Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 17:44:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8751191.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_SRR8751191 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8751191.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 17:44:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8751191.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,726,391
Mapped reads	5,433,558 / 94.89%
Unmapped reads	292,833 / 5.11%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	136,204 / 2.38%
Read min/max/mean length	30 / 101 / 101.99
Duplicated reads (estimated)	136,533 / 2.38%
Duplication rate	1.64%
Clipped reads	854,370 / 14.92%

2.2. ACGT Content

Number/percentage of A's	155,824,220 / 29.12%
Number/percentage of C's	111,688,975 / 20.87%
Number/percentage of T's	156,572,813 / 29.26%
Number/percentage of G's	111,052,513 / 20.75%
Number/percentage of N's	2,941 / 0%
GC Percentage	41.62%

2.3. Coverage

Mean	0.1729

Standard Deviation	1.1699

2.4. Mapping Quality

Mean Mapping Quality	51.51

2.5. Mismatches and indels

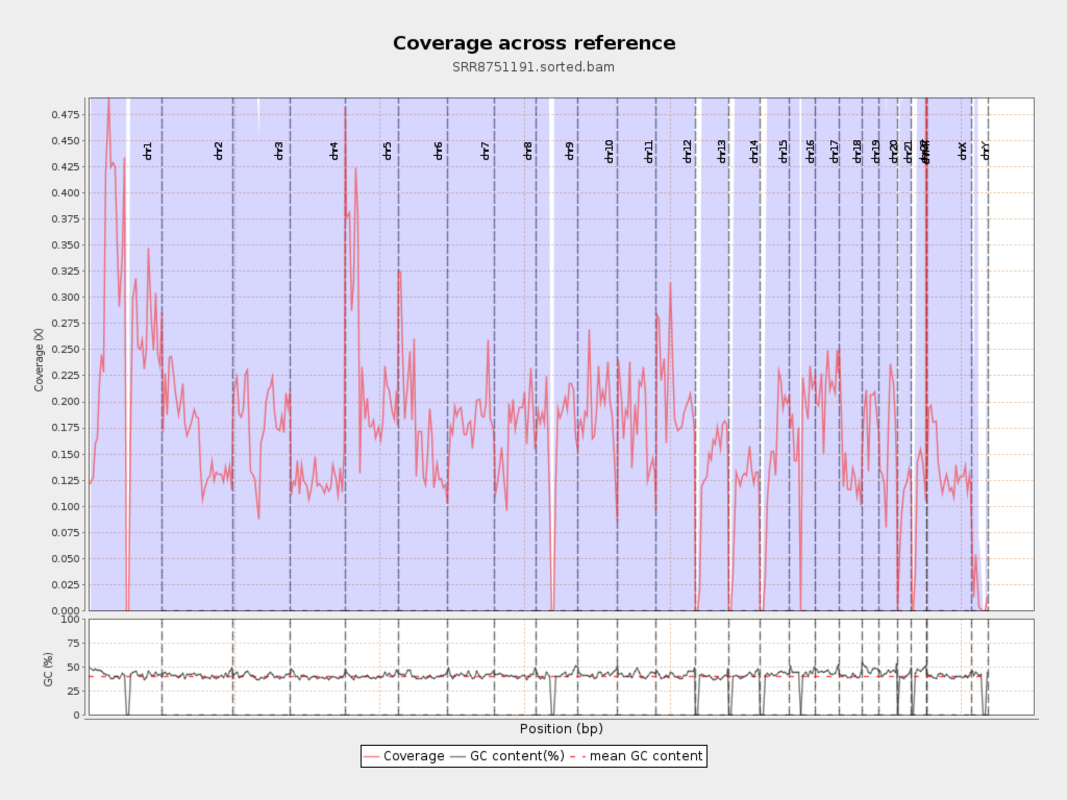
General error rate	0.35%
Mismatches	1,737,300
Insertions	83,531
Mapped reads with at least one insertion	1.51%
Deletions	67,561
Mapped reads with at least one deletion	1.22%
Homopolymer indels	47.65%

2.6. Chromosome stats

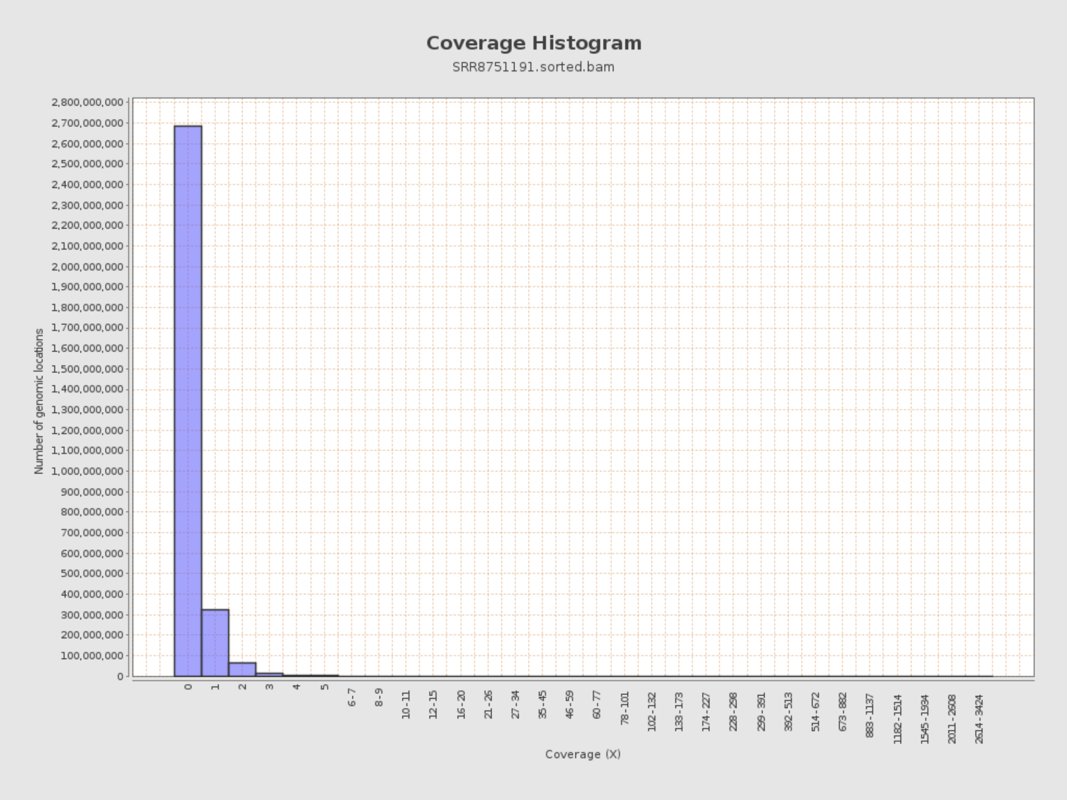
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	66829520	0.2681	3.2219
chr2	243199373	40344221	0.1659	0.5488
chr3	198022430	35920249	0.1814	0.5173
chr4	191154276	23705718	0.124	0.4584
chr5	180915260	42385436	0.2343	0.5821
chr6	171115067	30309567	0.1771	0.9138
chr7	159138663	29493305	0.1853	0.6483

chr8	146364022	24874775	0.17	0.5322
chr9	141213431	23350690	0.1654	0.5945
chr10	135534747	25990901	0.1918	1.3734
chr11	135006516	24642719	0.1825	0.6456
chr12	133851895	28695547	0.2144	0.5535
chr13	115169878	14845665	0.1289	0.4228
chr14	107349540	11574922	0.1078	0.3941
chr15	102531392	14181249	0.1383	0.4447
chr16	90354753	15807979	0.175	0.7355
chr17	81195210	17348384	0.2137	0.745
chr18	78077248	10574114	0.1354	0.9368
chr19	59128983	11154782	0.1887	2.287
chr20	63025520	10005400	0.1588	0.4829
chr21	48129895	4667263	0.097	0.3966
chr22	51304566	4840547	0.0943	0.3667
chrMT	16571	1509744	91.1076	31.6442
chrX	155270560	21344856	0.1375	0.4751
chrY	59373566	889196	0.015	0.4821

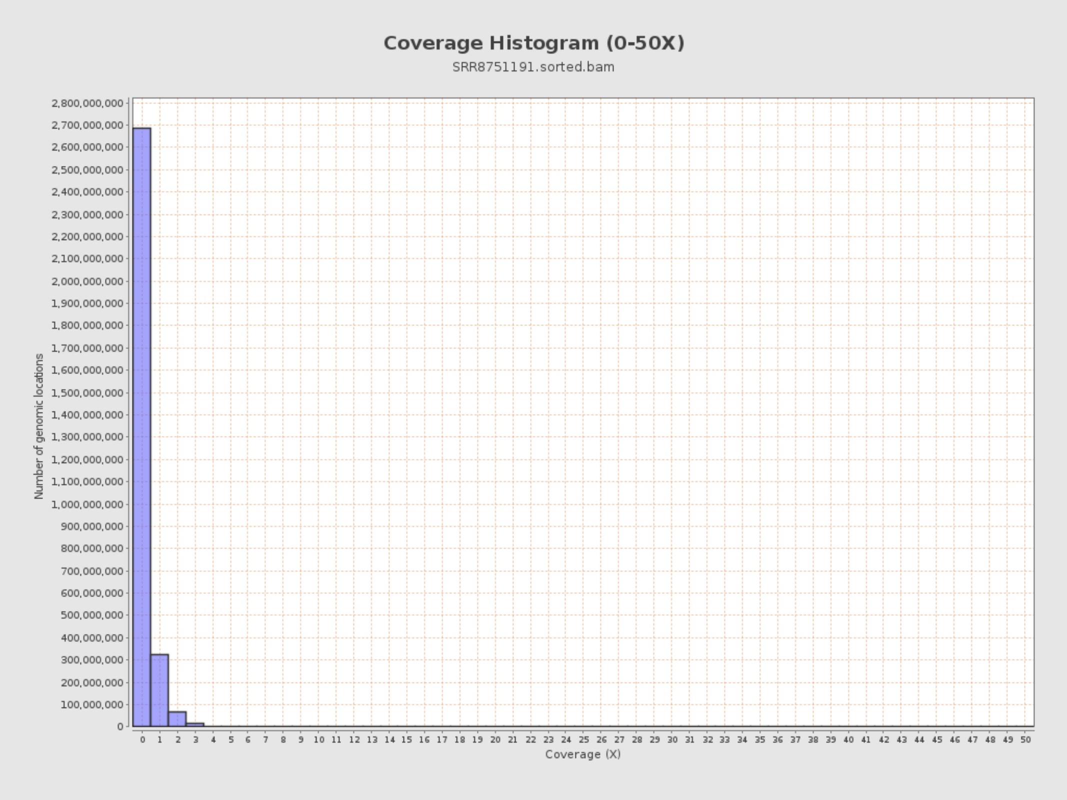
3. Results : Coverage across reference



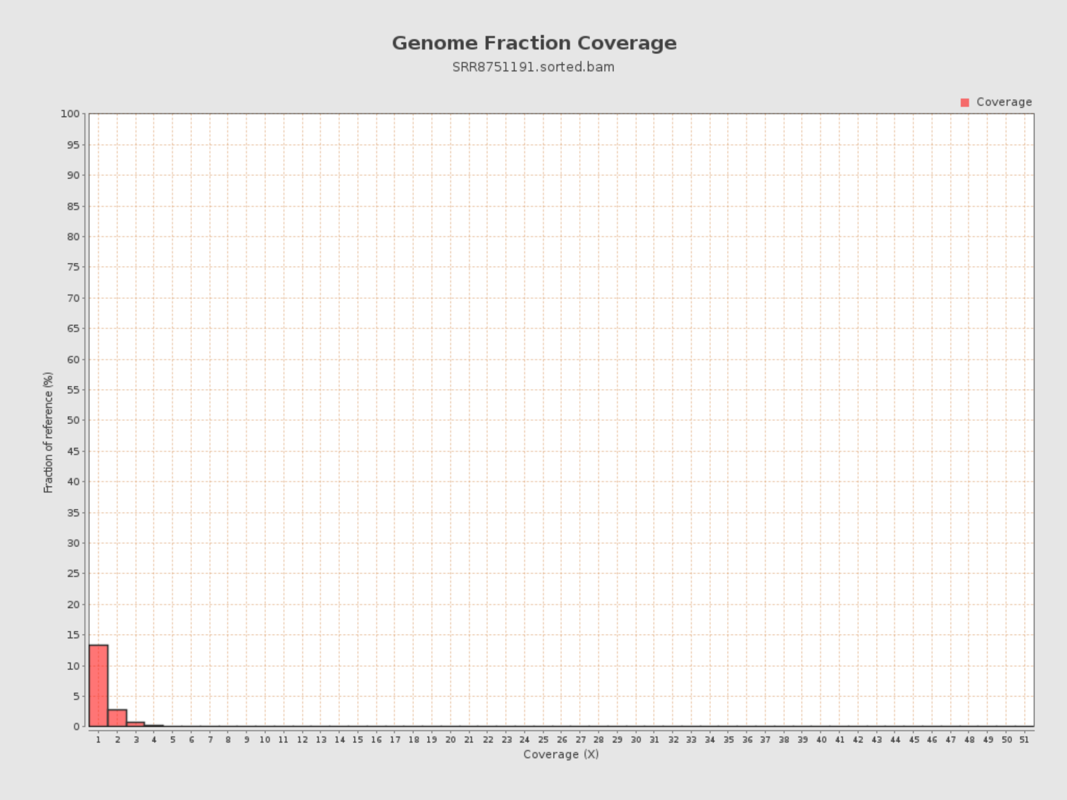
4. Results : Coverage Histogram



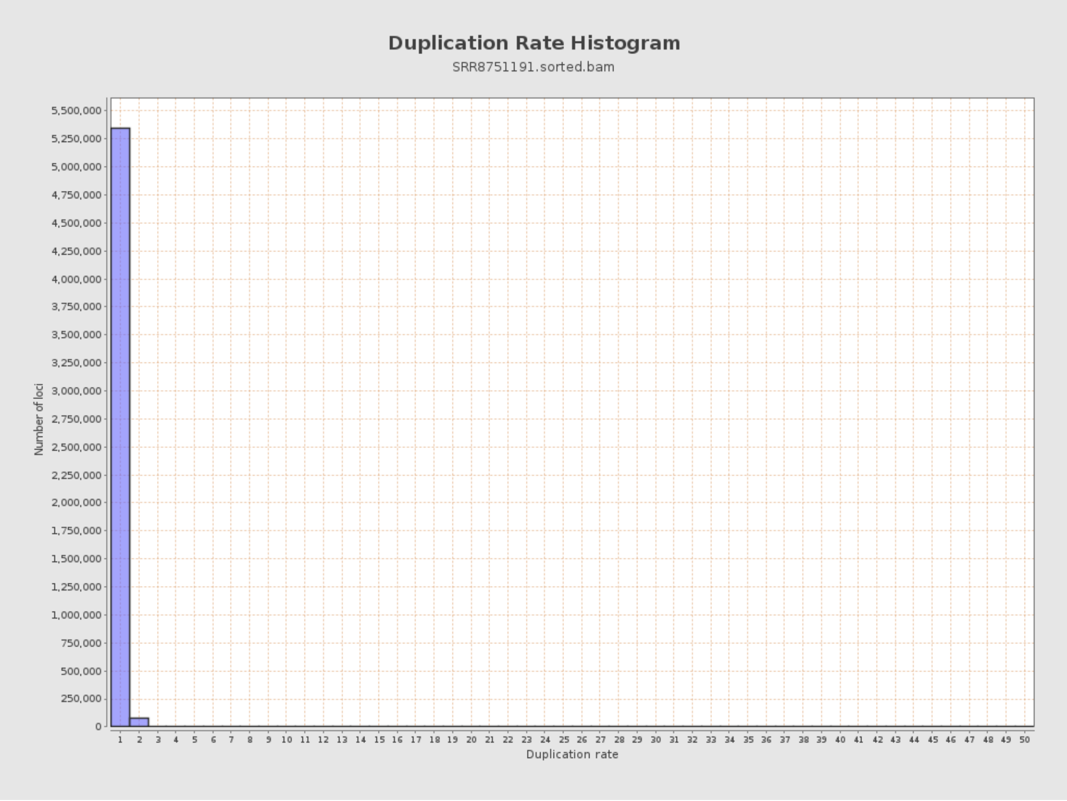
5. Results : Coverage Histogram (0-50X)



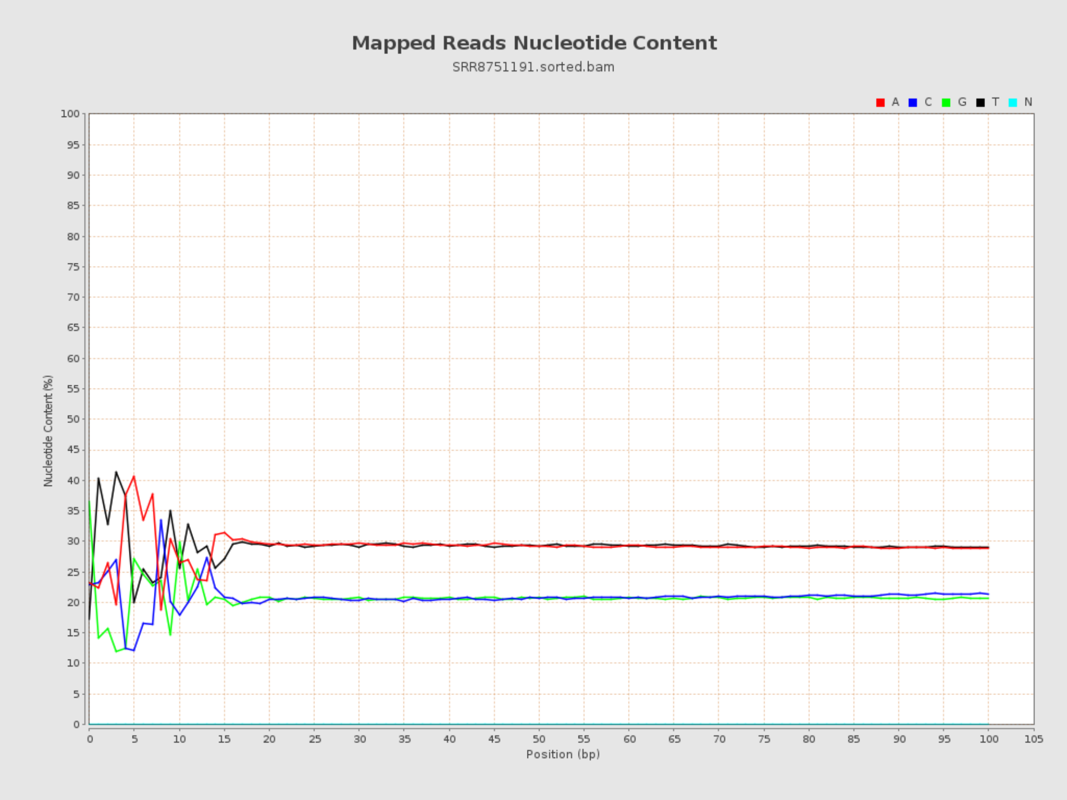
6. Results : Genome Fraction Coverage



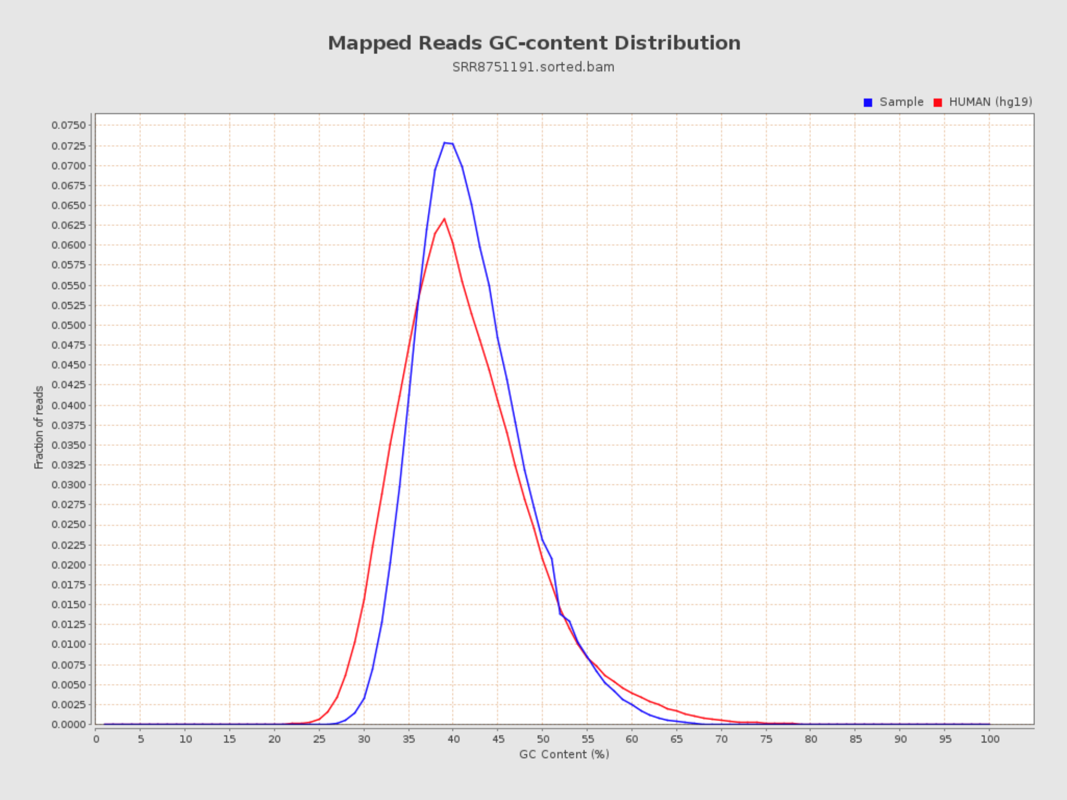
7. Results : Duplication Rate Histogram



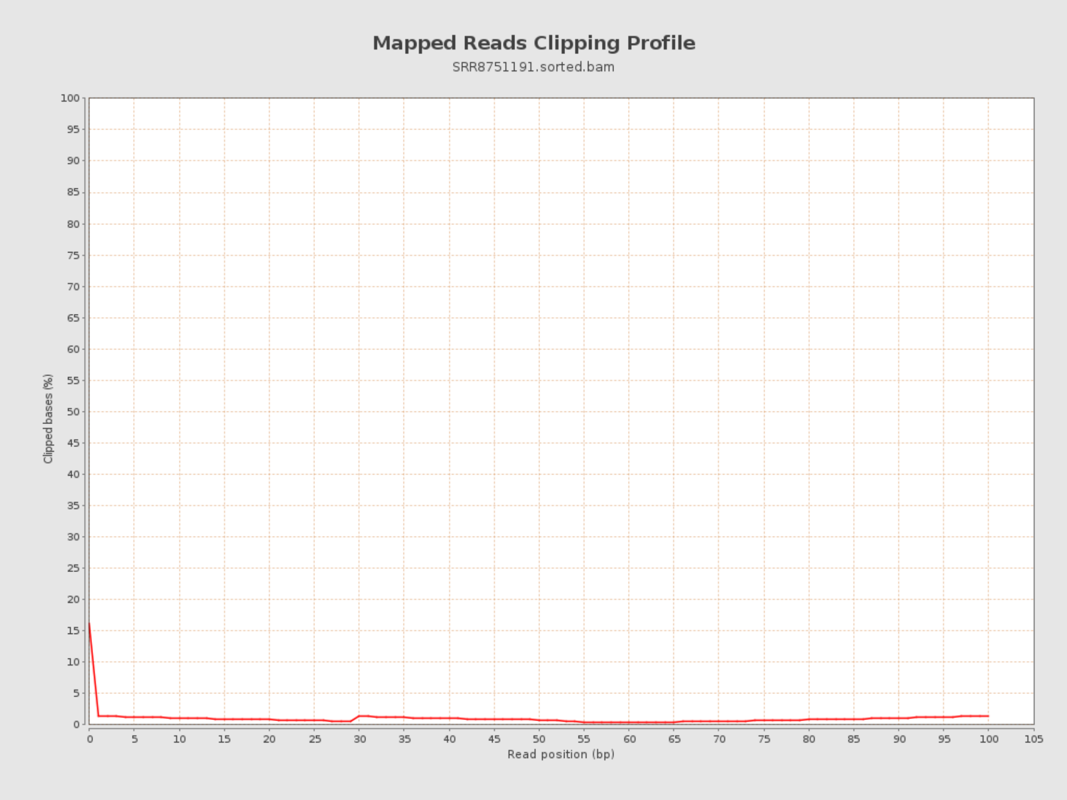
8. Results : Mapped Reads Nucleotide Content



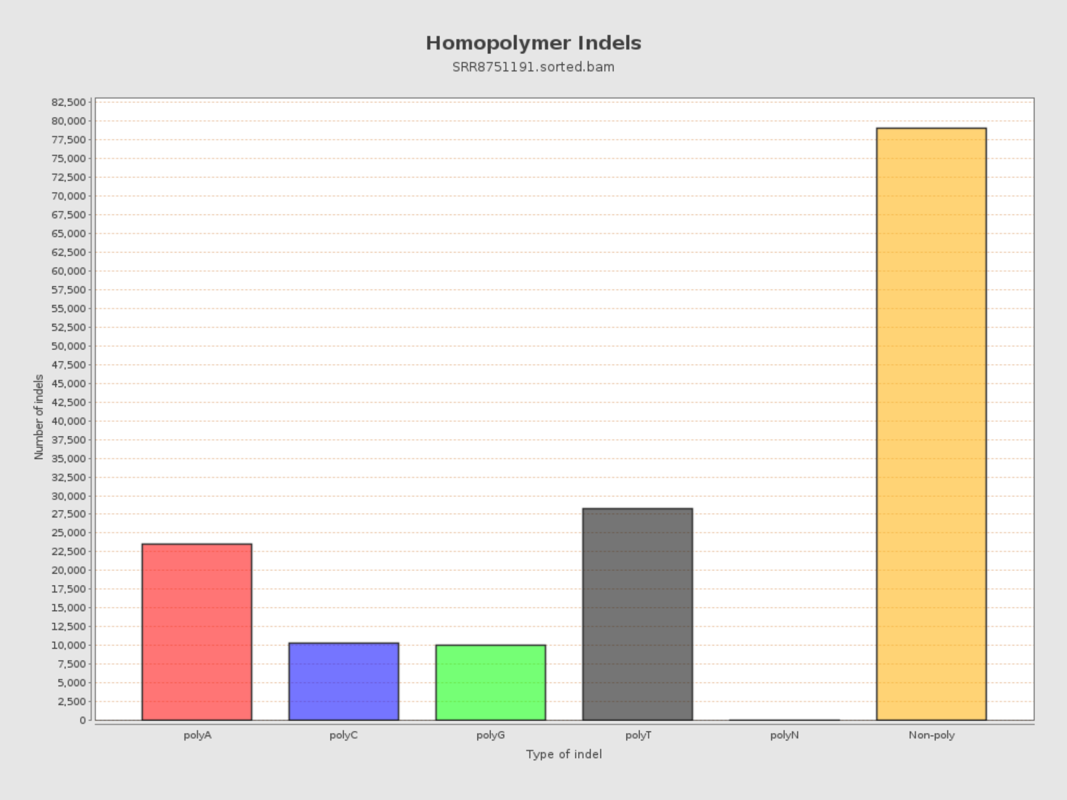
9. Results : Mapped Reads GC-content Distribution



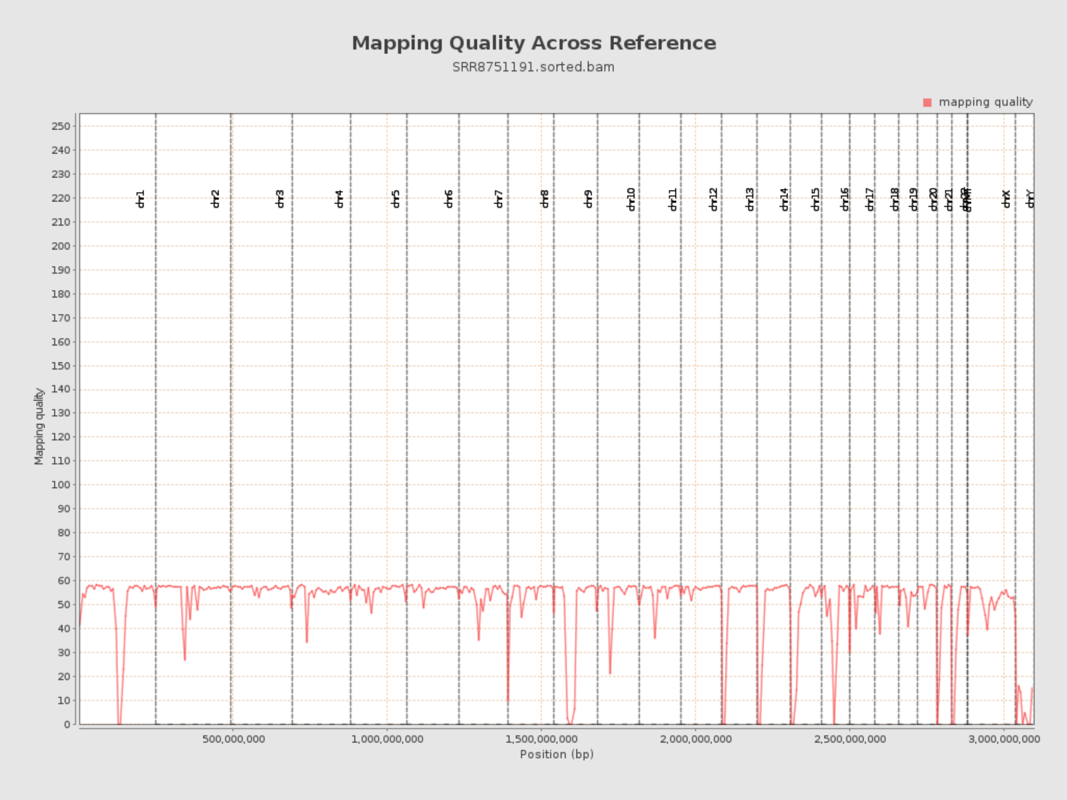
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram