Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 20:18:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6230376.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_SRR6230376 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6230376.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 20:18:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6230376.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,290,046
Mapped reads	1,486,352 / 64.9%
Unmapped reads	803,694 / 35.1%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,658 / 0.55%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	423,641 / 18.5%
Duplication rate	15.09%
Clipped reads	886,468 / 38.71%

2.2. ACGT Content

Number/percentage of A's	25,055,198 / 26.9%
Number/percentage of C's	16,781,164 / 18.02%
Number/percentage of T's	29,943,124 / 32.15%
Number/percentage of G's	21,313,239 / 22.88%
Number/percentage of N's	49,908 / 0.05%
GC Percentage	40.9%

2.3. Coverage

Mean	0.0301

Standard Deviation	0.5894

2.4. Mapping Quality

Mean Mapping Quality	45.16

2.5. Mismatches and indels

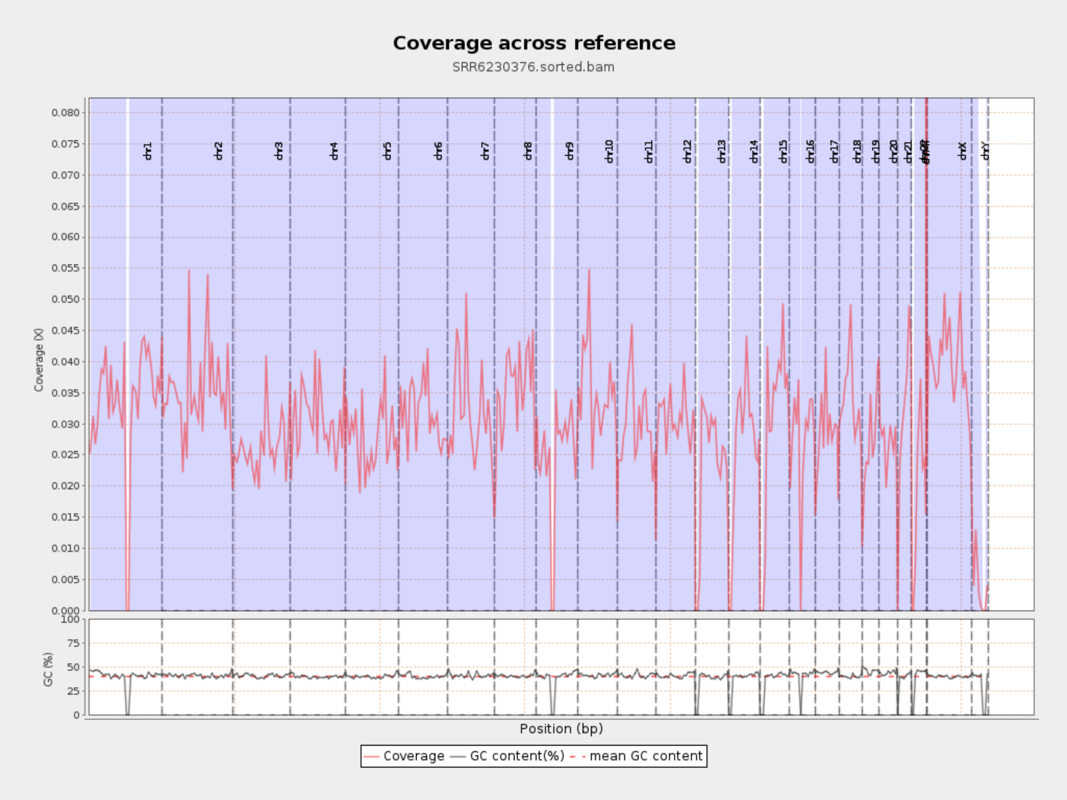
General error rate	0.96%
Mismatches	878,590
Insertions	7,302
Mapped reads with at least one insertion	0.49%
Deletions	27,245
Mapped reads with at least one deletion	1.81%
Homopolymer indels	47.58%

2.6. Chromosome stats

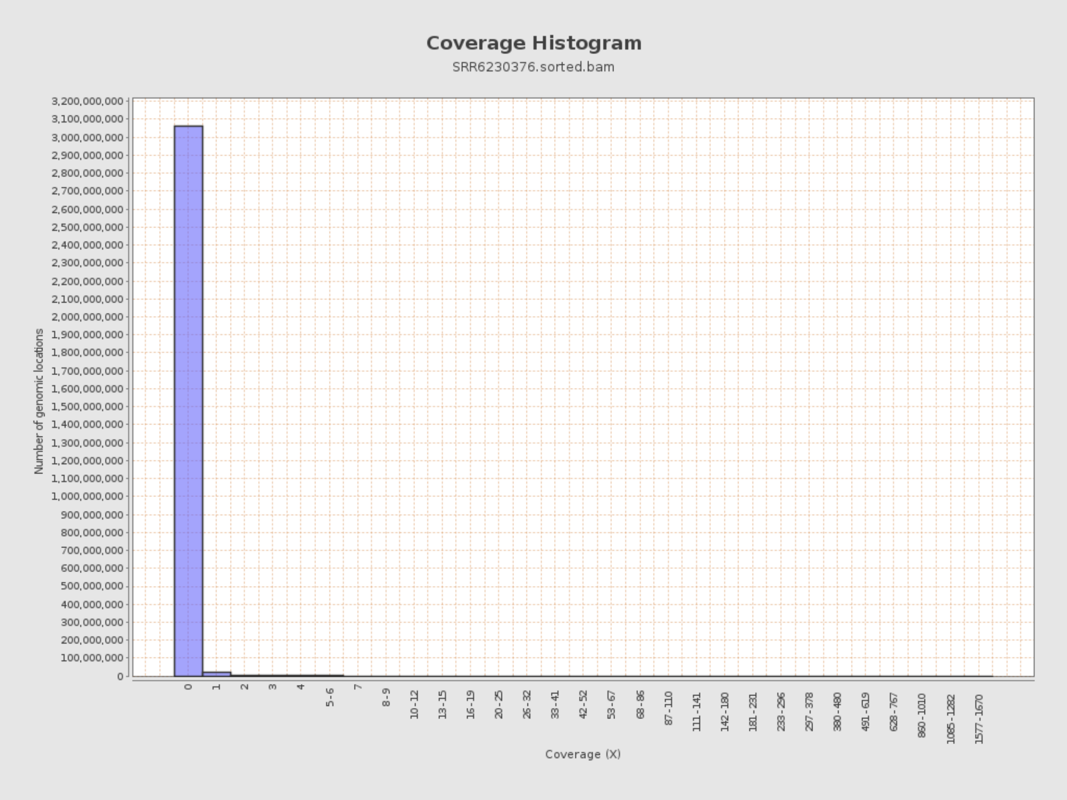
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8315422	0.0334	0.6608
chr2	243199373	8533090	0.0351	0.7786
chr3	198022430	5177933	0.0261	0.4605
chr4	191154276	5867086	0.0307	0.5113
chr5	180915260	5041630	0.0279	0.4681
chr6	171115067	5408646	0.0316	0.5702
chr7	159138663	5103464	0.0321	0.6057

chr8	146364022	5163641	0.0353	0.5585
chr9	141213431	3460077	0.0245	0.44
chr10	135534747	4819646	0.0356	0.5155
chr11	135006516	4032912	0.0299	0.5006
chr12	133851895	4146675	0.031	0.4859
chr13	115169878	2677868	0.0233	0.4901
chr14	107349540	2793432	0.026	0.8505
chr15	102531392	3038115	0.0296	1.0765
chr16	90354753	2481823	0.0275	0.4626
chr17	81195210	2326981	0.0287	0.4723
chr18	78077248	2656656	0.034	0.623
chr19	59128983	1612145	0.0273	0.4651
chr20	63025520	1690143	0.0268	0.4158
chr21	48129895	1531296	0.0318	0.4801
chr22	51304566	937688	0.0183	0.3408
chrMT	16571	23219	1.4012	3.5491
chrX	155270560	6103050	0.0393	0.6412
chrY	59373566	243579	0.0041	0.2022

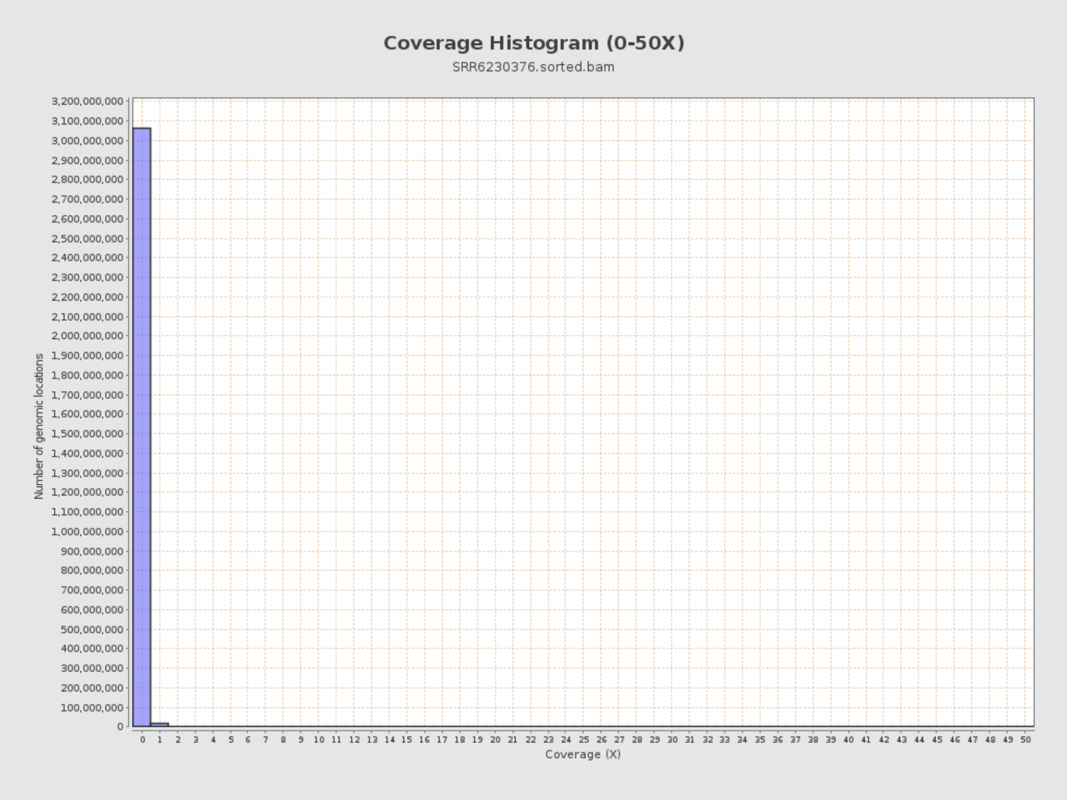
3. Results : Coverage across reference



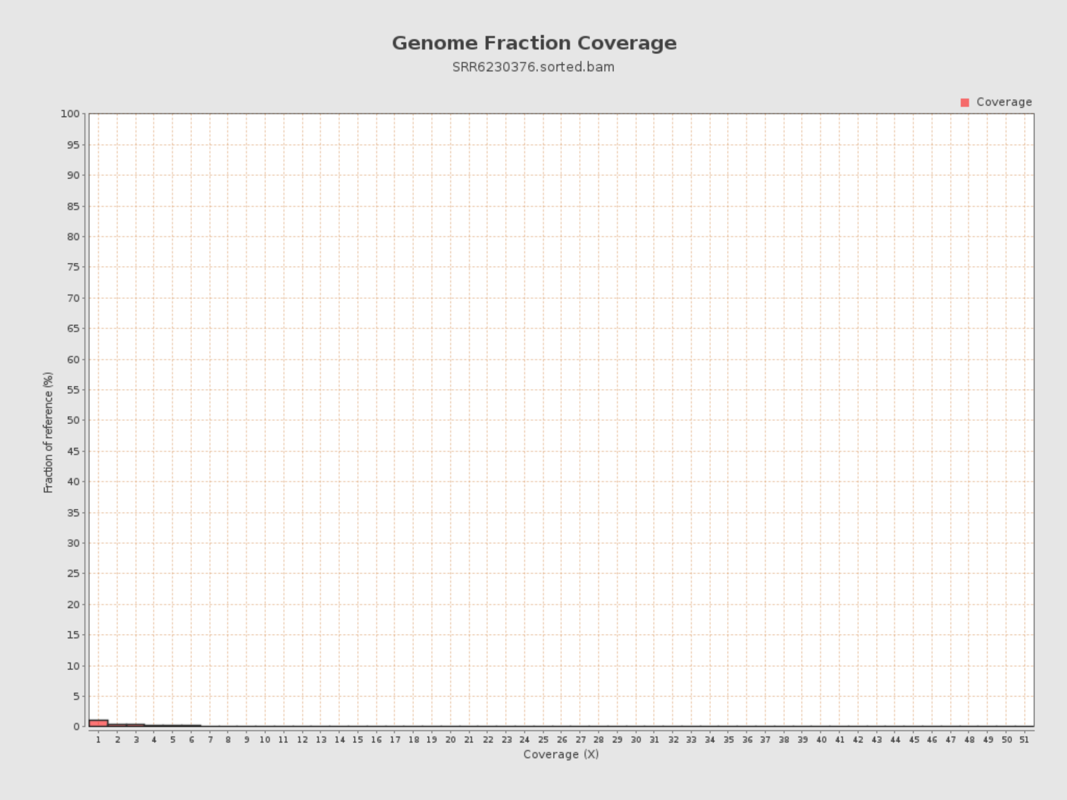
4. Results : Coverage Histogram



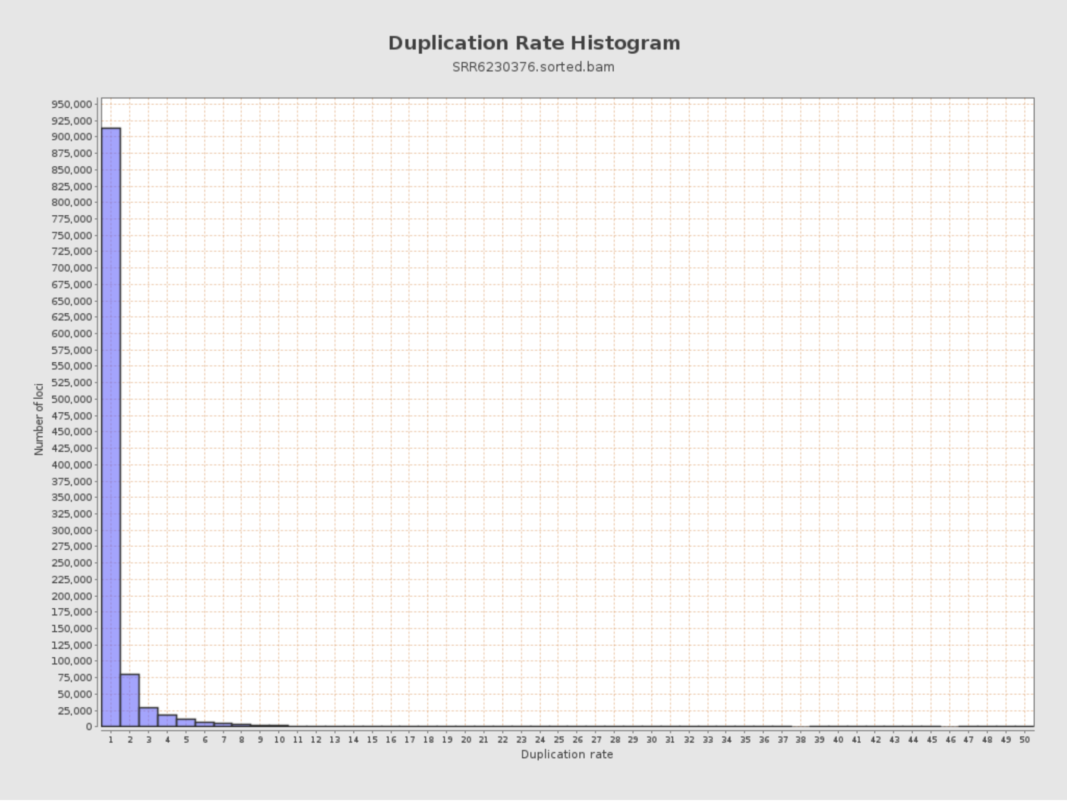
5. Results : Coverage Histogram (0-50X)



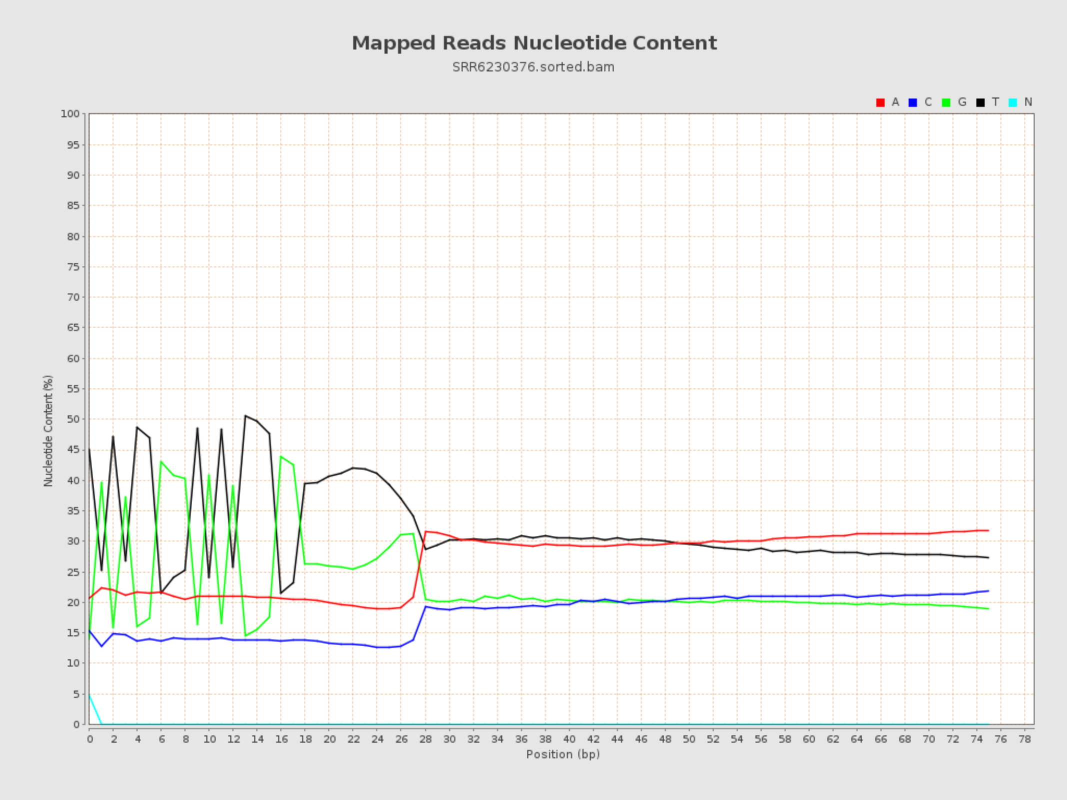
6. Results : Genome Fraction Coverage



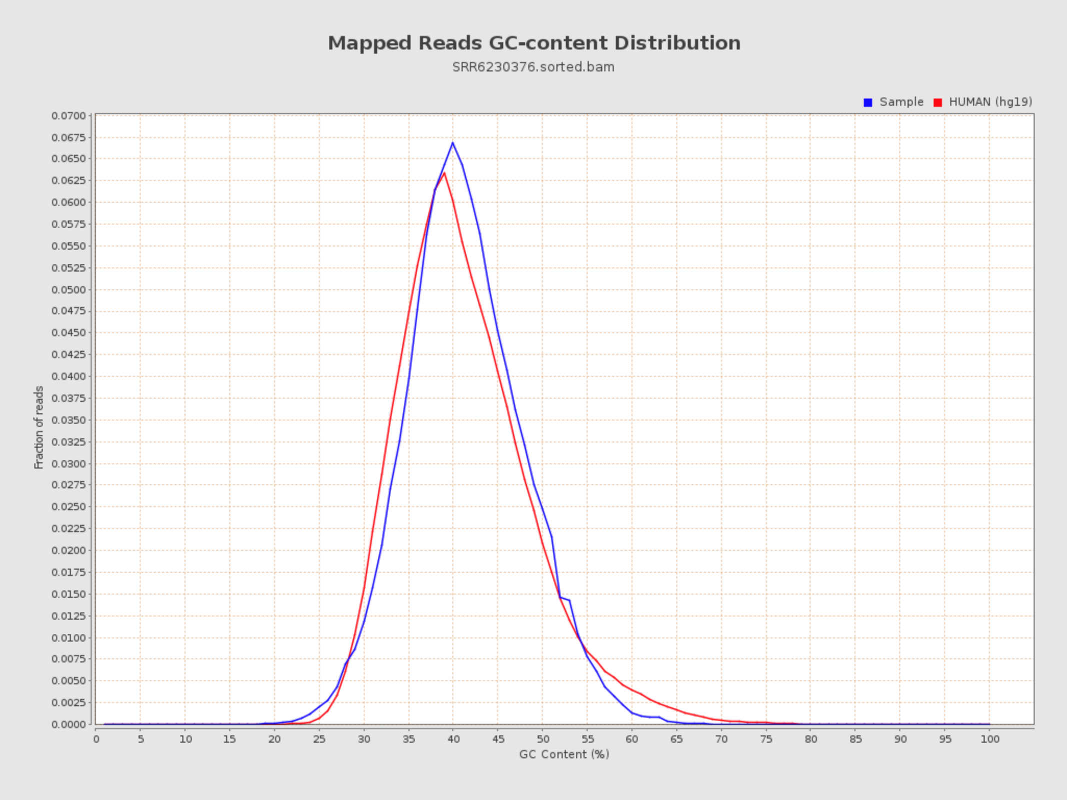
7. Results : Duplication Rate Histogram



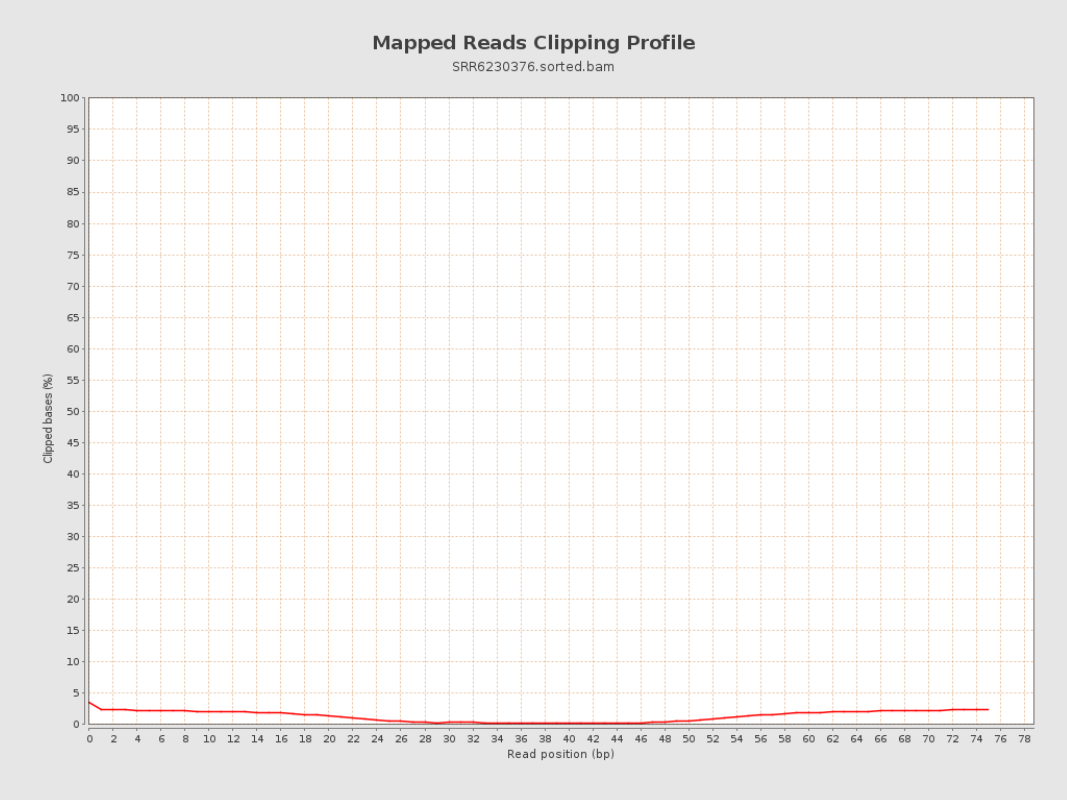
8. Results : Mapped Reads Nucleotide Content



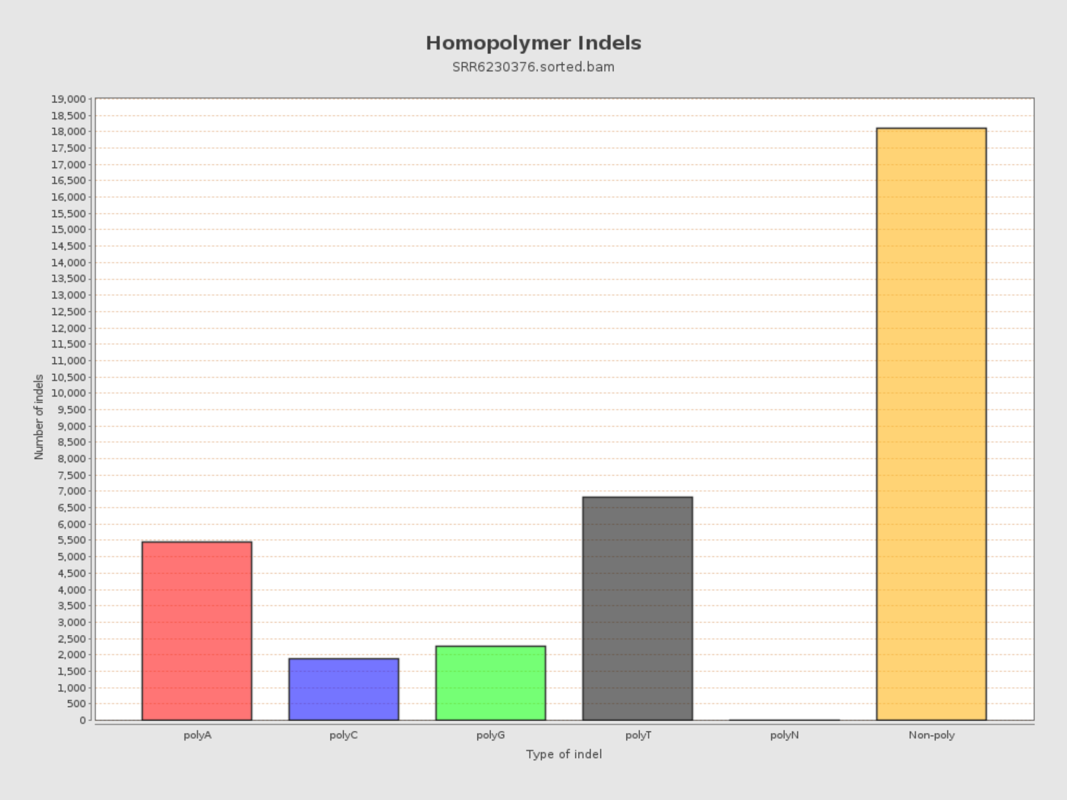
9. Results : Mapped Reads GC-content Distribution



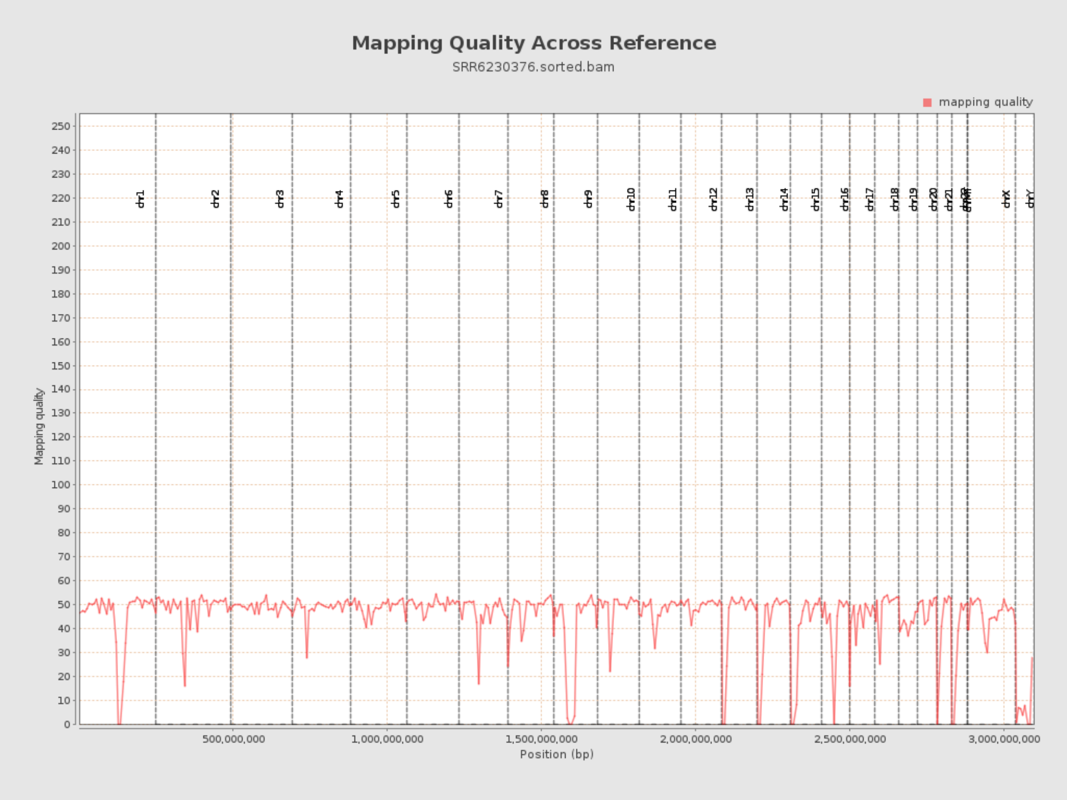
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram