16571	70166	4.2343	3.7504
chrX	155270560	22442092	0.1445	0.6157
chrY	59373566	681389	0.0115	0.1754

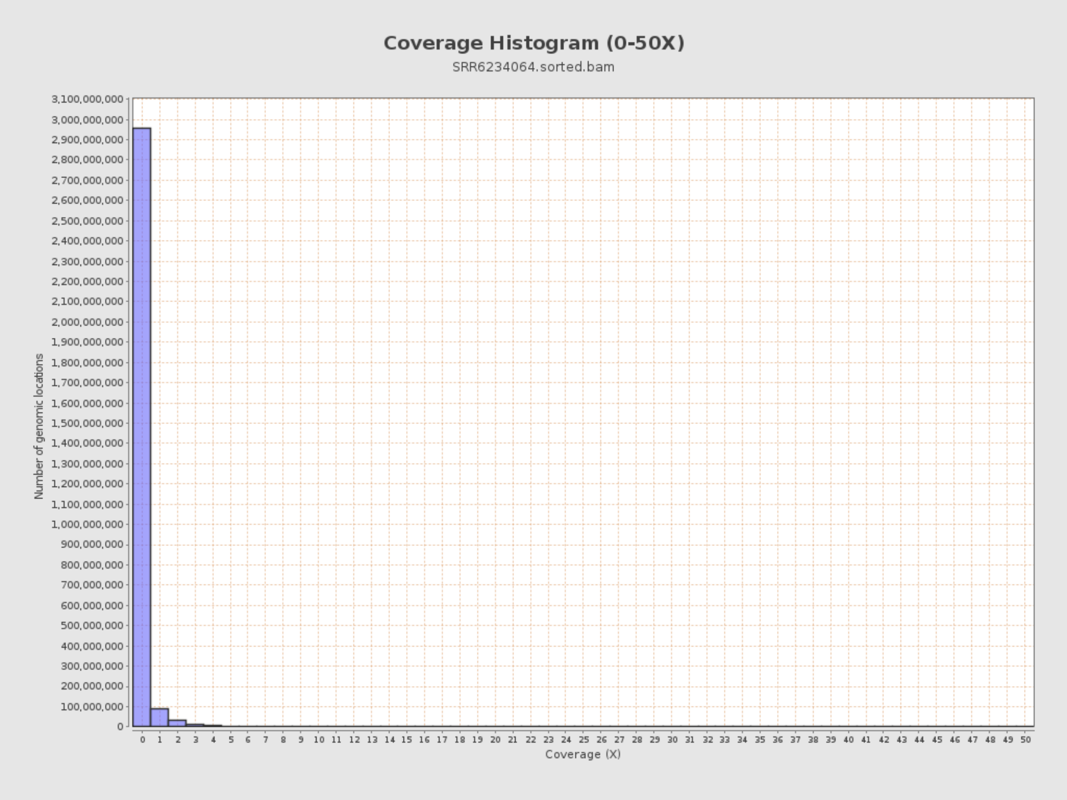
3. Results : Coverage across reference



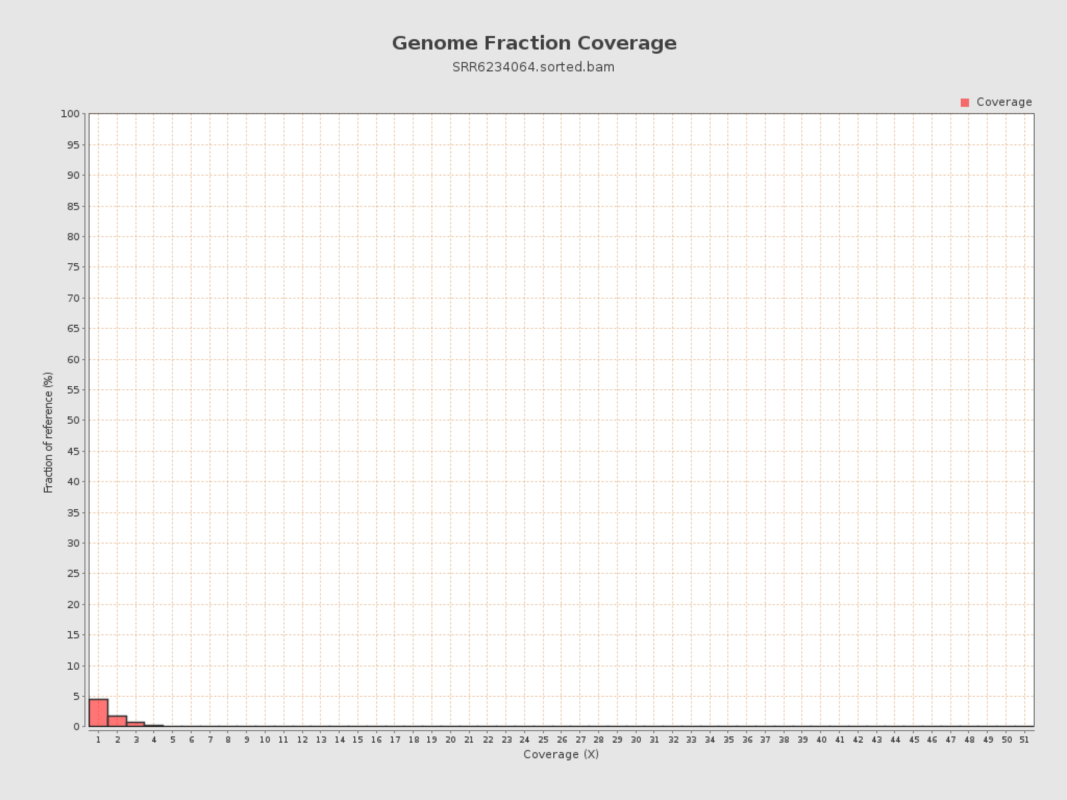
4. Results : Coverage Histogram



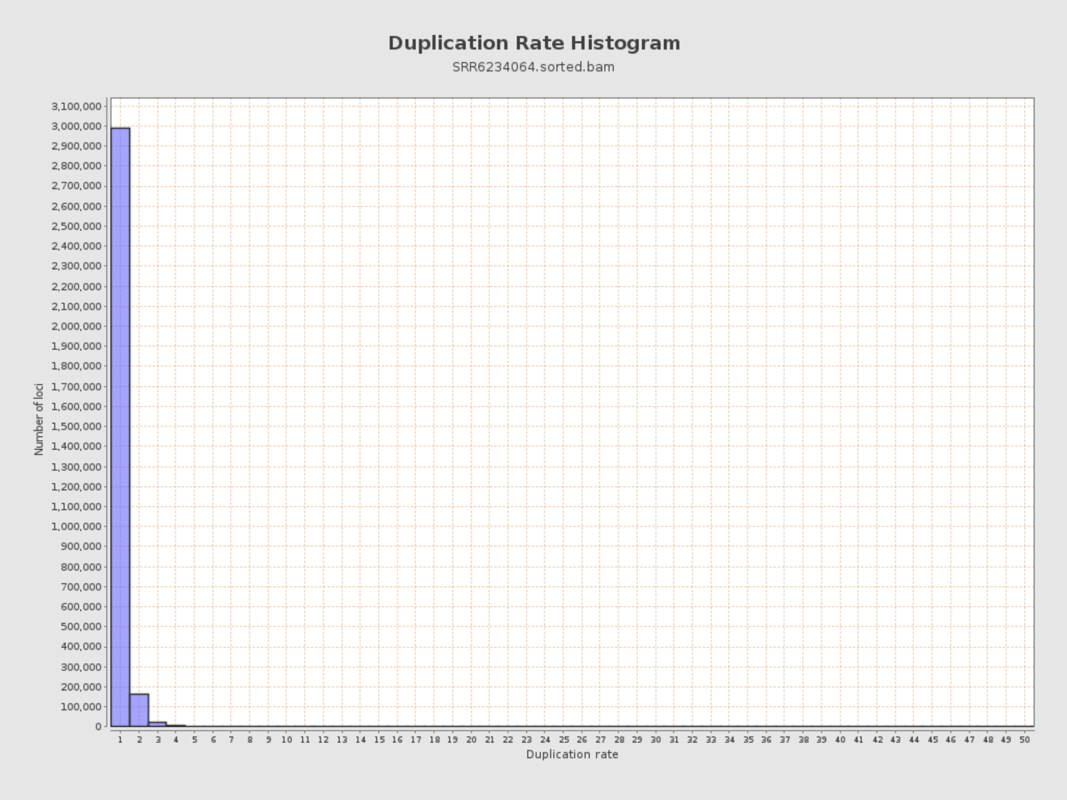
5. Results : Coverage Histogram (0-50X)



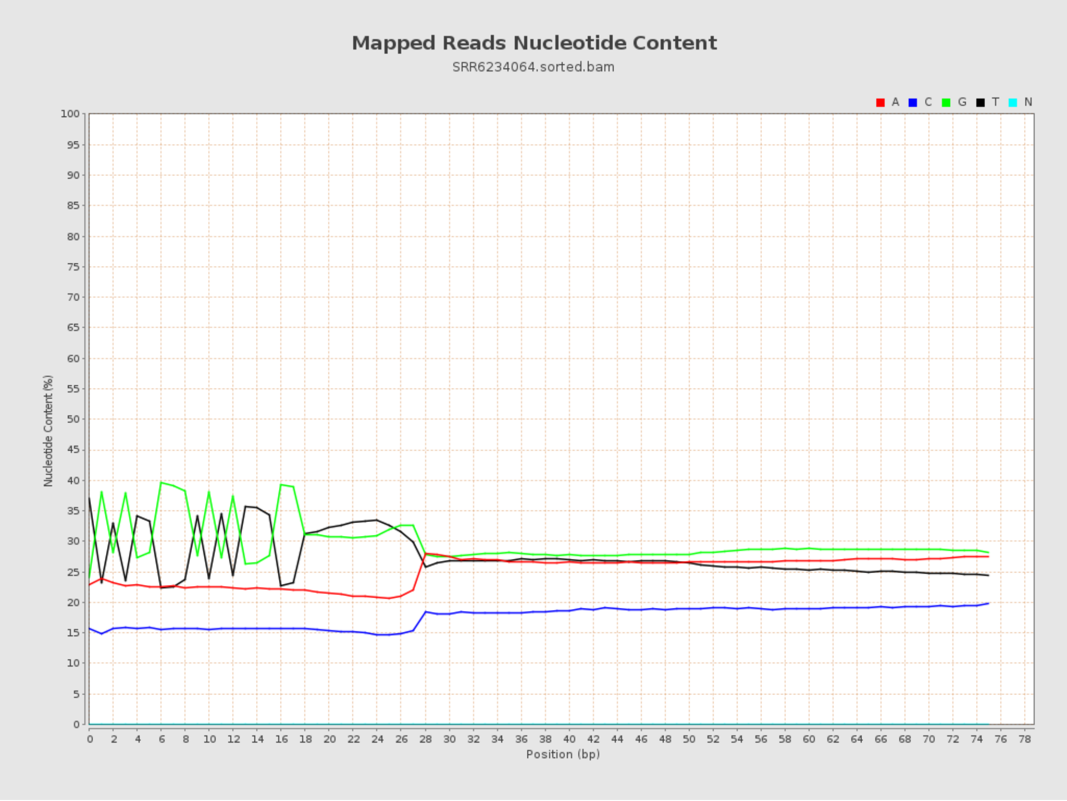
6. Results : Genome Fraction Coverage



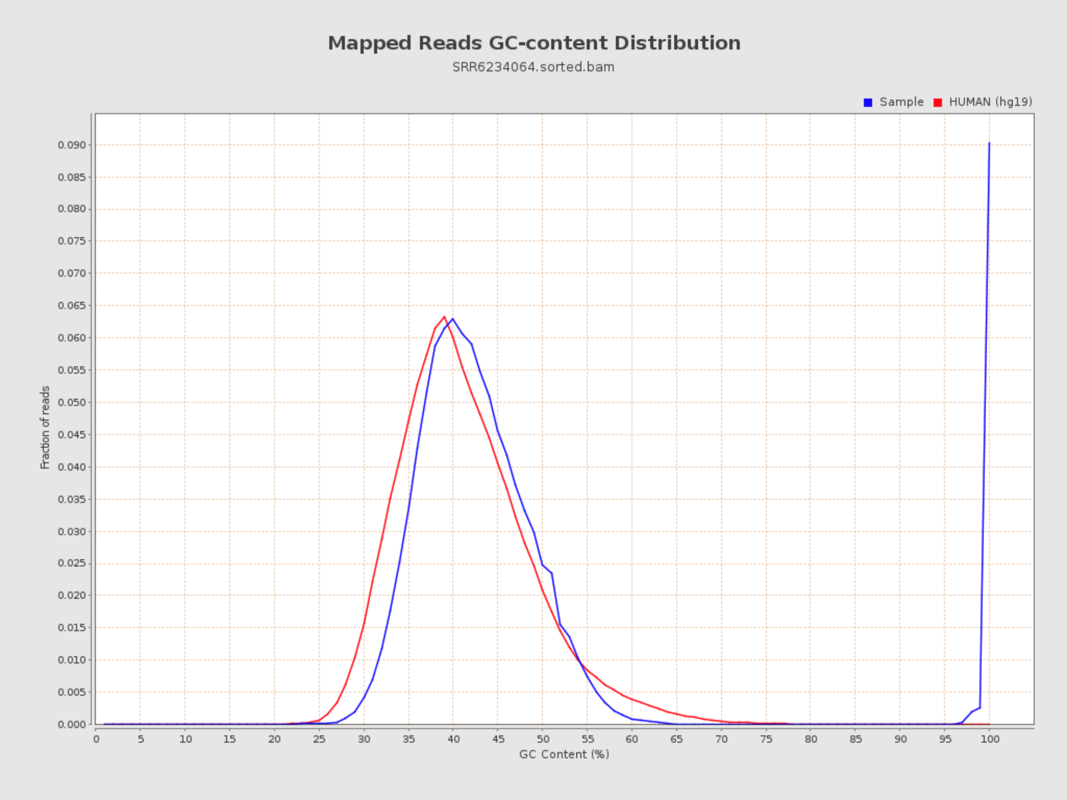
7. Results : Duplication Rate Histogram



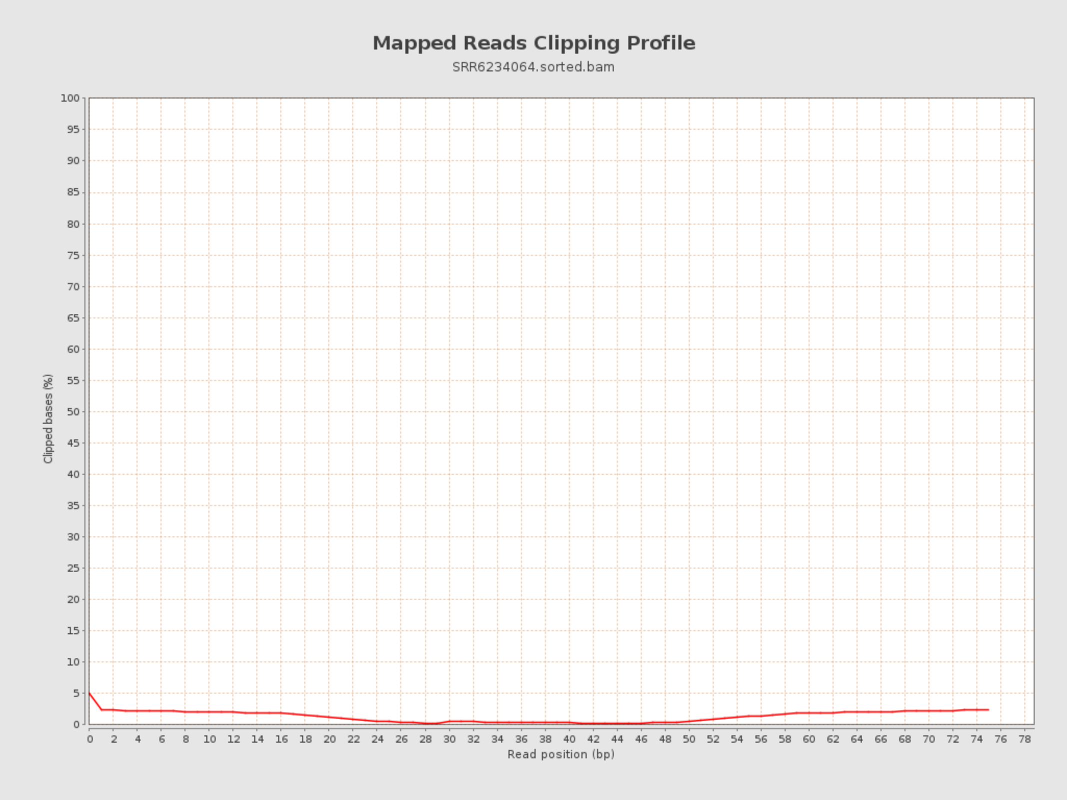
8. Results : Mapped Reads Nucleotide Content



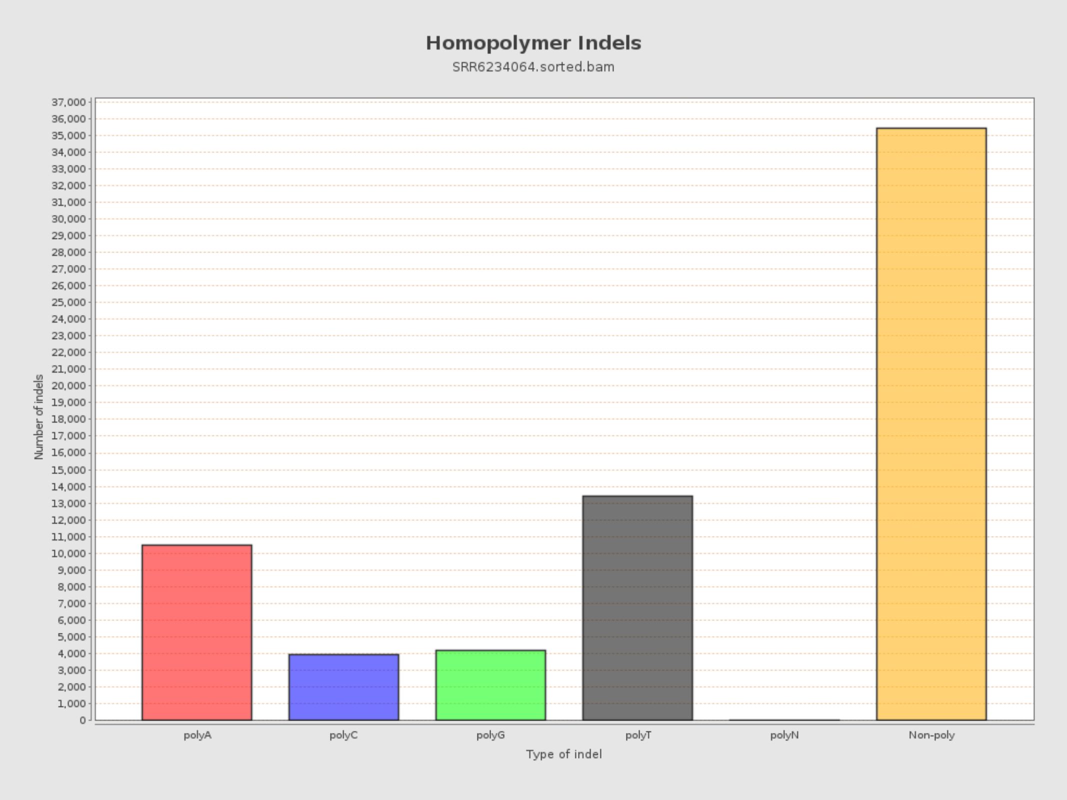
9. Results : Mapped Reads GC-content Distribution



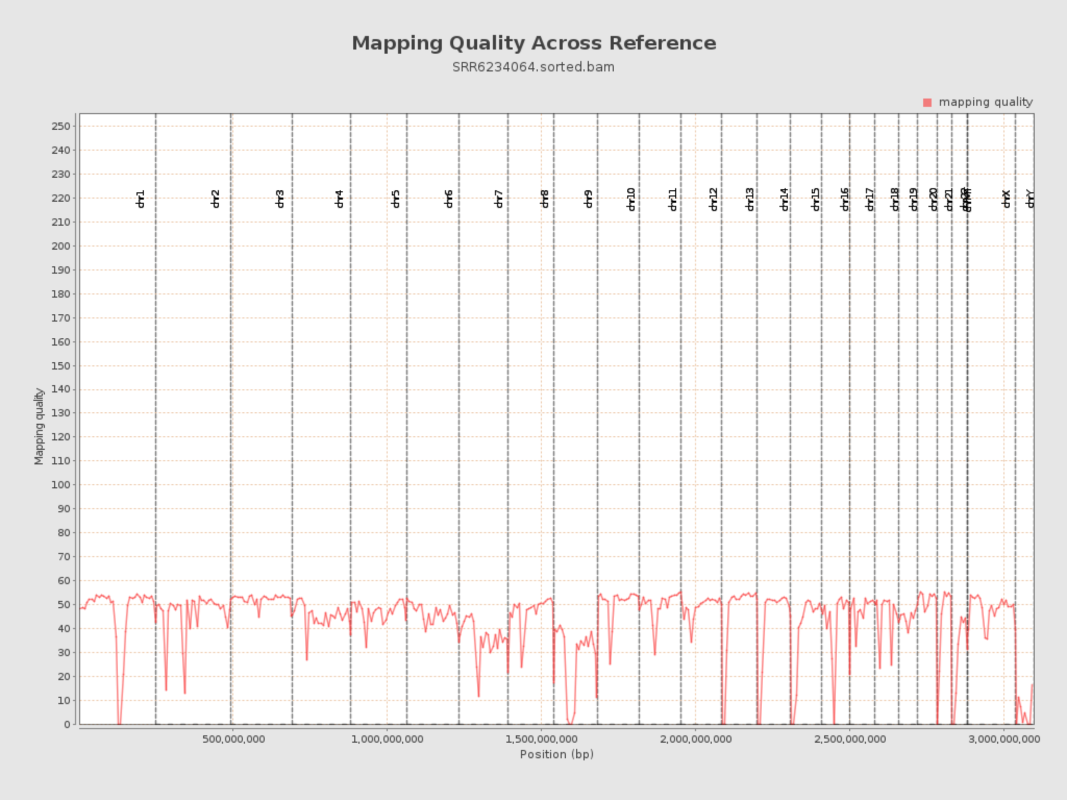
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram