Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 10:47:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234020.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_SRR6234020 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234020.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 10:47:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234020.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	768,038
Mapped reads	538,784 / 70.15%
Unmapped reads	229,254 / 29.85%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,243 / 0.68%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	48,757 / 6.35%
Duplication rate	7.36%
Clipped reads	284,451 / 37.04%

2.2. ACGT Content

Number/percentage of A's	9,597,866 / 27.65%
Number/percentage of C's	5,799,863 / 16.71%
Number/percentage of T's	11,747,245 / 33.84%
Number/percentage of G's	7,558,367 / 21.78%
Number/percentage of N's	7,102 / 0.02%
GC Percentage	38.48%

2.3. Coverage

Mean	0.0112

Standard Deviation	0.2193

2.4. Mapping Quality

Mean Mapping Quality	45.52

2.5. Mismatches and indels

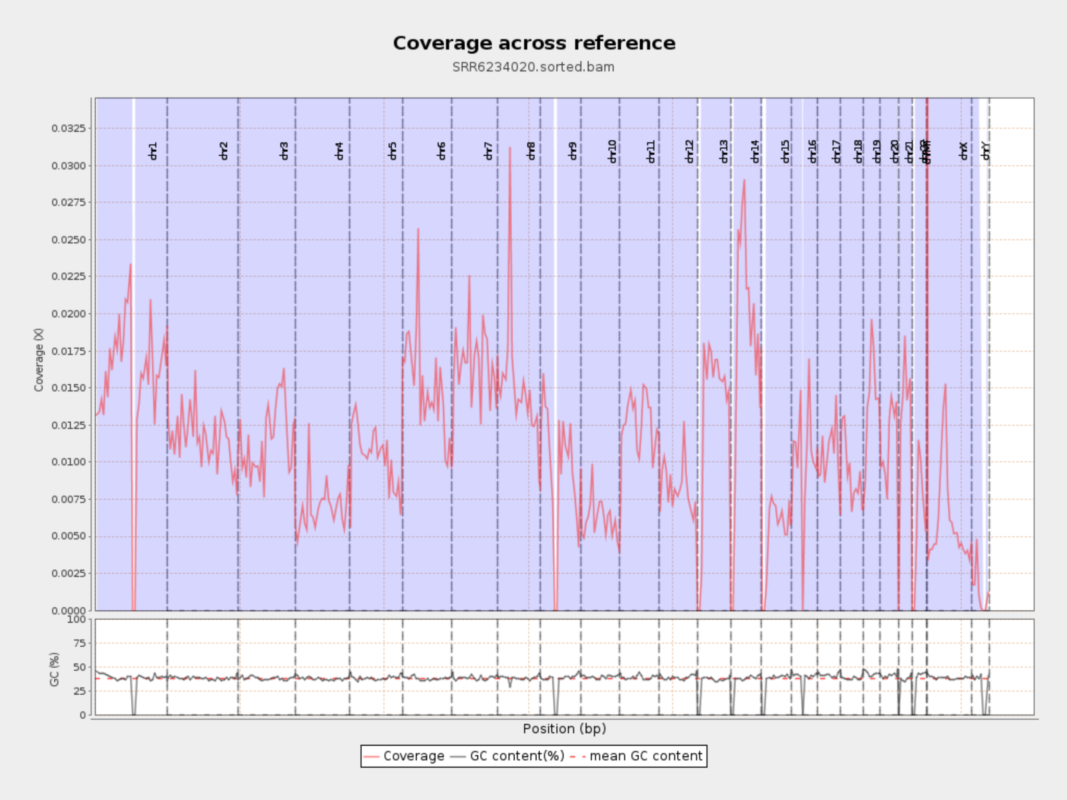
General error rate	0.89%
Mismatches	304,040
Insertions	3,059
Mapped reads with at least one insertion	0.56%
Deletions	12,430
Mapped reads with at least one deletion	2.28%
Homopolymer indels	42.97%

2.6. Chromosome stats

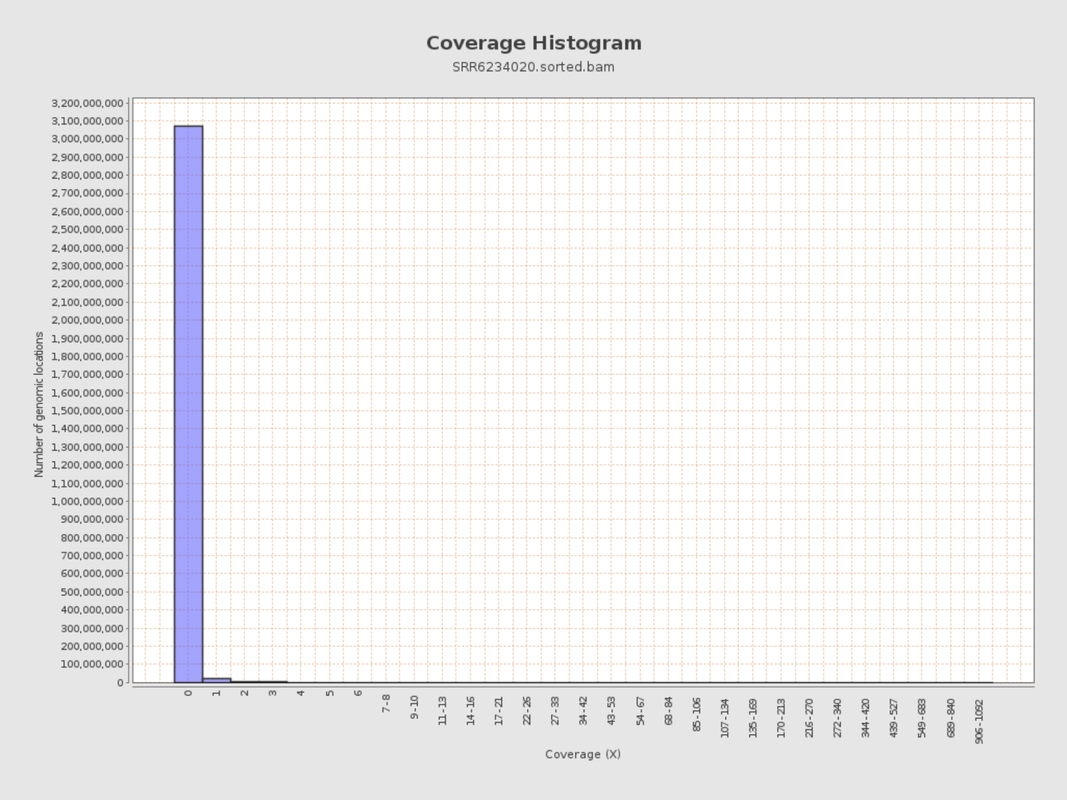
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3894963	0.0156	0.274
chr2	243199373	2821219	0.0116	0.1956
chr3	198022430	2281117	0.0115	0.1429
chr4	191154276	1338307	0.007	0.1146
chr5	180915260	1902249	0.0105	0.1381
chr6	171115067	2593759	0.0152	0.1785
chr7	159138663	2638436	0.0166	0.2043

chr8	146364022	2233209	0.0153	0.6747
chr9	141213431	1340718	0.0095	0.1457
chr10	135534747	834096	0.0062	0.1094
chr11	135006516	1704876	0.0126	0.173
chr12	133851895	1105287	0.0083	0.1225
chr13	115169878	1540035	0.0134	0.1575
chr14	107349540	1918879	0.0179	0.1849
chr15	102531392	533565	0.0052	0.0947
chr16	90354753	910086	0.0101	0.1358
chr17	81195210	849705	0.0105	0.1351
chr18	78077248	735130	0.0094	0.2229
chr19	59128983	844097	0.0143	0.1863
chr20	63025520	706899	0.0112	0.1403
chr21	48129895	634958	0.0132	0.1563
chr22	51304566	321600	0.0063	0.0995
chrMT	16571	23721	1.4315	1.8556
chrX	155270560	945898	0.0061	0.1062
chrY	59373566	79642	0.0013	0.0471

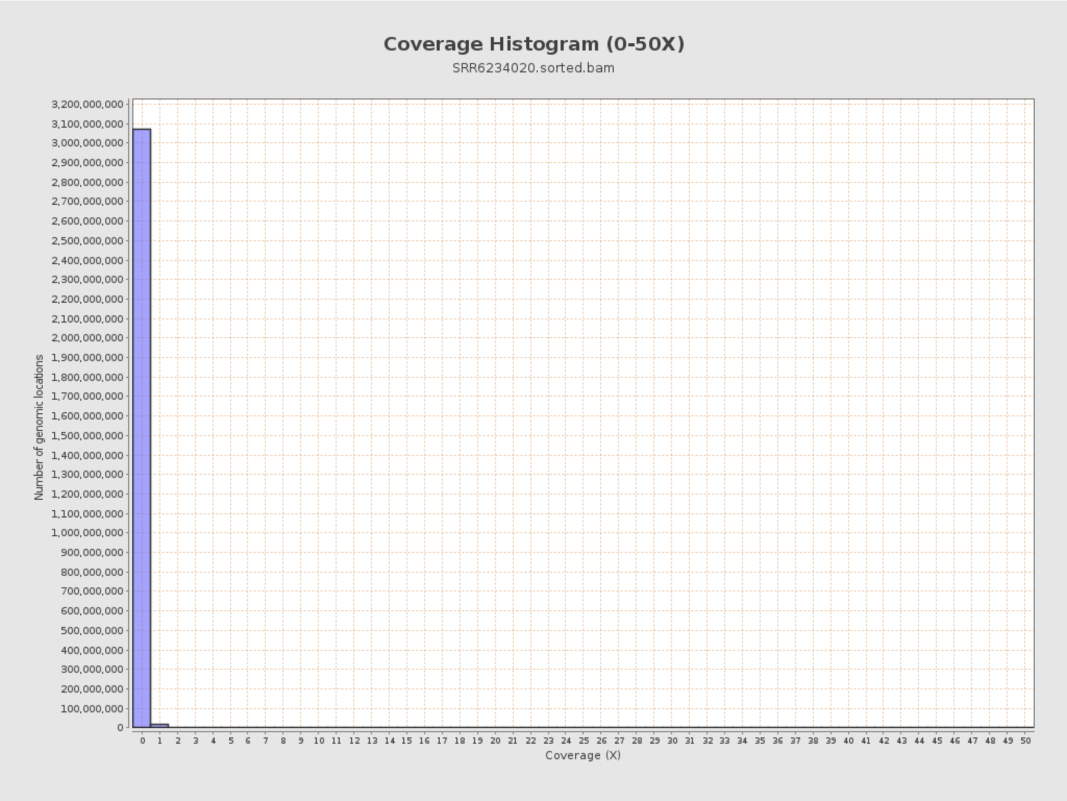
3. Results : Coverage across reference



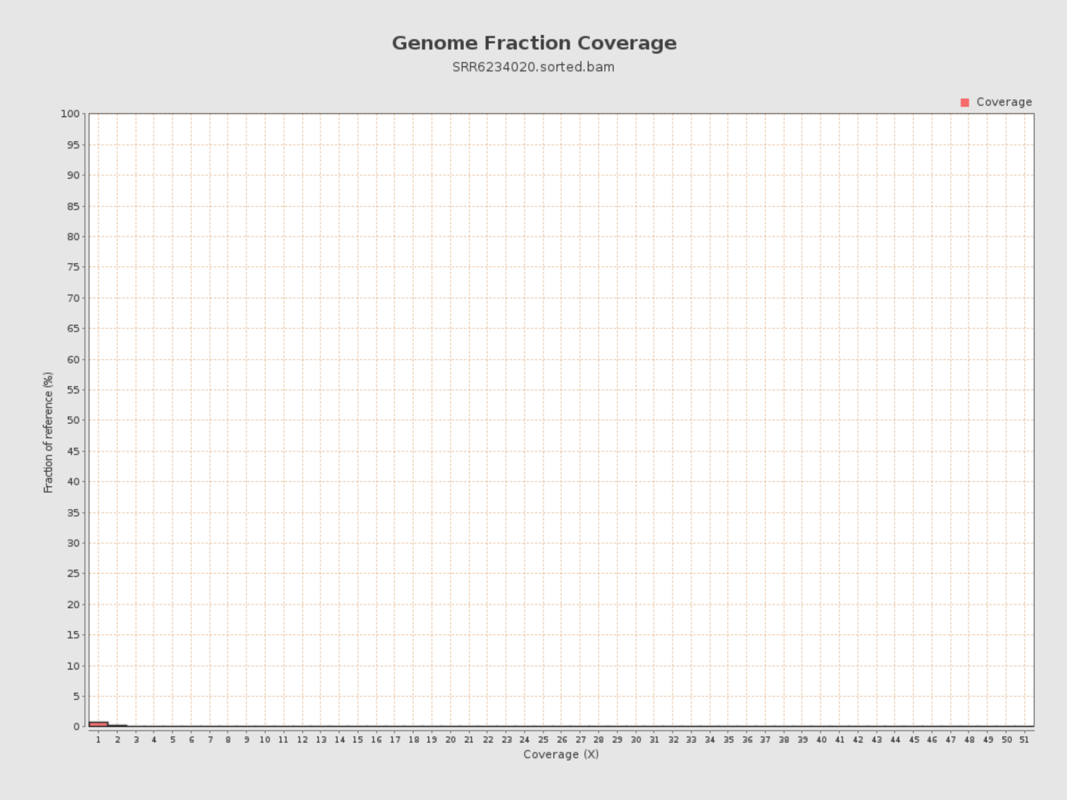
4. Results : Coverage Histogram



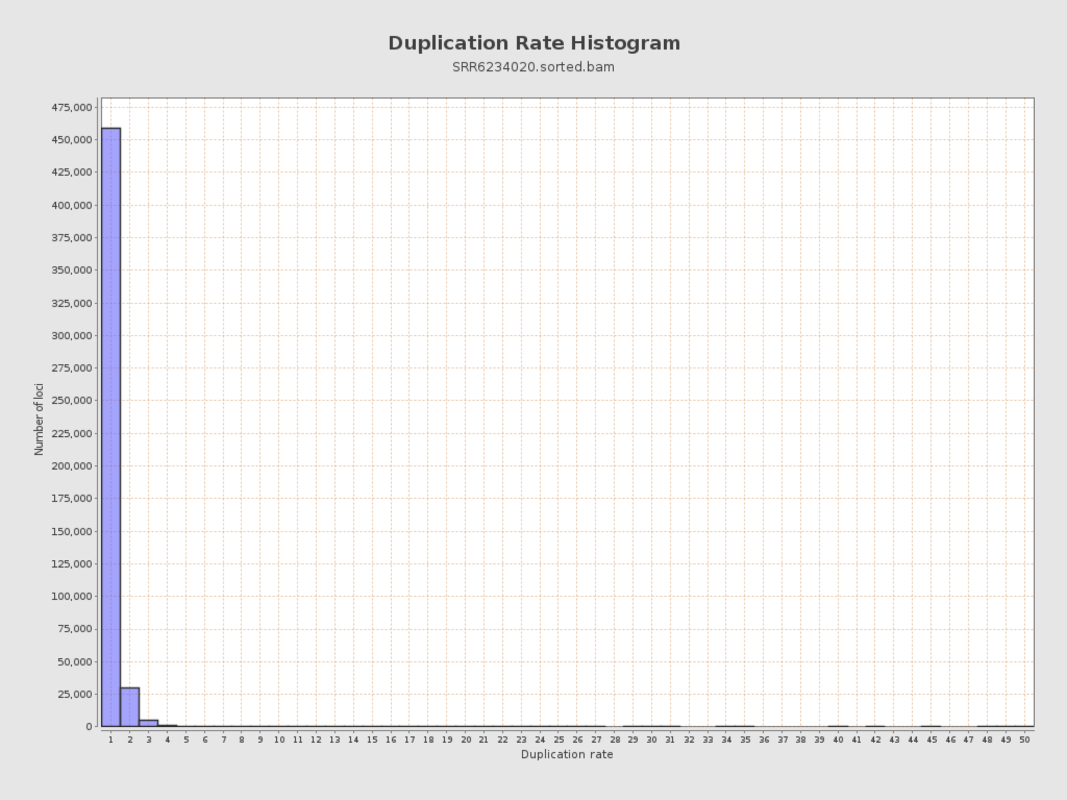
5. Results : Coverage Histogram (0-50X)



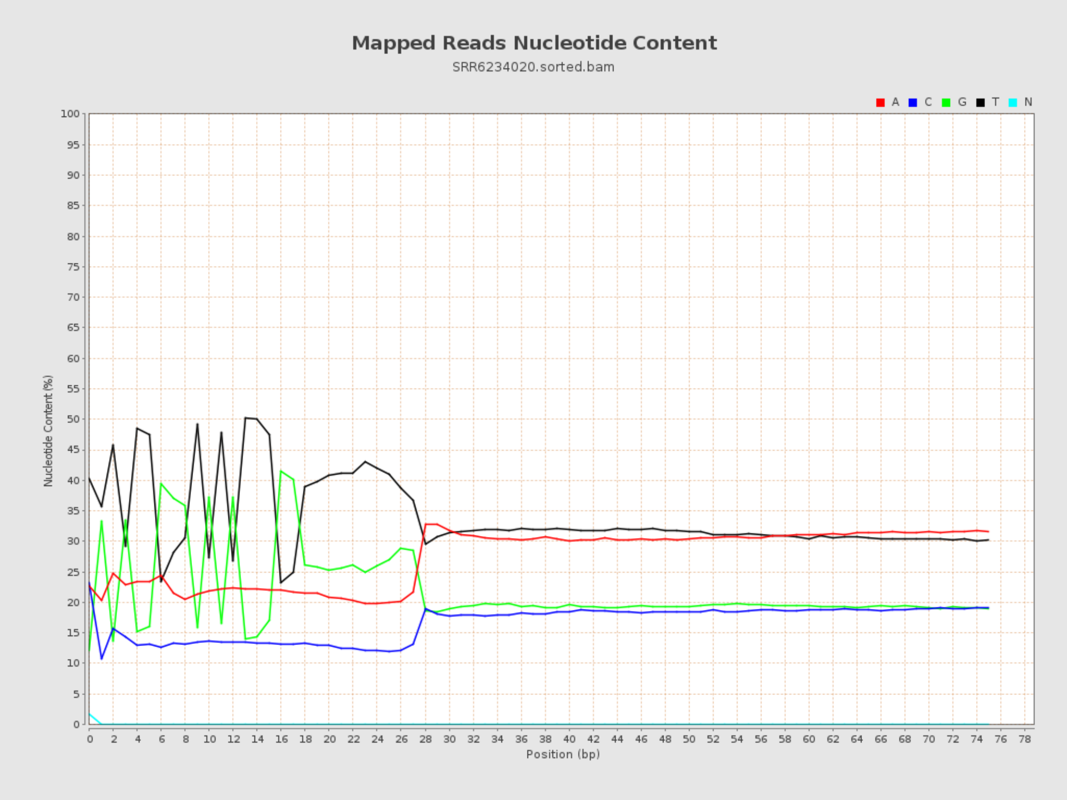
6. Results : Genome Fraction Coverage



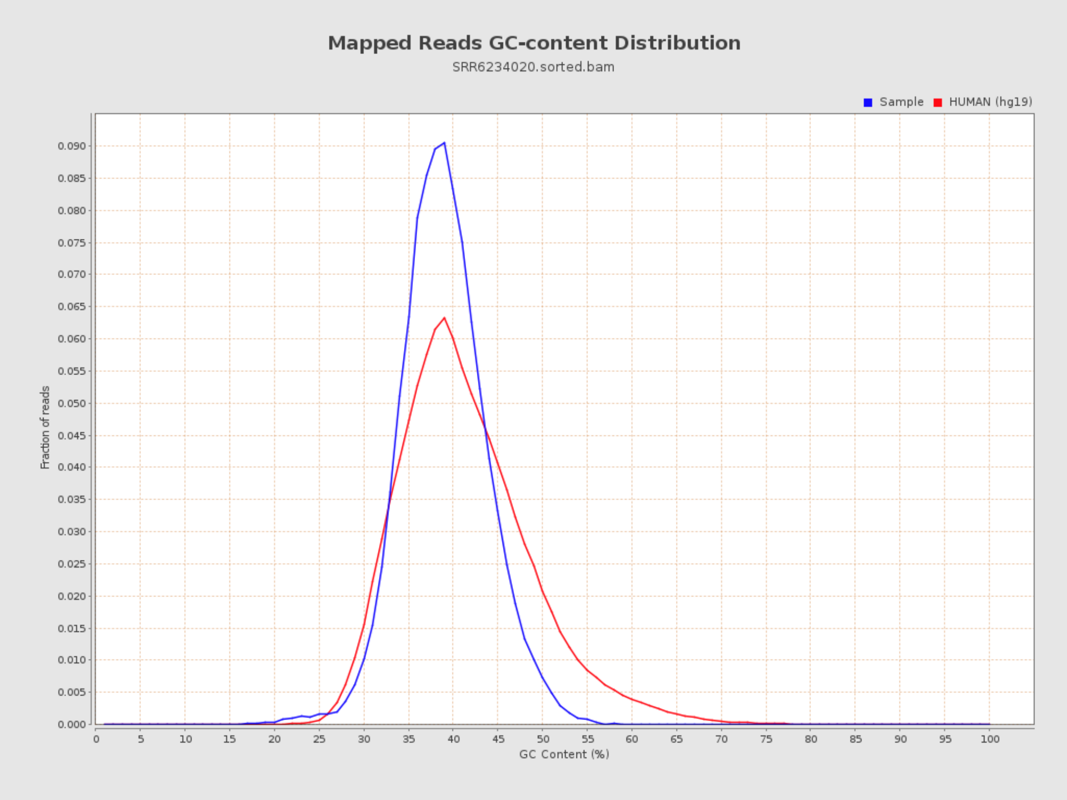
7. Results : Duplication Rate Histogram



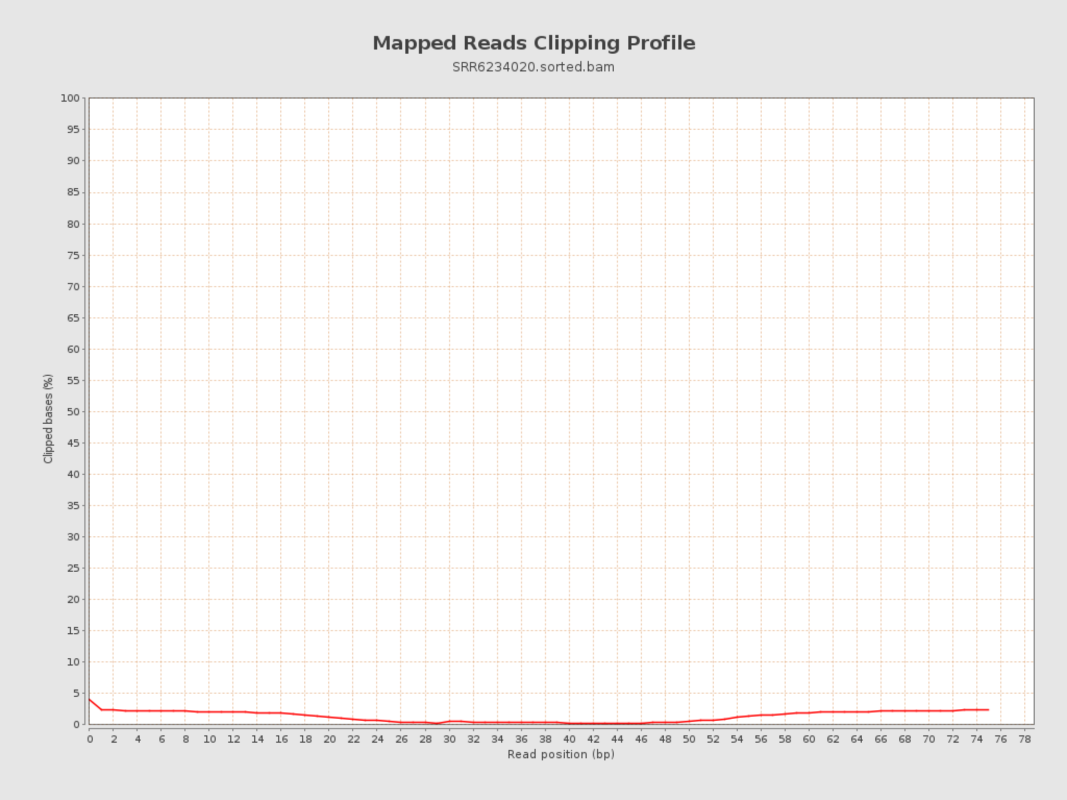
8. Results : Mapped Reads Nucleotide Content



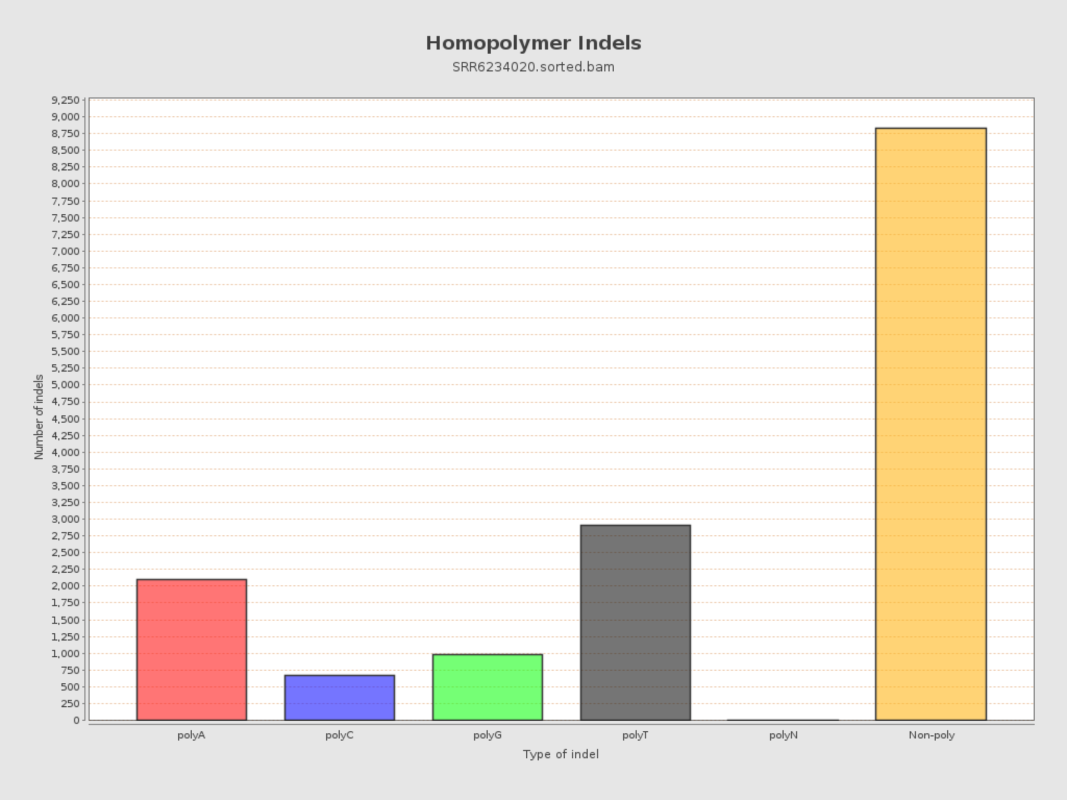
9. Results : Mapped Reads GC-content Distribution



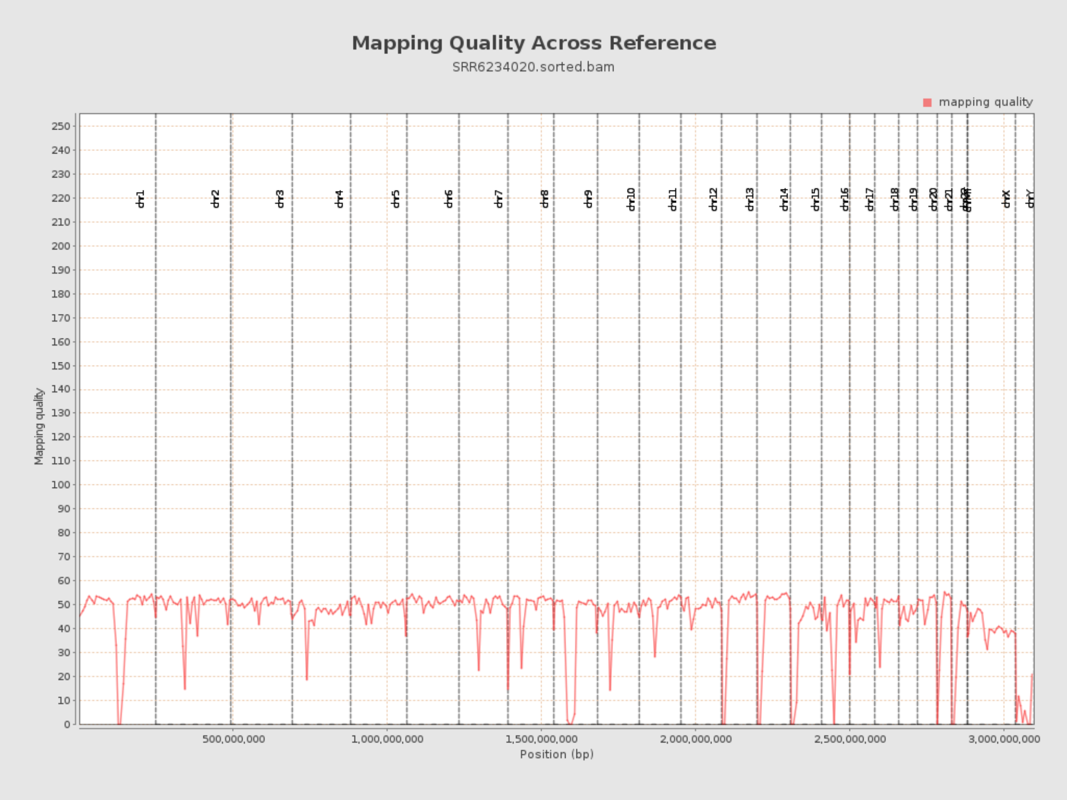
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram