

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 22:25:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231726.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_SRR6231726 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231726.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 22:25:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231726.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,533,045
Mapped reads	5,164,275 / 93.34%
Unmapped reads	368,770 / 6.66%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	44,129 / 0.8%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	601,786 / 10.88%
Duplication rate	5.38%
Clipped reads	2,025,079 / 36.6%

2.2. ACGT Content

Number/percentage of A's	92,832,294 / 26.46%
Number/percentage of C's	63,776,294 / 18.18%
Number/percentage of T's	101,439,356 / 28.91%
Number/percentage of G's	92,755,375 / 26.44%
Number/percentage of N's	76,506 / 0.02%
GC Percentage	44.61%

2.3. Coverage

Mean	0.1134

Standard Deviation	38.3236
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2.4. Mapping Quality

Mean Mapping Quality	45.5
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2.5. Mismatches and indels

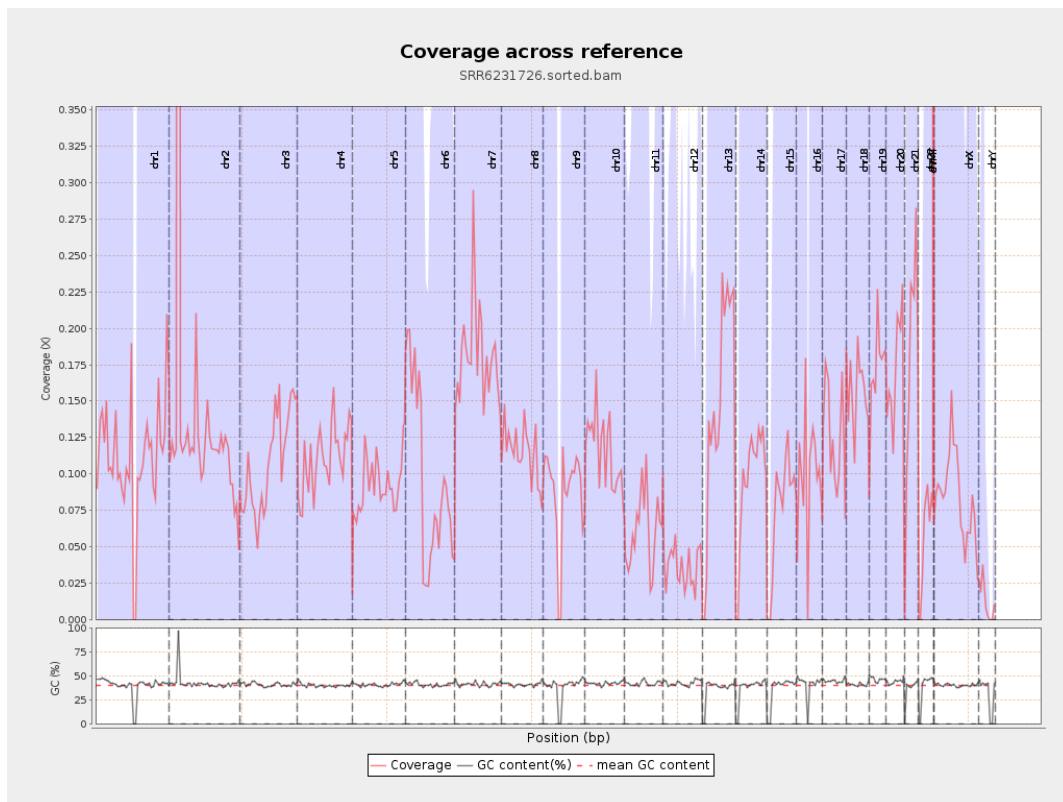
General error rate	0.67%
Mismatches	2,298,612
Insertions	23,635
Mapped reads with at least one insertion	0.45%
Deletions	79,469
Mapped reads with at least one deletion	1.52%
Homopolymer indels	46.3%

2.6. Chromosome stats

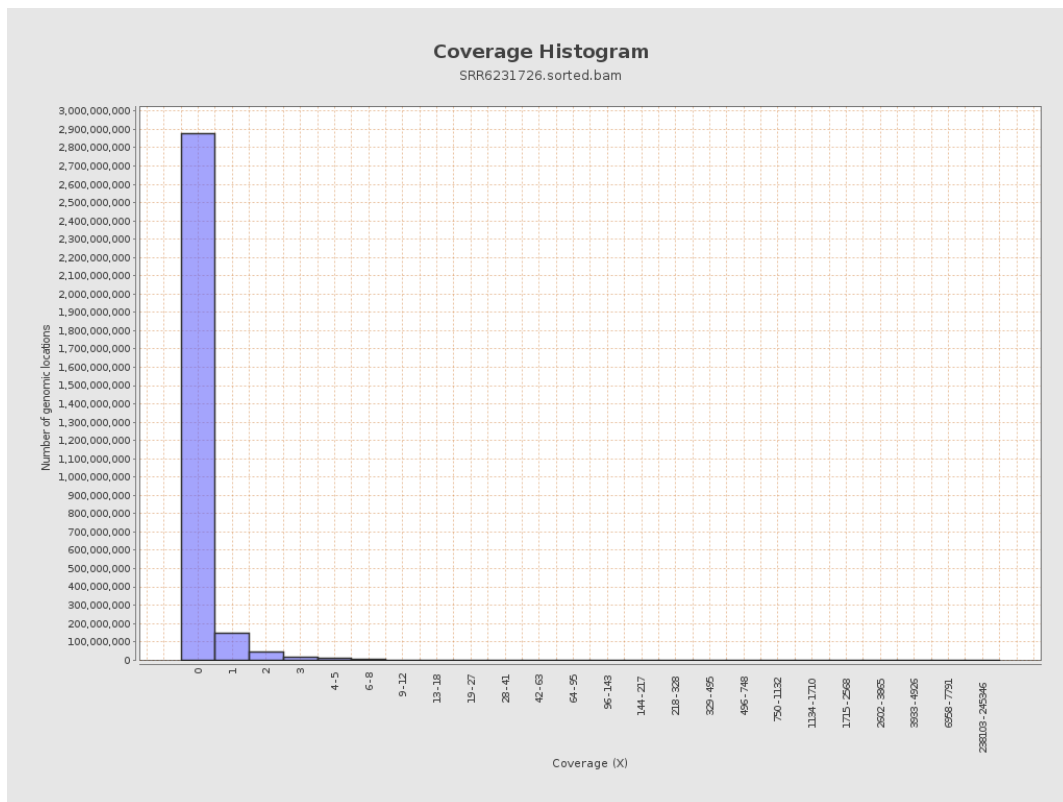
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	27793472	0.1115	1.8322
chr2	243199373	47636980	0.1959	136.6915
chr3	198022430	21407819	0.1081	0.4628
chr4	191154276	21351185	0.1117	0.4887
chr5	180915260	16811992	0.0929	0.4378
chr6	171115067	16725280	0.0977	0.5611
chr7	159138663	29150805	0.1832	2.0934

chr8	146364022	16793807	0.1147	0.9592
chr9	141213431	12206230	0.0864	0.7349
chr10	135534747	15787925	0.1165	0.7143
chr11	135006516	8273275	0.0613	0.6146
chr12	133851895	4784507	0.0357	0.2859
chr13	115169878	16847195	0.1463	0.548
chr14	107349540	10176280	0.0948	0.5703
chr15	102531392	7779735	0.0759	0.3887
chr16	90354753	8936097	0.0989	0.5168
chr17	81195210	10034070	0.1236	0.623
chr18	78077248	12259239	0.157	1.4265
chr19	59128983	10339679	0.1749	1.2979
chr20	63025520	10552438	0.1674	0.615
chr21	48129895	8381512	0.1741	0.6436
chr22	51304566	2871341	0.056	0.3302
chrMT	16571	327601	19.7695	12.8316
chrX	155270560	13075241	0.0842	0.5284
chrY	59373566	707857	0.0119	0.2227

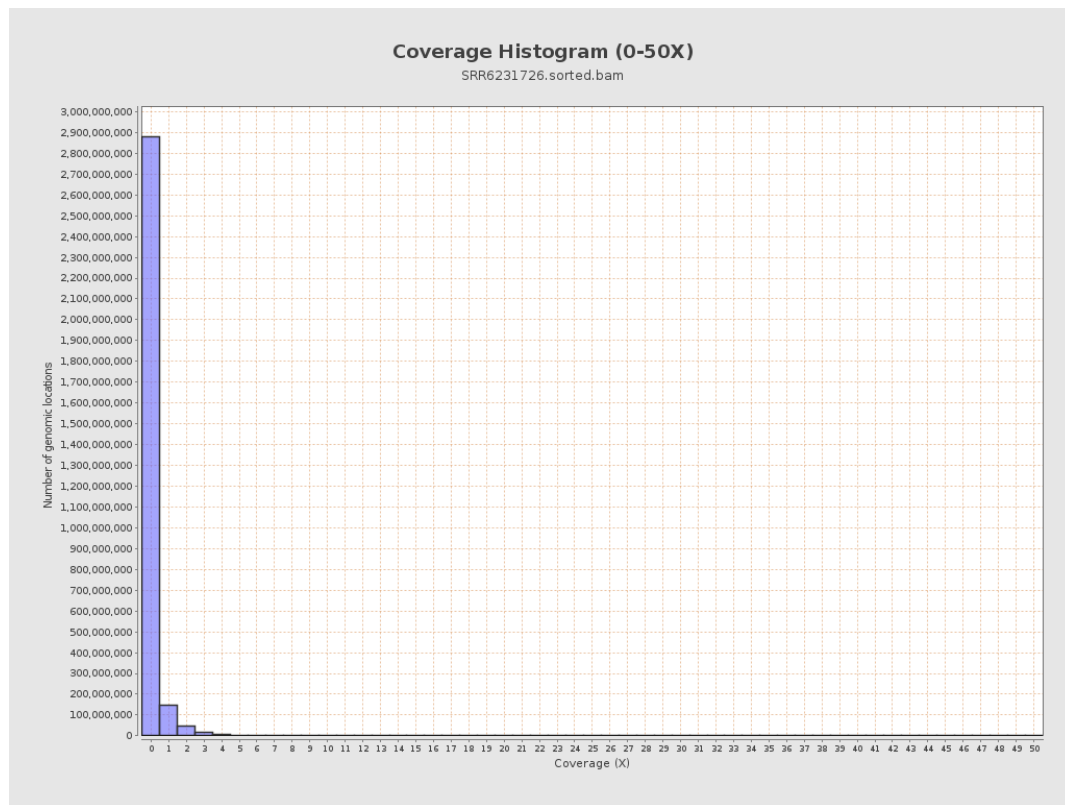
3. Results : Coverage across reference



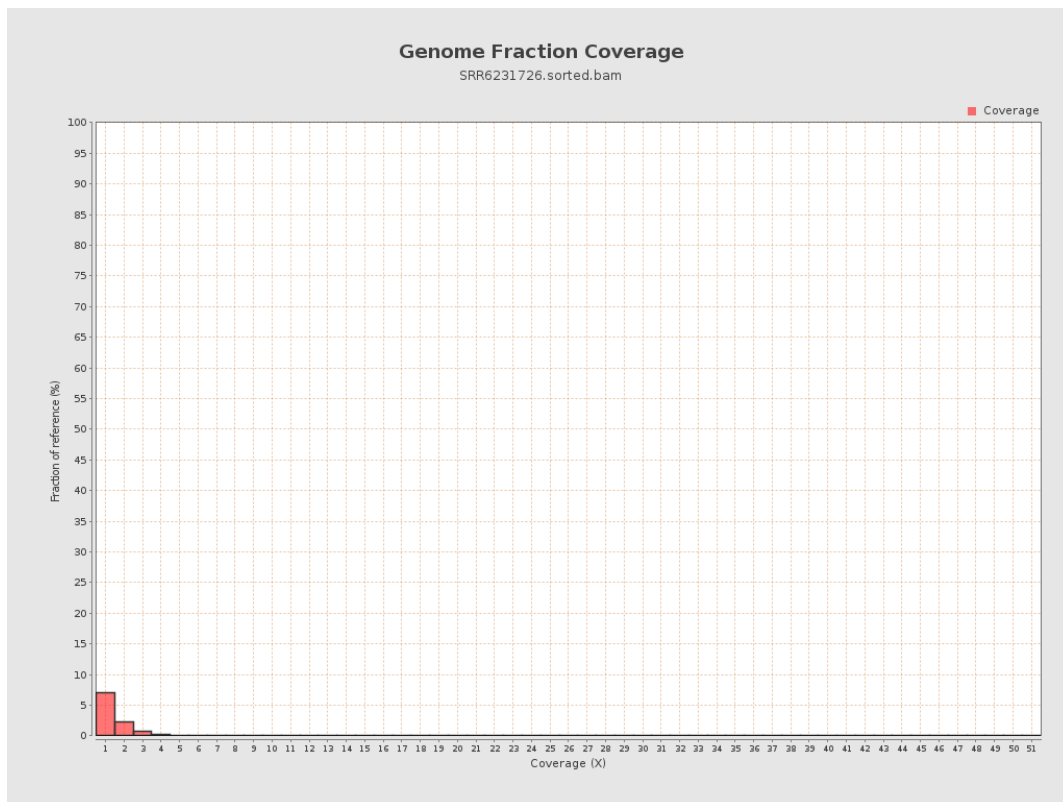
4. Results : Coverage Histogram



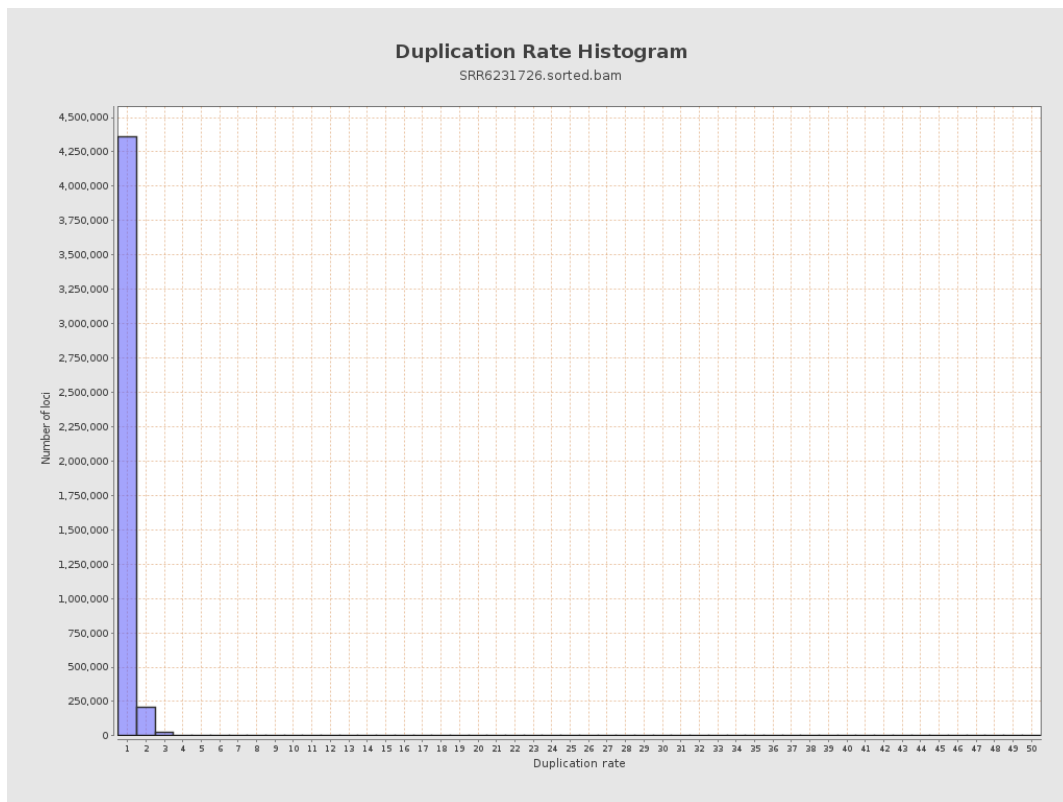
5. Results : Coverage Histogram (0-50X)



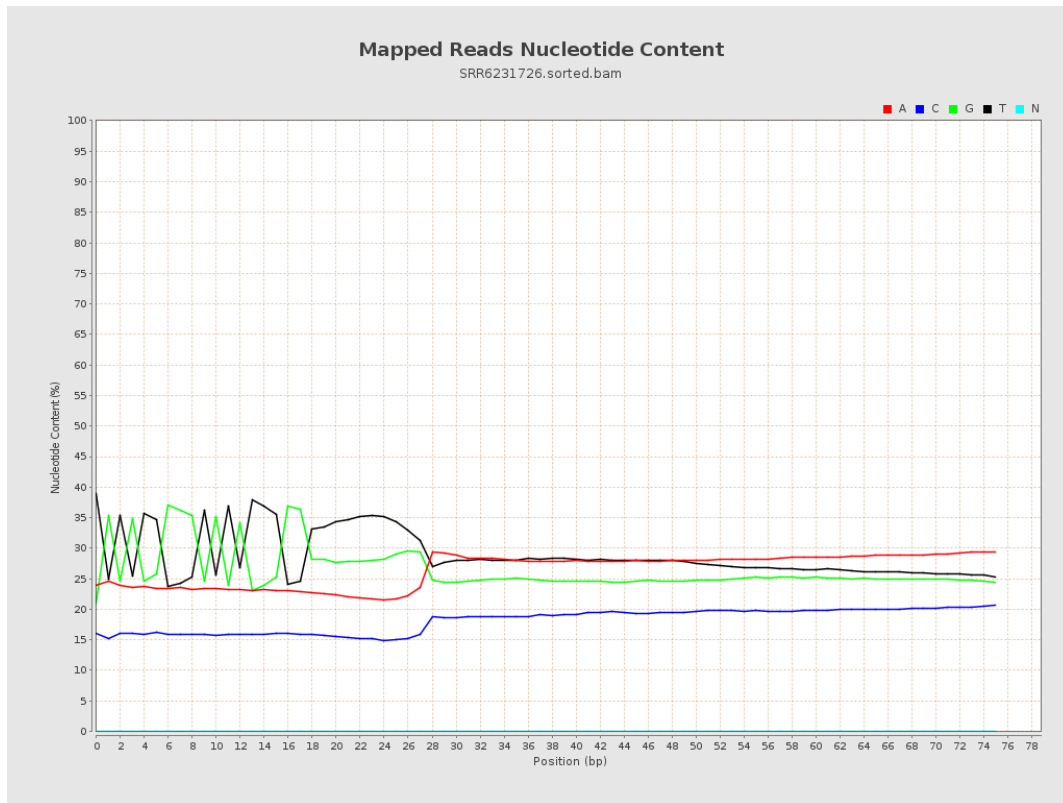
6. Results : Genome Fraction Coverage



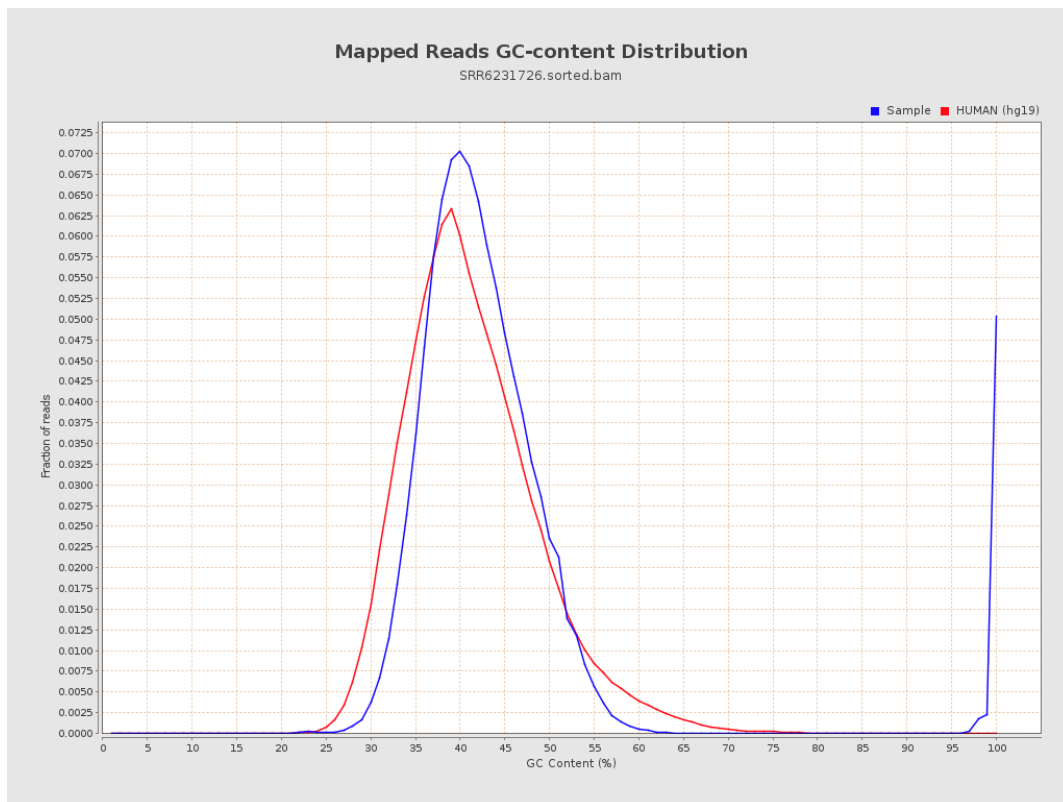
7. Results : Duplication Rate Histogram



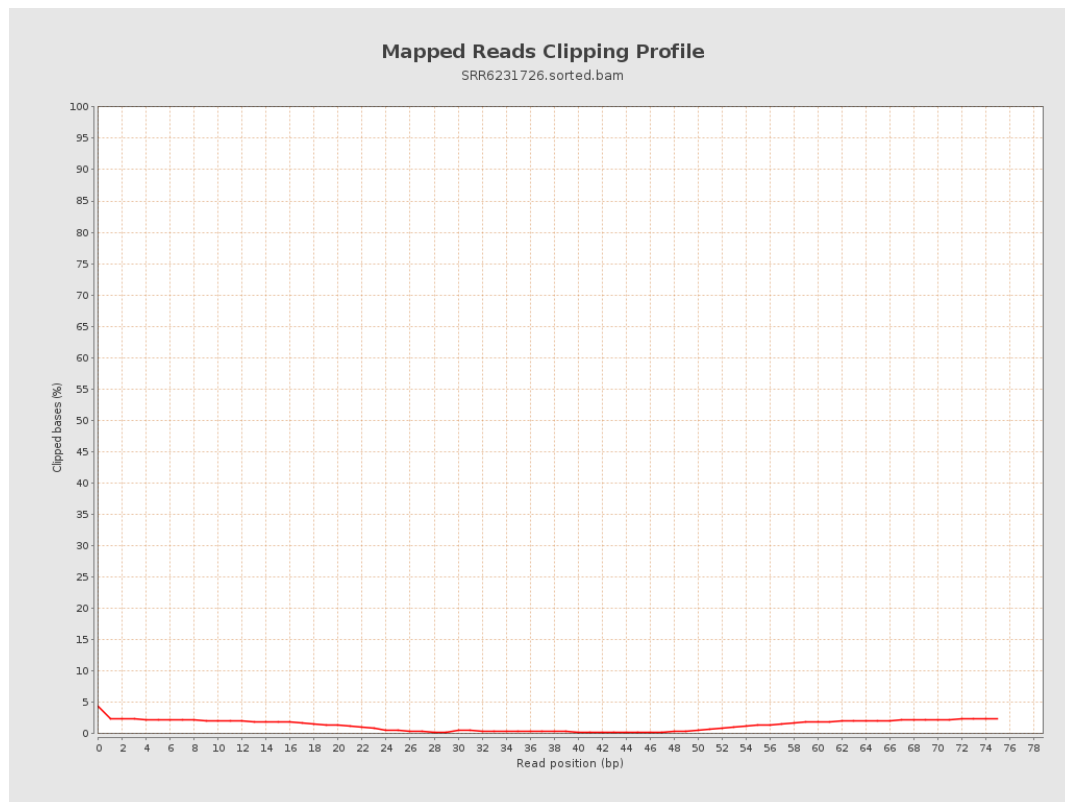
8. Results : Mapped Reads Nucleotide Content



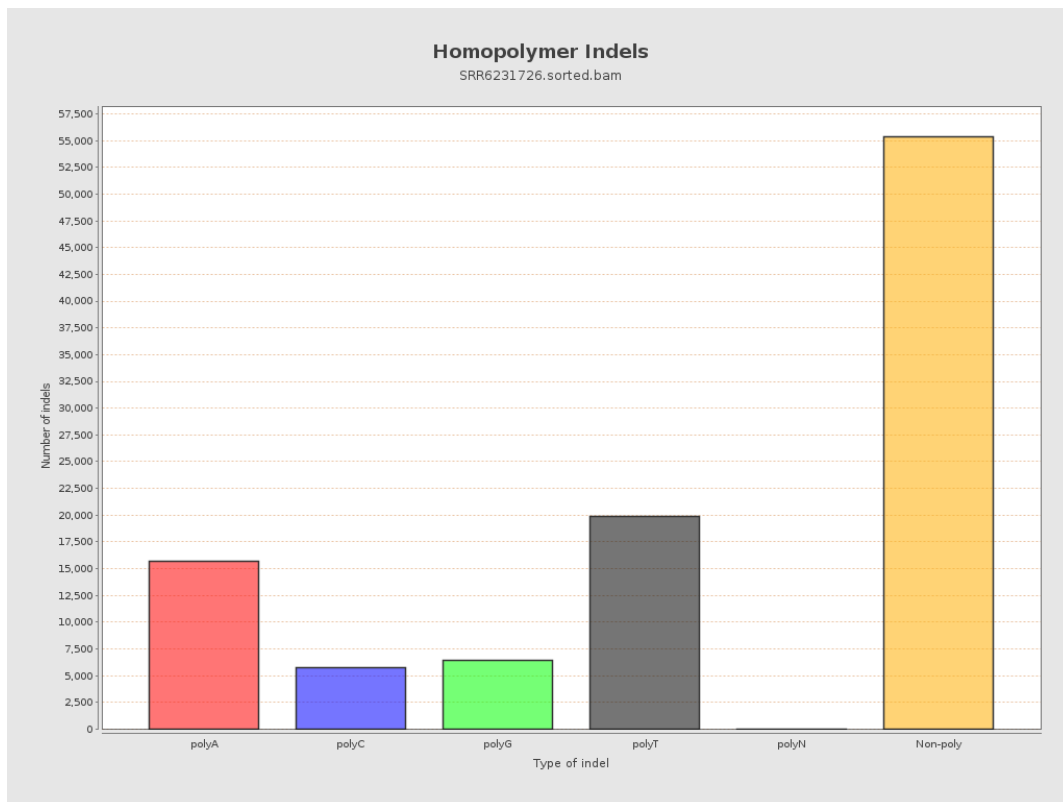
9. Results : Mapped Reads GC-content Distribution



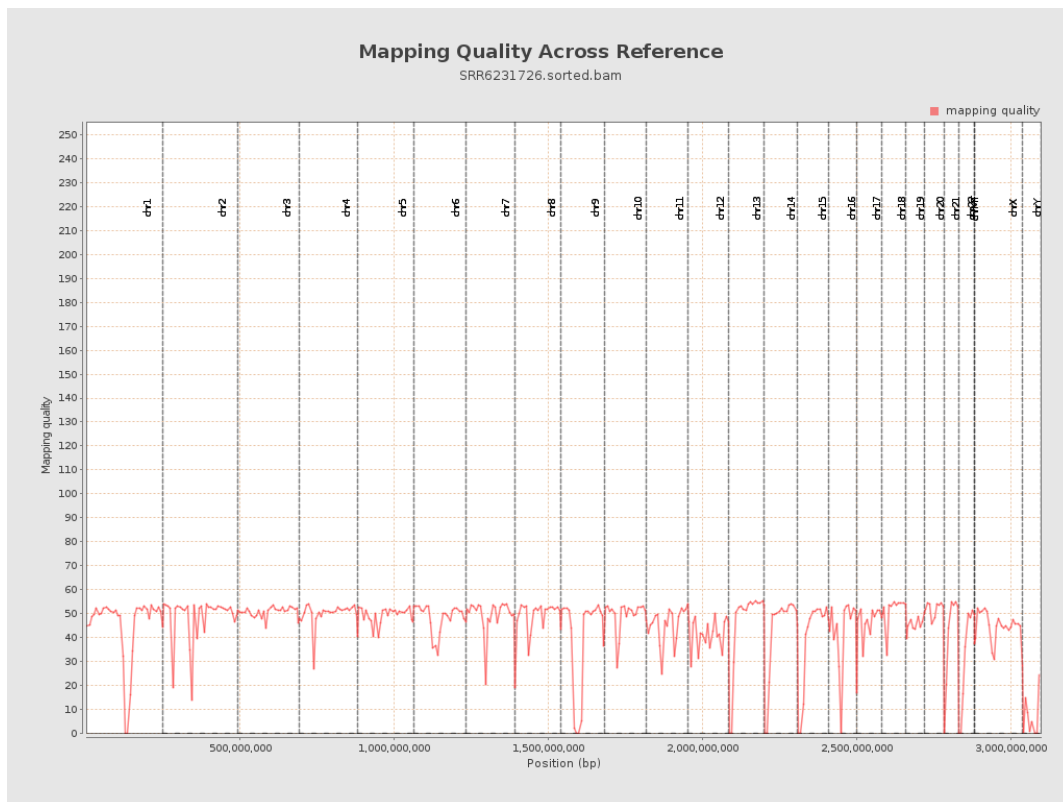
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

