Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 09:30:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231874.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_SRR6231874 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231874.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 09:30:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231874.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,720,455
Mapped reads	2,874,031 / 60.88%
Unmapped reads	1,846,424 / 39.12%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	21,992 / 0.47%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	149,209 / 3.16%
Duplication rate	2.54%
Clipped reads	1,579,988 / 33.47%

2.2. ACGT Content

Number/percentage of A's	53,118,228 / 28.8%
Number/percentage of C's	37,374,985 / 20.27%
Number/percentage of T's	52,105,903 / 28.25%
Number/percentage of G's	41,803,799 / 22.67%
Number/percentage of N's	13,724 / 0.01%
GC Percentage	42.93%

2.3. Coverage

Mean	0.0596

Standard Deviation	4.6431

2.4. Mapping Quality

Mean Mapping Quality	42.13

2.5. Mismatches and indels

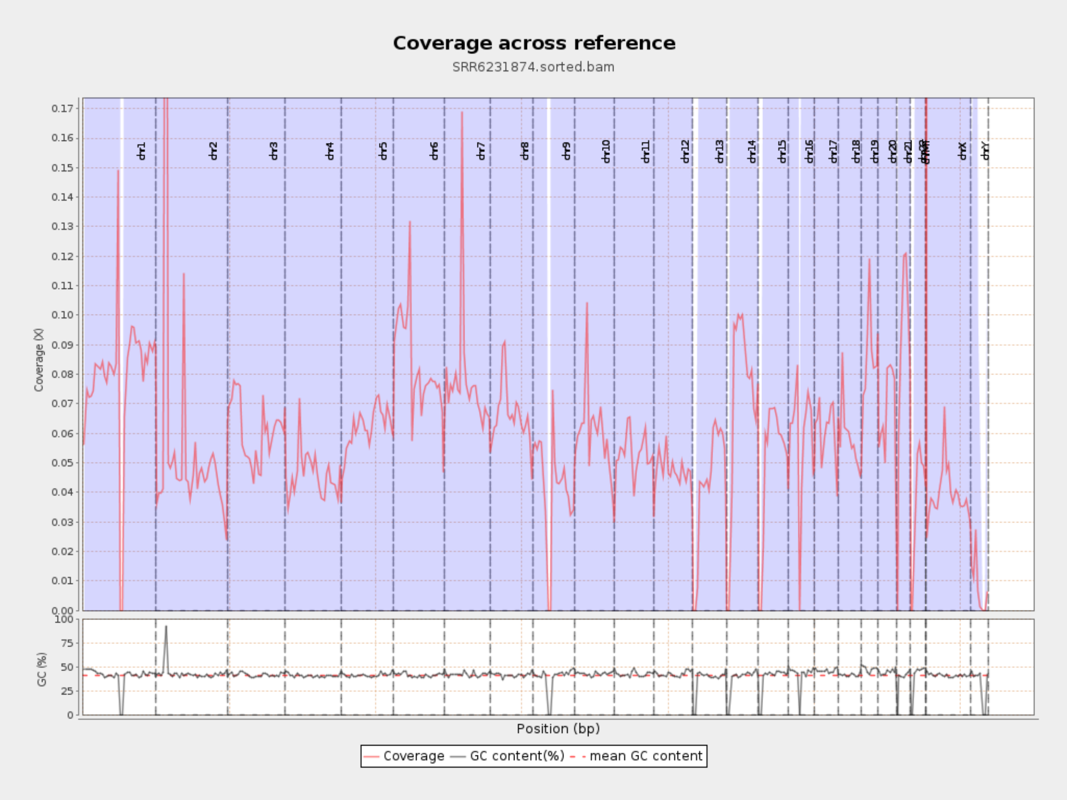
General error rate	0.67%
Mismatches	1,217,183
Insertions	13,952
Mapped reads with at least one insertion	0.48%
Deletions	41,612
Mapped reads with at least one deletion	1.43%
Homopolymer indels	43.85%

2.6. Chromosome stats

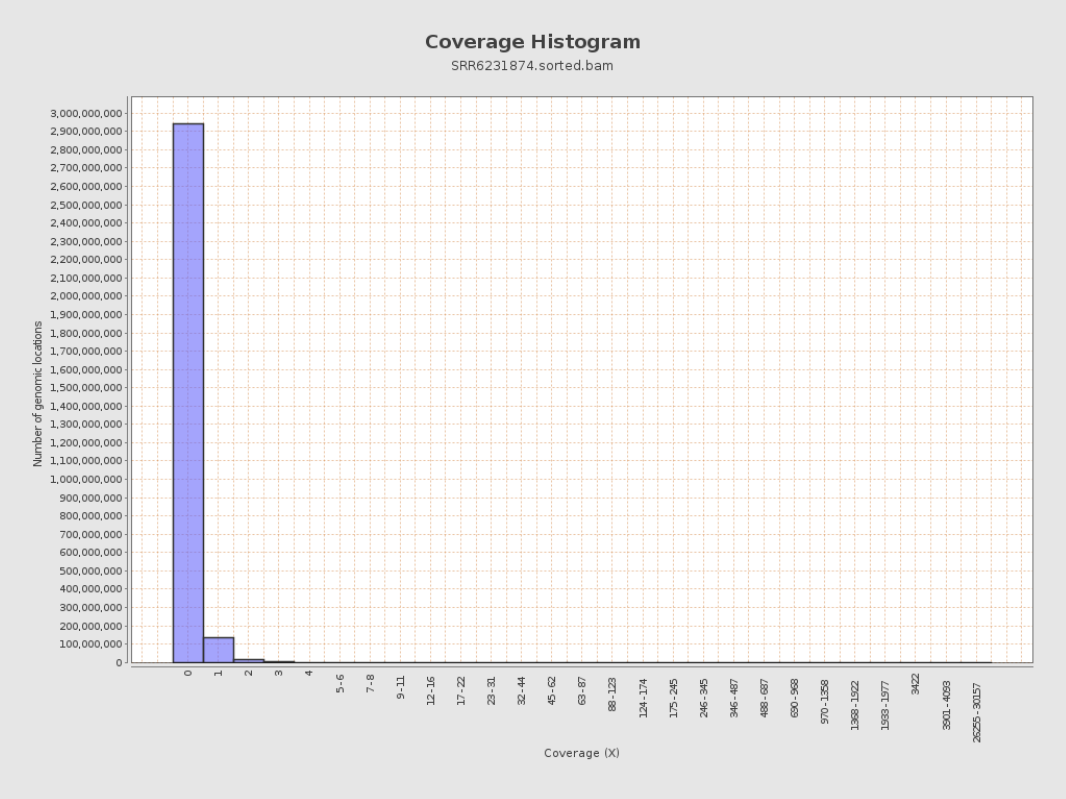
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	19808516	0.0795	1.6582
chr2	243199373	13772061	0.0566	16.3771
chr3	198022430	12081783	0.061	0.2801
chr4	191154276	8813798	0.0461	0.2682
chr5	180915260	11169239	0.0617	0.2919
chr6	171115067	14337516	0.0838	0.4794
chr7	159138663	12384579	0.0778	1.2321

chr8	146364022	9701968	0.0663	0.9797
chr9	141213431	5940347	0.0421	0.5074
chr10	135534747	8179337	0.0603	0.5301
chr11	135006516	7172094	0.0531	0.5409
chr12	133851895	6371095	0.0476	0.2616
chr13	115169878	4962915	0.0431	0.2327
chr14	107349540	7748029	0.0722	0.3765
chr15	102531392	5096496	0.0497	0.2578
chr16	90354753	5154553	0.057	0.3237
chr17	81195210	5007473	0.0617	0.3491
chr18	78077248	4615893	0.0591	1.1205
chr19	59128983	5082629	0.086	0.9885
chr20	63025520	4321216	0.0686	0.3161
chr21	48129895	4209052	0.0875	0.3634
chr22	51304566	1864827	0.0363	0.2127
chrMT	16571	84784	5.1164	3.7825
chrX	155270560	6118069	0.0394	0.3118
chrY	59373566	486216	0.0082	0.1767

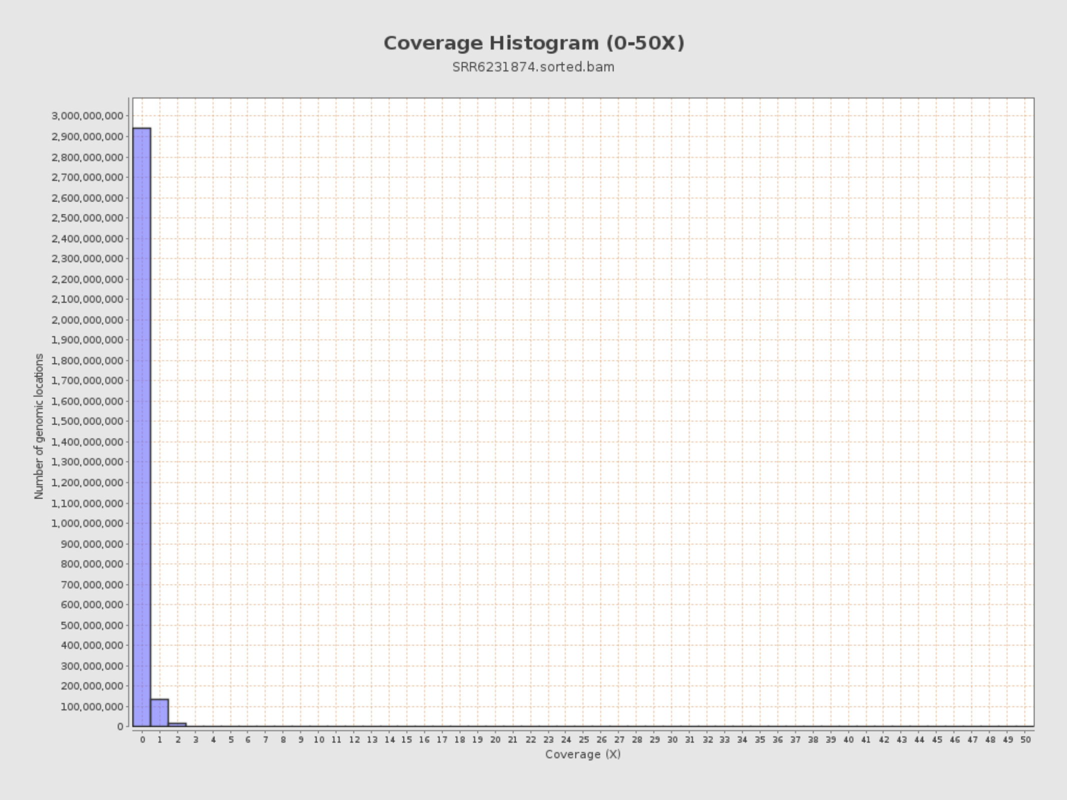
3. Results : Coverage across reference



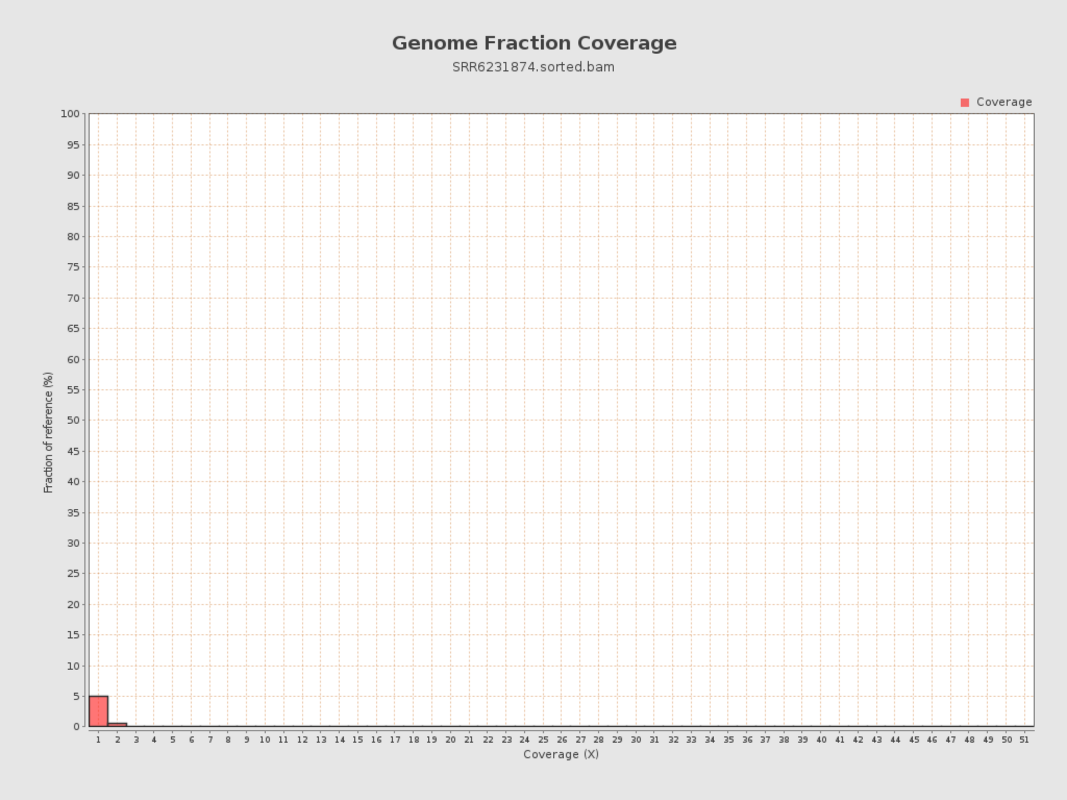
4. Results : Coverage Histogram



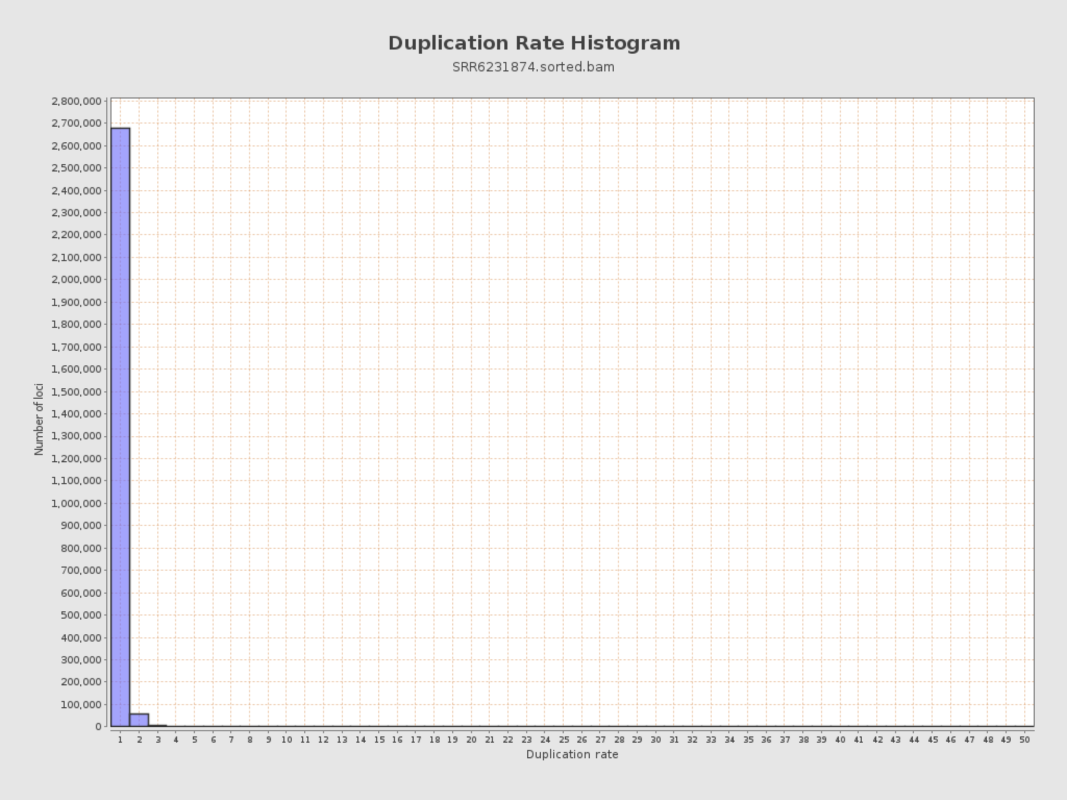
5. Results : Coverage Histogram (0-50X)



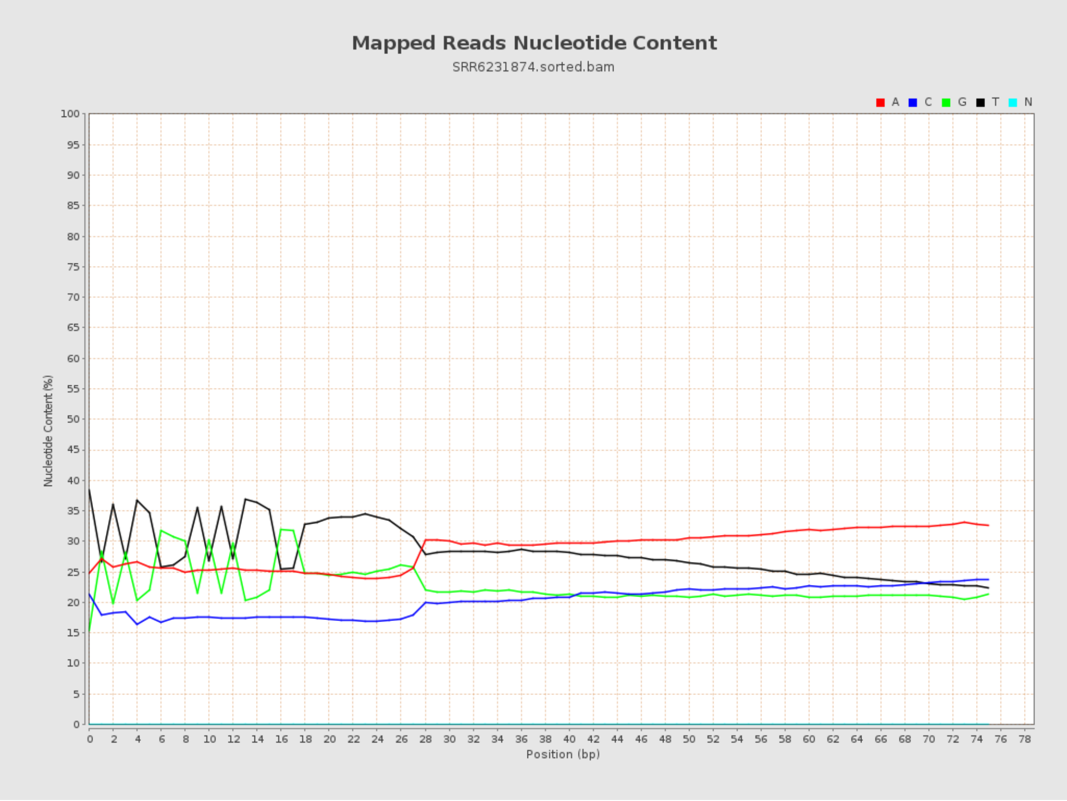
6. Results : Genome Fraction Coverage



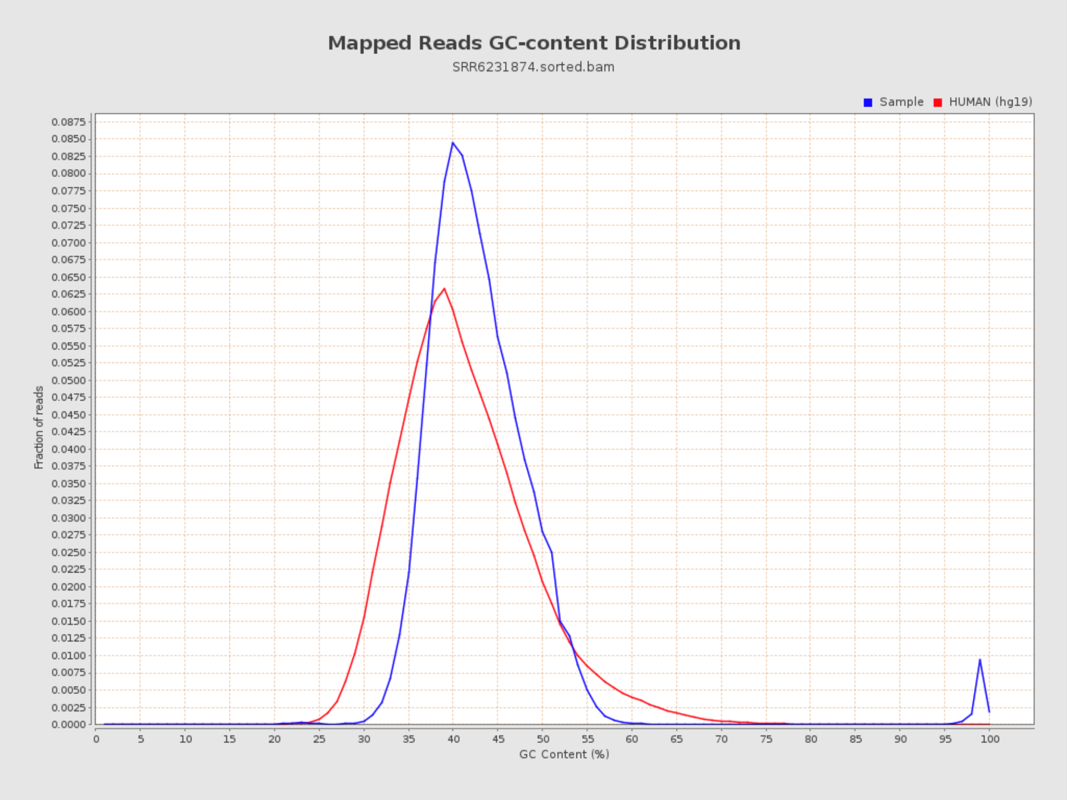
7. Results : Duplication Rate Histogram



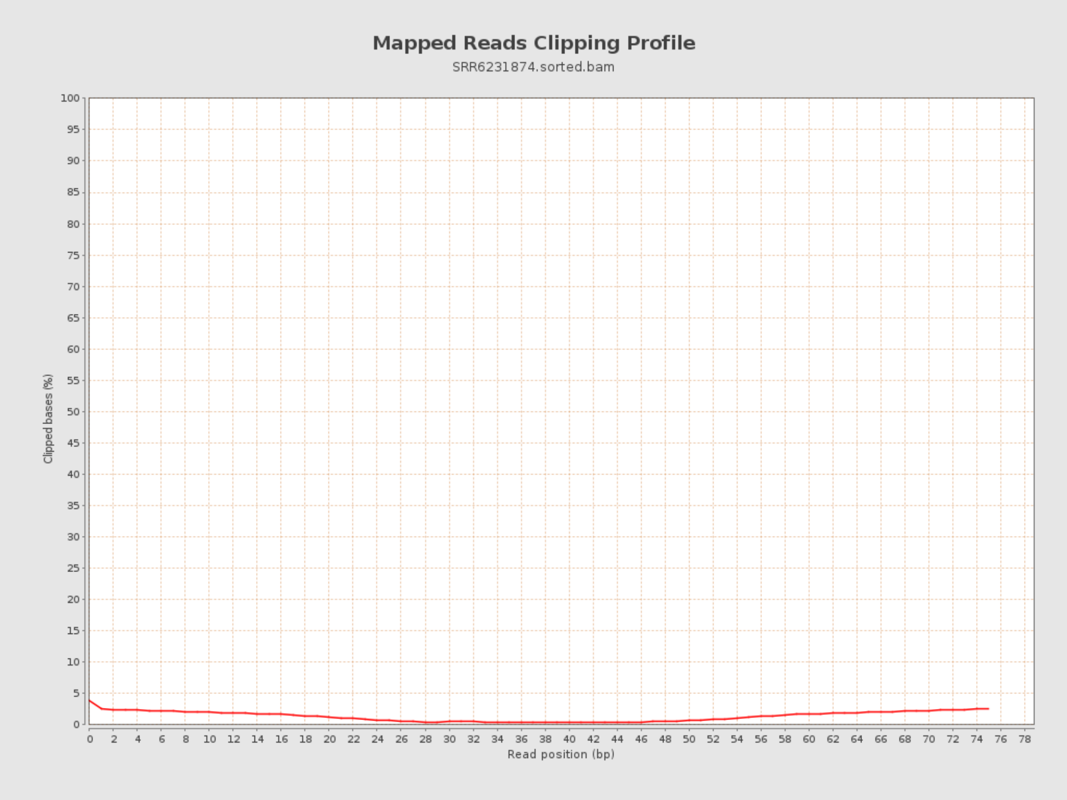
8. Results : Mapped Reads Nucleotide Content



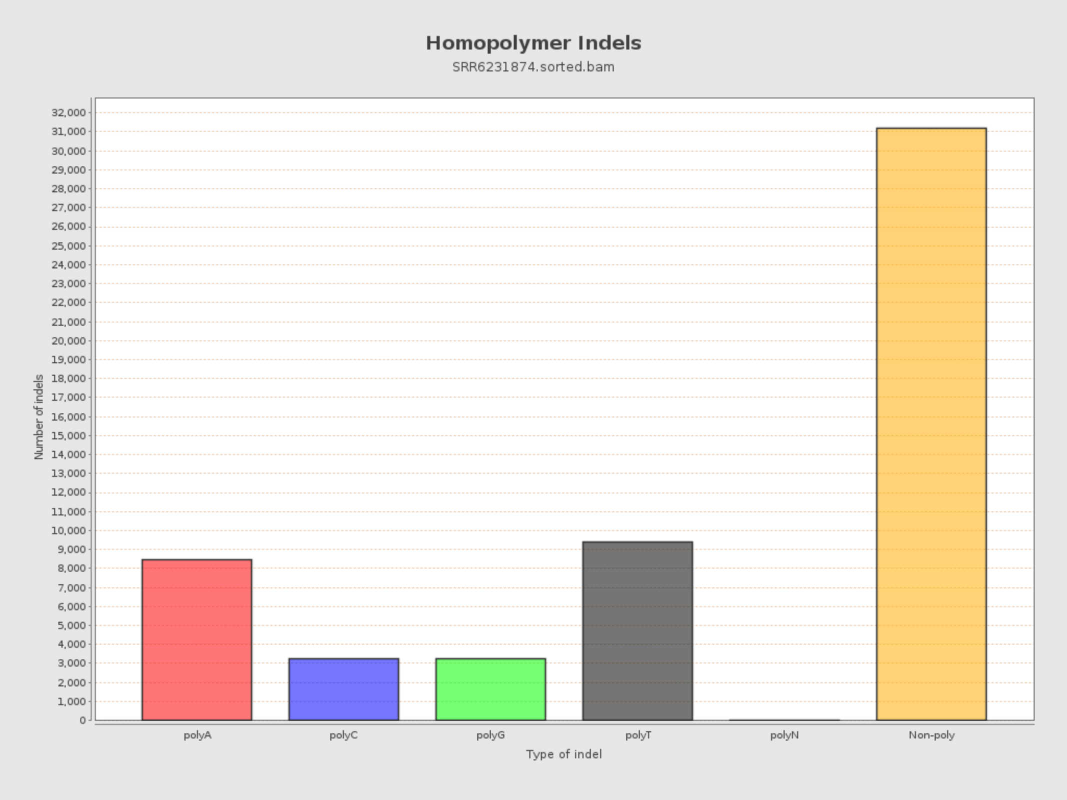
9. Results : Mapped Reads GC-content Distribution



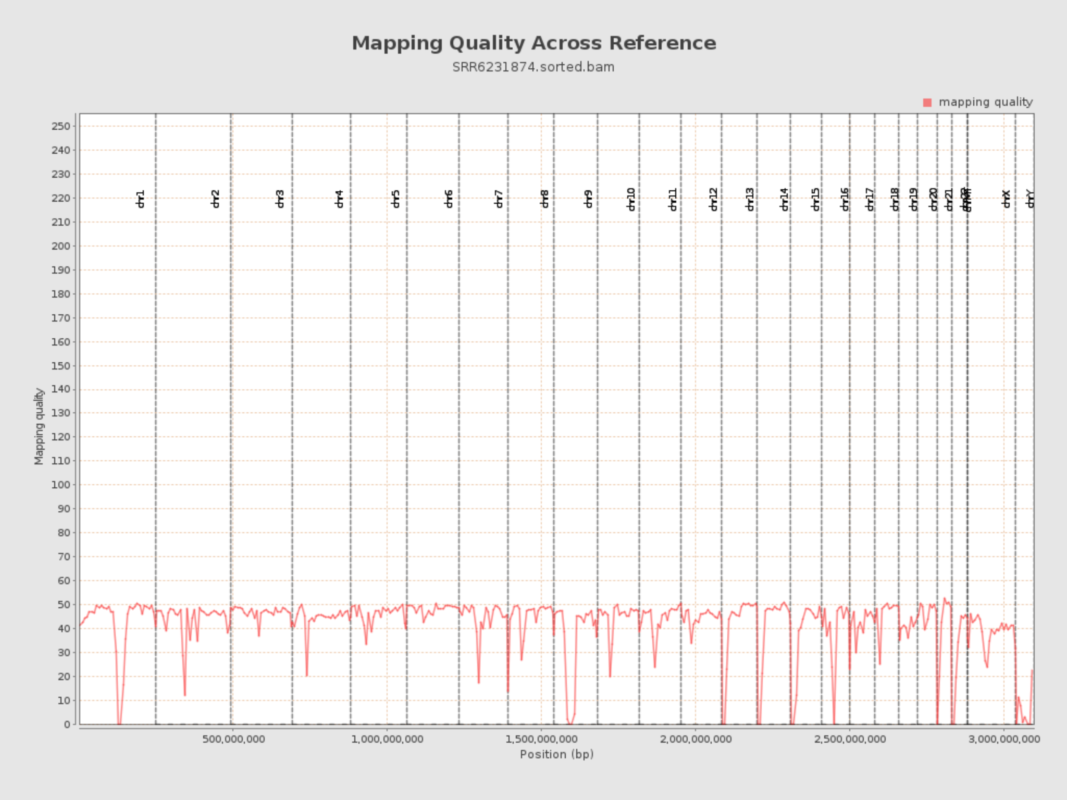
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram