Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 11:15:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234030.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_SRR6234030 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234030.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 11:15:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234030.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,179,282
Mapped reads	898,353 / 76.18%
Unmapped reads	280,929 / 23.82%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,479 / 0.3%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	30,943 / 2.62%
Duplication rate	2.91%
Clipped reads	374,726 / 31.78%

2.2. ACGT Content

Number/percentage of A's	16,683,354 / 27.92%
Number/percentage of C's	10,439,650 / 17.47%
Number/percentage of T's	19,526,116 / 32.67%
Number/percentage of G's	13,101,017 / 21.92%
Number/percentage of N's	11,096 / 0.02%
GC Percentage	39.39%

2.3. Coverage

Mean	0.0193

Standard Deviation	0.1898

2.4. Mapping Quality

Mean Mapping Quality	46.23

2.5. Mismatches and indels

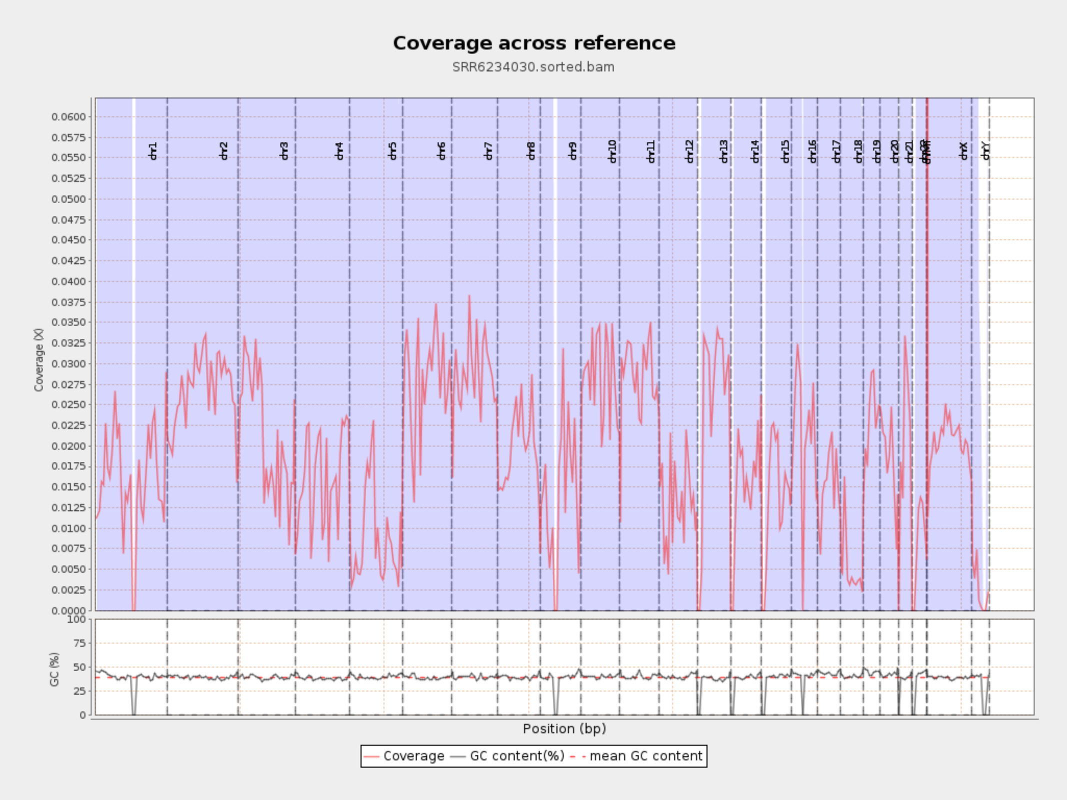
General error rate	0.79%
Mismatches	464,357
Insertions	4,886
Mapped reads with at least one insertion	0.54%
Deletions	16,377
Mapped reads with at least one deletion	1.8%
Homopolymer indels	47.27%

2.6. Chromosome stats

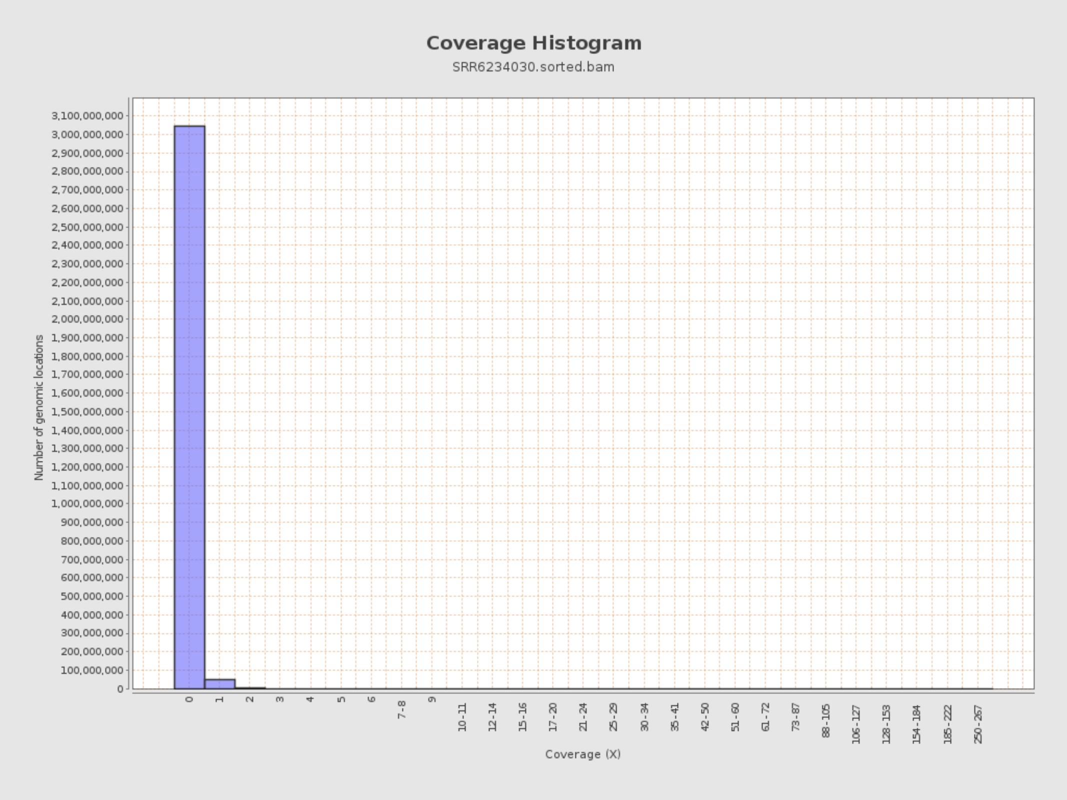
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3985437	0.016	0.2292
chr2	243199373	6590310	0.0271	0.2182
chr3	198022430	4224838	0.0213	0.1626
chr4	191154276	3038511	0.0159	0.1455
chr5	180915260	1598156	0.0088	0.1044
chr6	171115067	4806189	0.0281	0.203
chr7	159138663	4578361	0.0288	0.2924

chr8	146364022	2905613	0.0199	0.2279
chr9	141213431	1991366	0.0141	0.1494
chr10	135534747	3824752	0.0282	0.2059
chr11	135006516	3875124	0.0287	0.217
chr12	133851895	1739602	0.013	0.1286
chr13	115169878	2876808	0.025	0.1778
chr14	107349540	1562667	0.0146	0.1492
chr15	102531392	1411909	0.0138	0.1309
chr16	90354753	1908910	0.0211	0.1732
chr17	81195210	1212970	0.0149	0.1456
chr18	78077248	382647	0.0049	0.3054
chr19	59128983	1386386	0.0234	0.1964
chr20	63025520	1143254	0.0181	0.1543
chr21	48129895	966088	0.0201	0.1628
chr22	51304566	425491	0.0083	0.0997
chrMT	16571	23704	1.4305	1.6733
chrX	155270560	3180944	0.0205	0.1648
chrY	59373566	150056	0.0025	0.0761

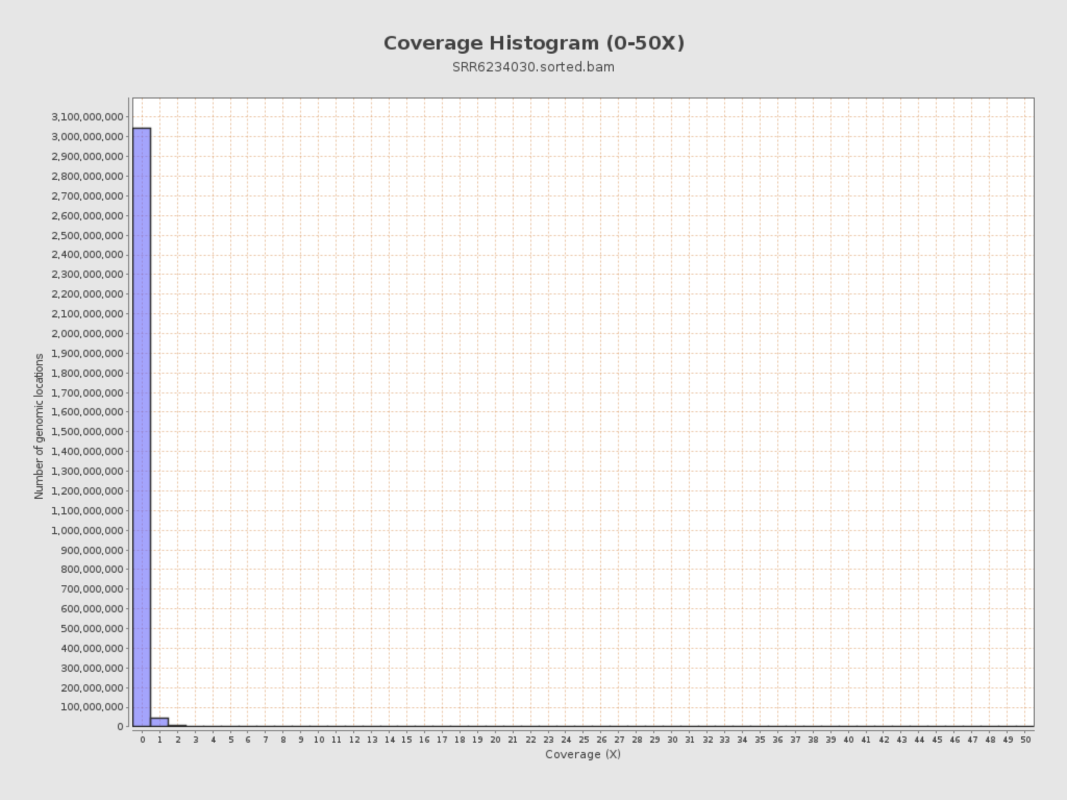
3. Results : Coverage across reference



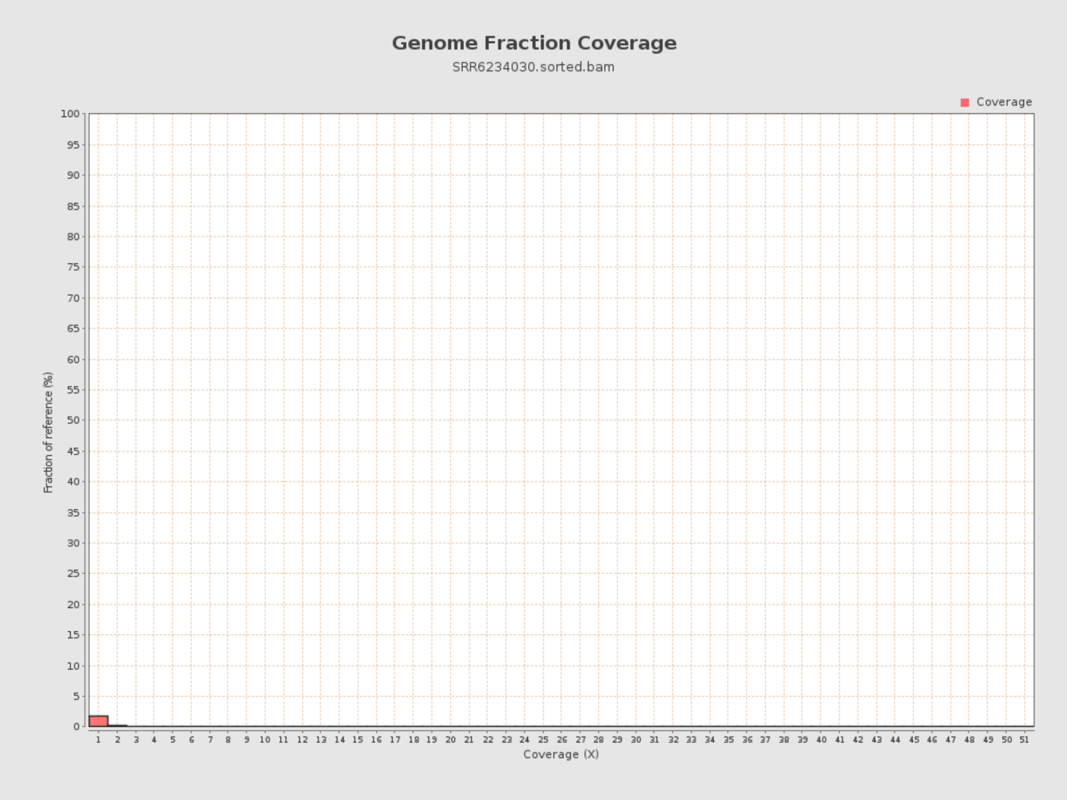
4. Results : Coverage Histogram



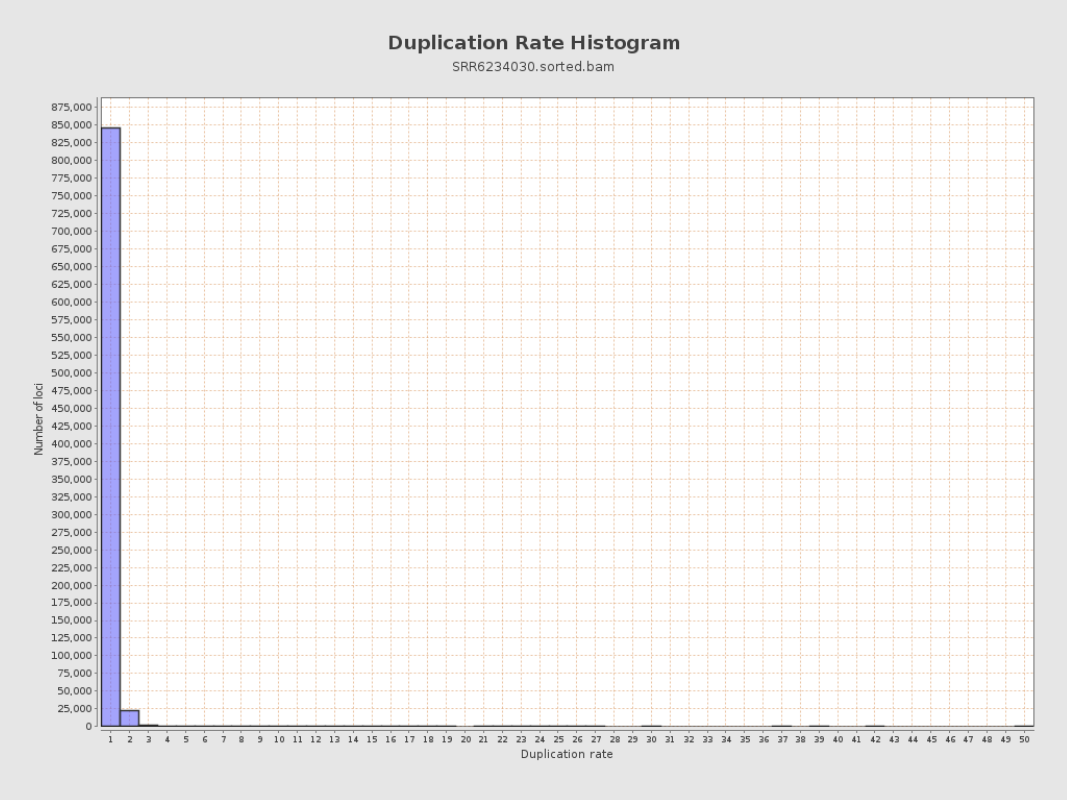
5. Results : Coverage Histogram (0-50X)



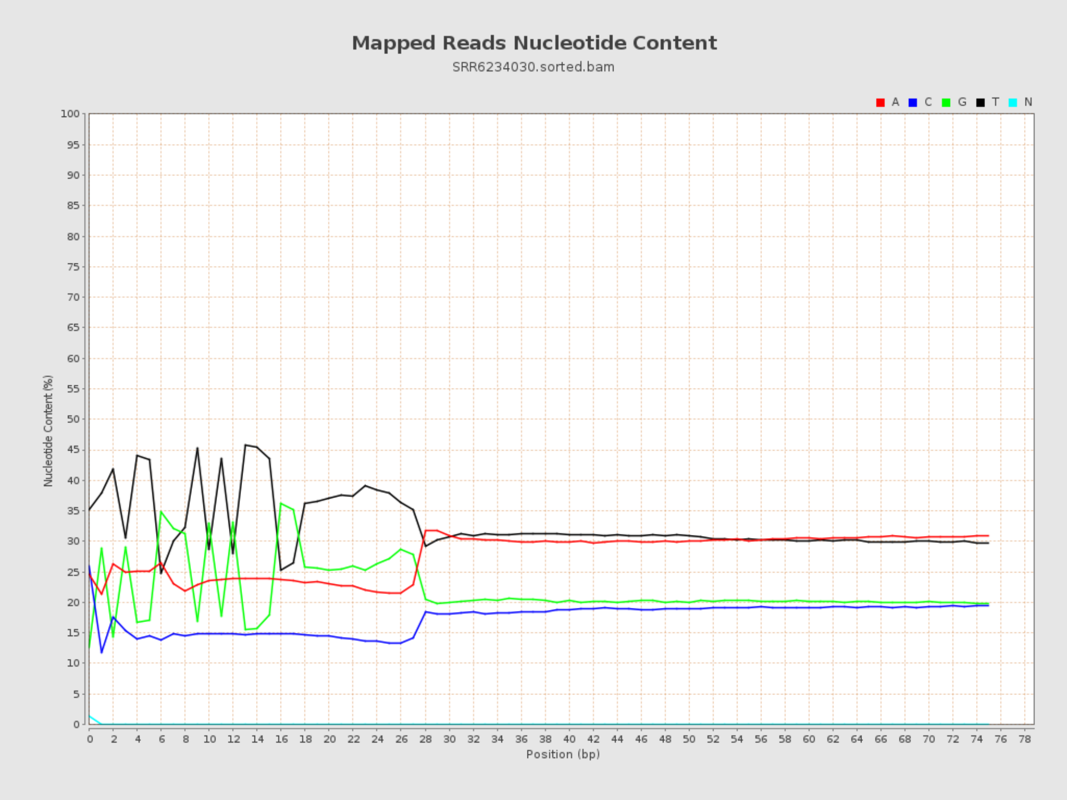
6. Results : Genome Fraction Coverage



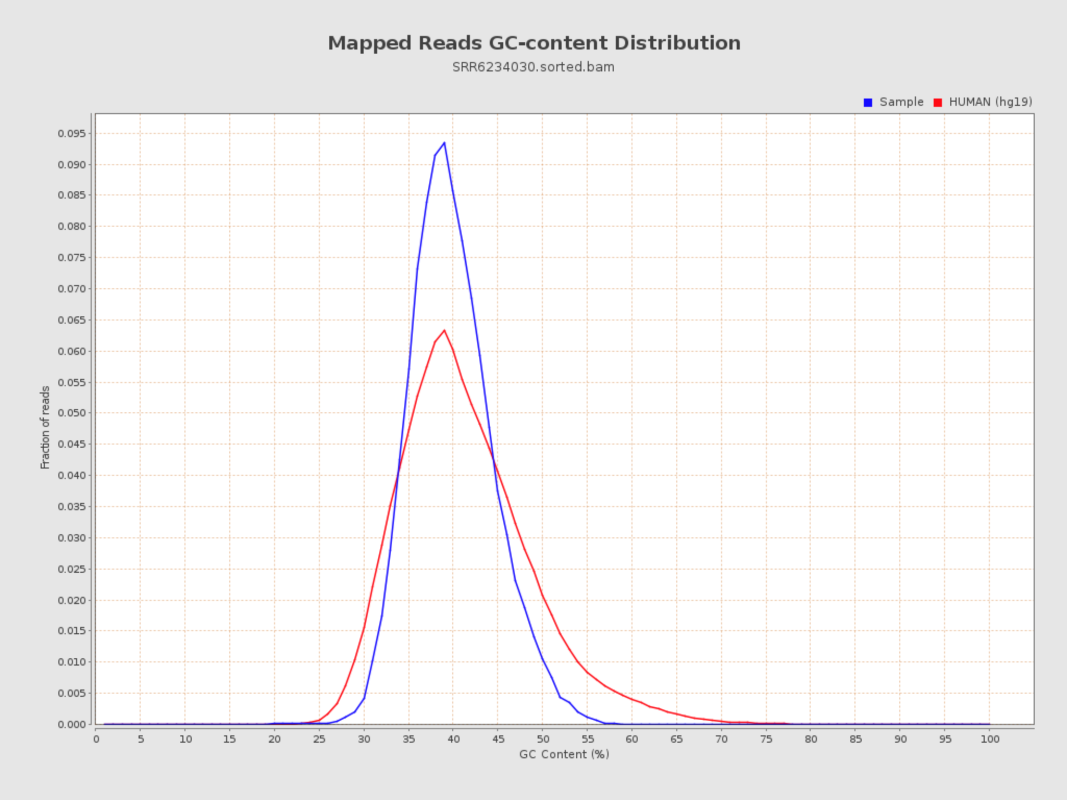
7. Results : Duplication Rate Histogram



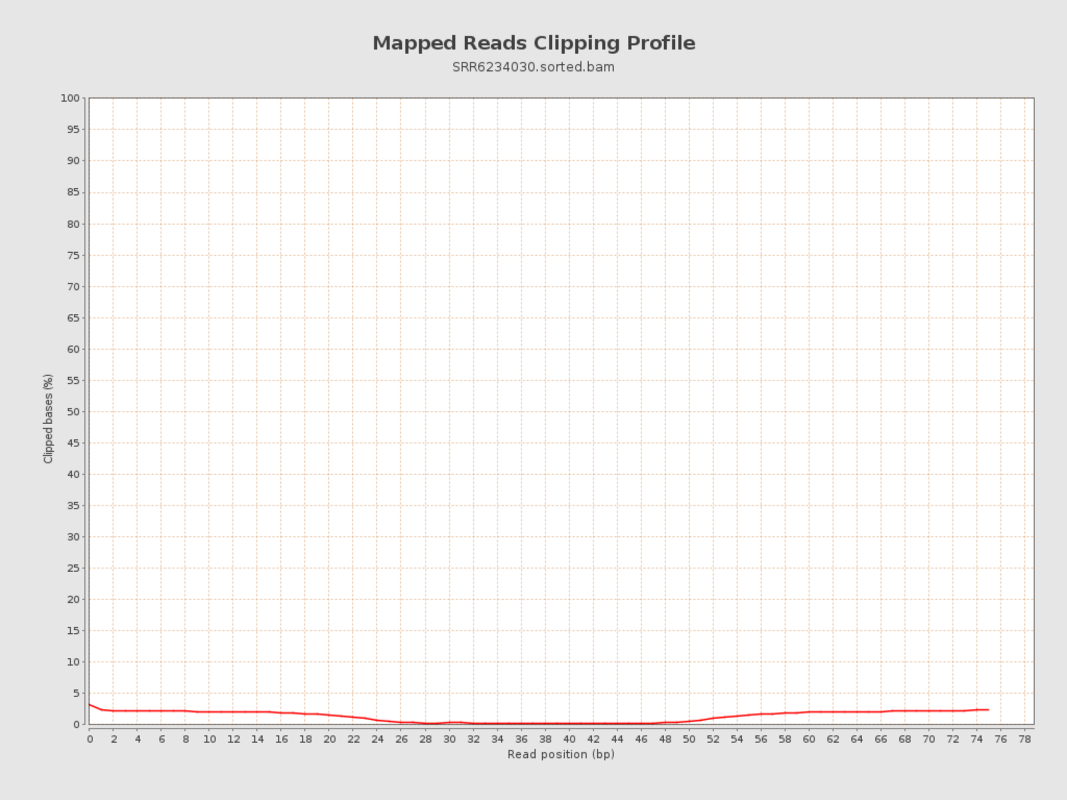
8. Results : Mapped Reads Nucleotide Content



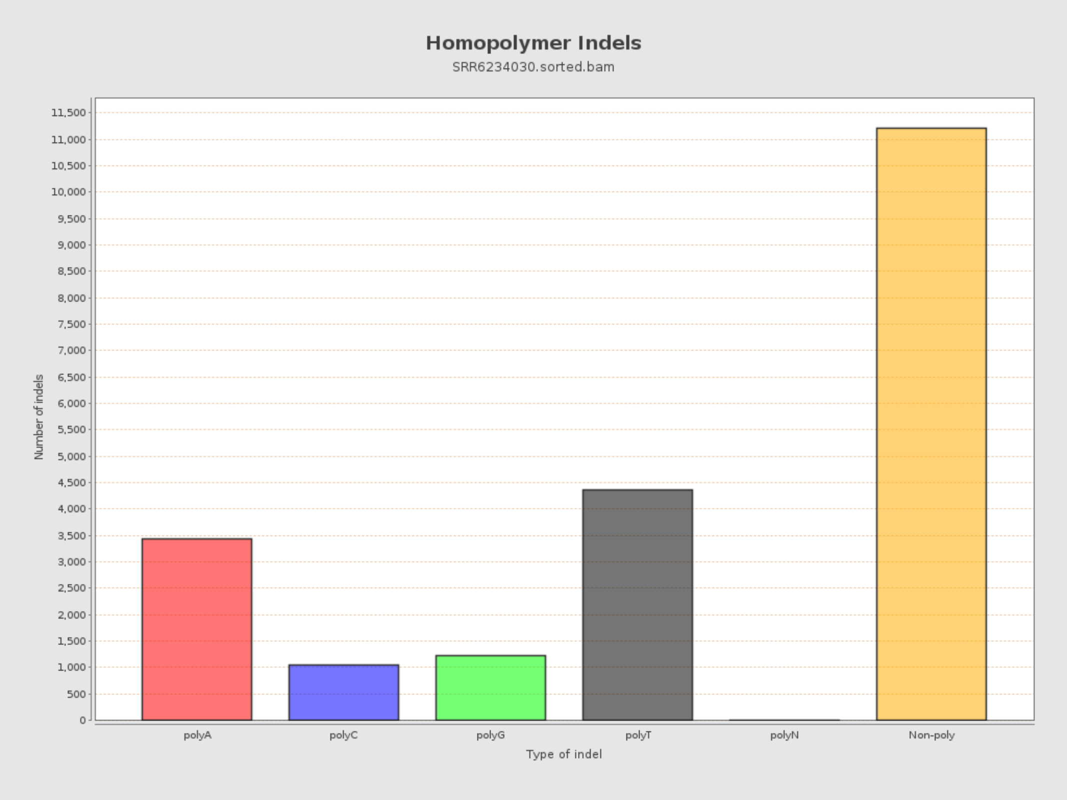
9. Results : Mapped Reads GC-content Distribution



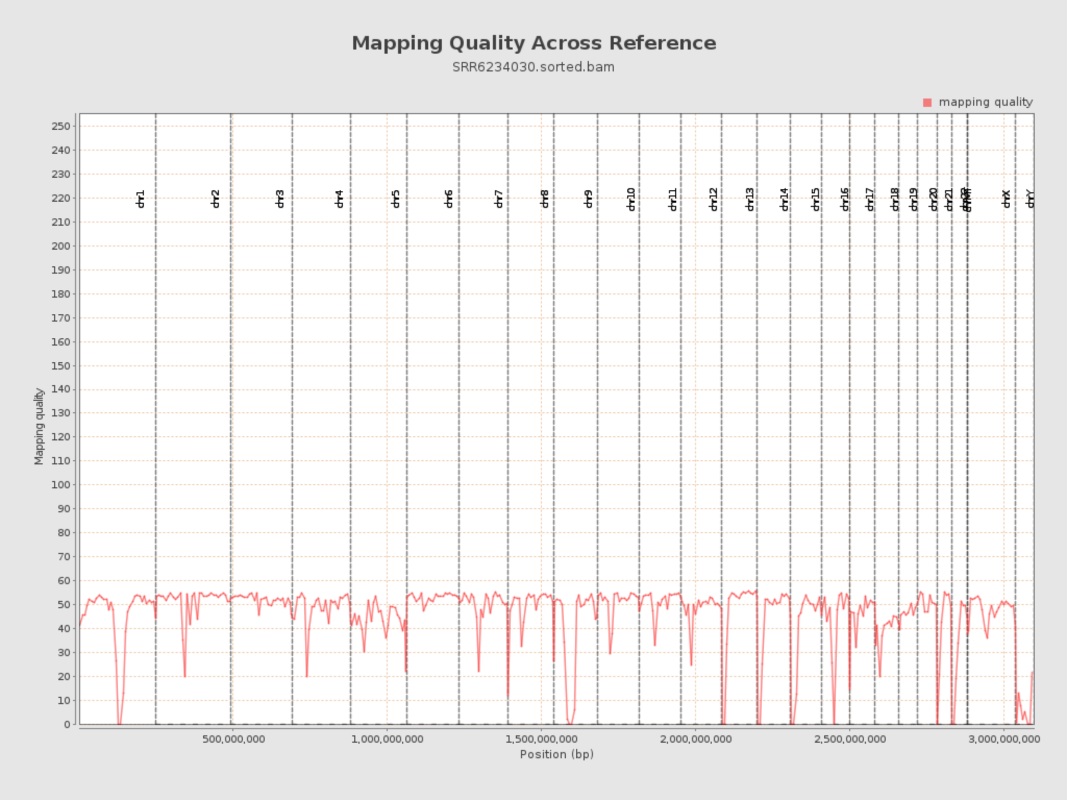
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram