Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 04:56:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3083761.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_SRR3083761 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3083761.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 04:56:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3083761.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,901,726
Mapped reads	1,247,615 / 65.6%
Unmapped reads	654,111 / 34.4%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,390 / 0.28%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	33,239 / 1.75%
Duplication rate	2.17%
Clipped reads	661,475 / 34.78%

2.2. ACGT Content

Number/percentage of A's	22,690,710 / 28.55%
Number/percentage of C's	15,123,541 / 19.03%
Number/percentage of T's	23,600,016 / 29.7%
Number/percentage of G's	18,053,057 / 22.72%
Number/percentage of N's	922 / 0%
GC Percentage	41.75%

2.3. Coverage

Mean	0.0257

Standard Deviation	0.2124

2.4. Mapping Quality

Mean Mapping Quality	45.07

2.5. Mismatches and indels

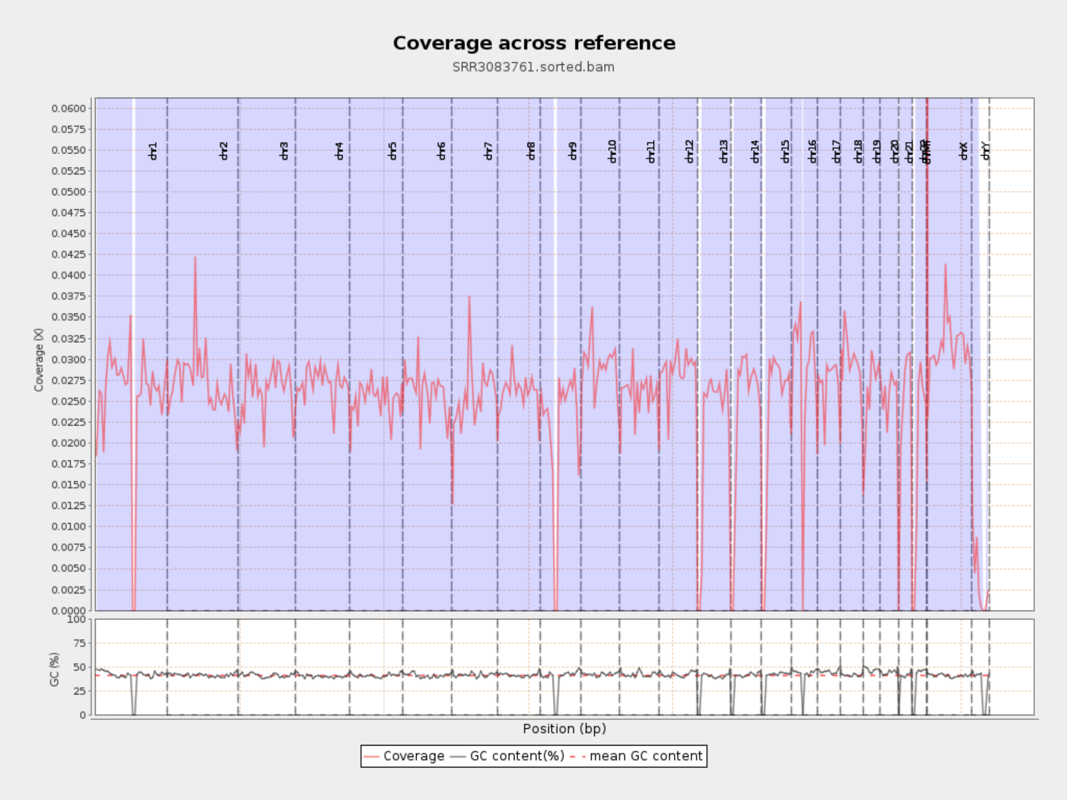
General error rate	0.88%
Mismatches	689,804
Insertions	5,805
Mapped reads with at least one insertion	0.46%
Deletions	16,519
Mapped reads with at least one deletion	1.31%
Homopolymer indels	45.38%

2.6. Chromosome stats

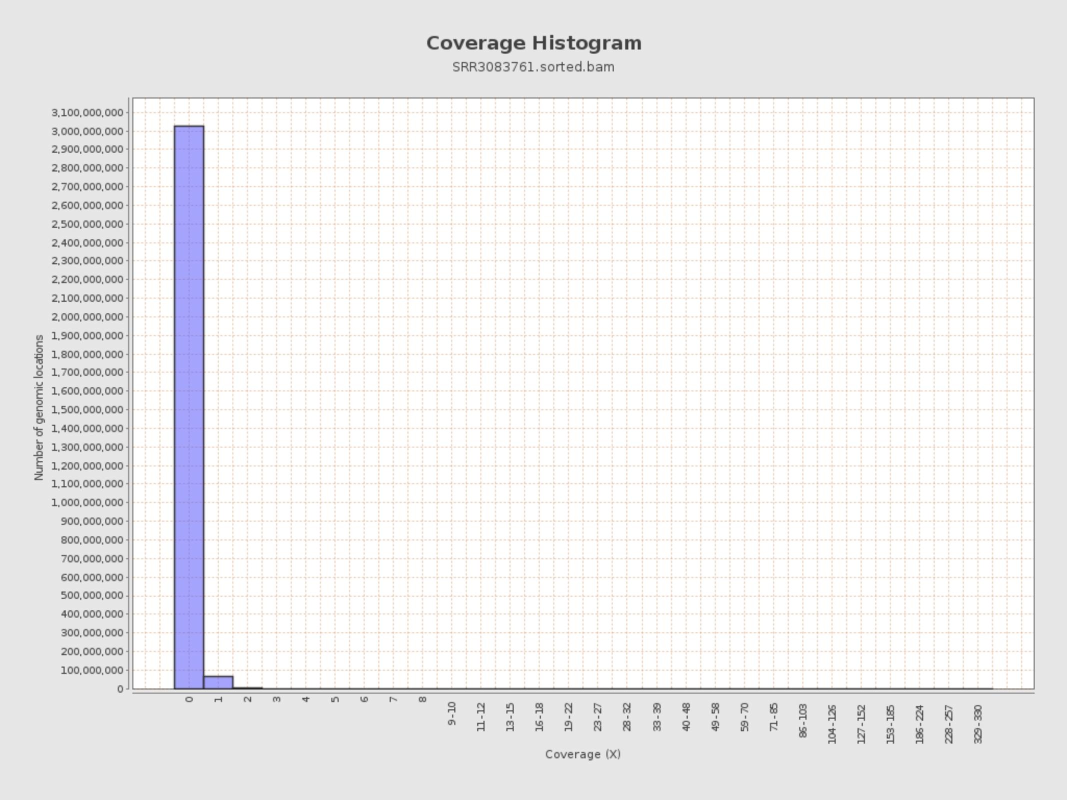
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6357510	0.0255	0.2692
chr2	243199373	6627737	0.0273	0.2687
chr3	198022430	5244397	0.0265	0.1749
chr4	191154276	5206988	0.0272	0.1799
chr5	180915260	4582910	0.0253	0.1717
chr6	171115067	4447128	0.026	0.1936
chr7	159138663	4082734	0.0257	0.233

chr8	146364022	3834898	0.0262	0.2205
chr9	141213431	3064716	0.0217	0.2053
chr10	135534747	3967348	0.0293	0.2168
chr11	135006516	3519275	0.0261	0.1996
chr12	133851895	3838768	0.0287	0.1836
chr13	115169878	2479584	0.0215	0.1591
chr14	107349540	2504081	0.0233	0.1719
chr15	102531392	2347053	0.0229	0.1692
chr16	90354753	2510570	0.0278	0.1936
chr17	81195210	2198496	0.0271	0.1892
chr18	78077248	2321271	0.0297	0.3924
chr19	59128983	1553532	0.0263	0.237
chr20	63025520	1605958	0.0255	0.1733
chr21	48129895	1142491	0.0237	0.1712
chr22	51304566	939182	0.0183	0.146
chrMT	16571	20483	1.2361	1.429
chrX	155270560	4899997	0.0316	0.2059
chrY	59373566	197371	0.0033	0.0702

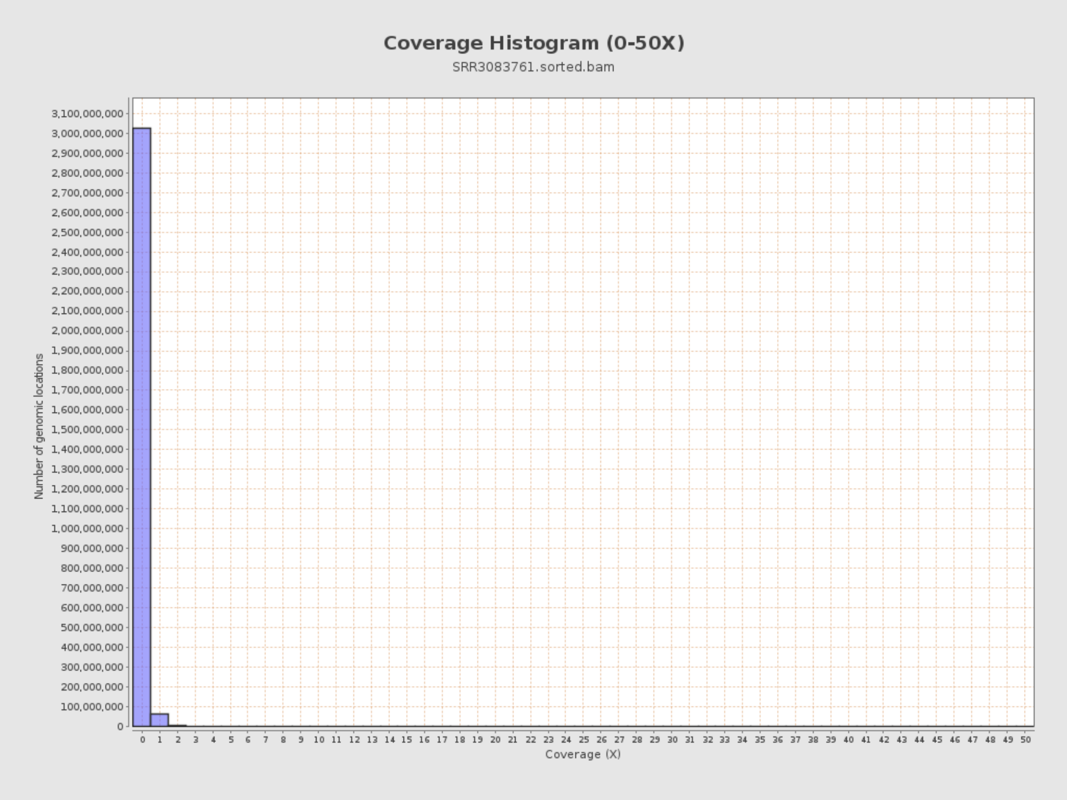
3. Results : Coverage across reference



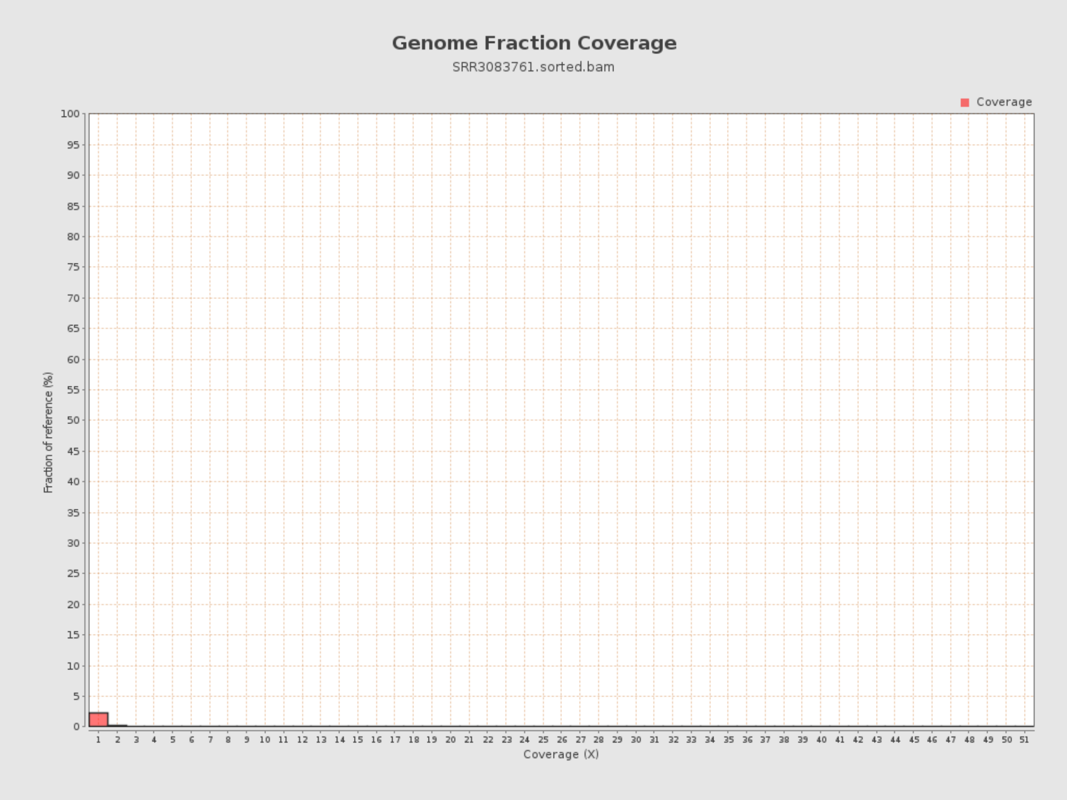
4. Results : Coverage Histogram



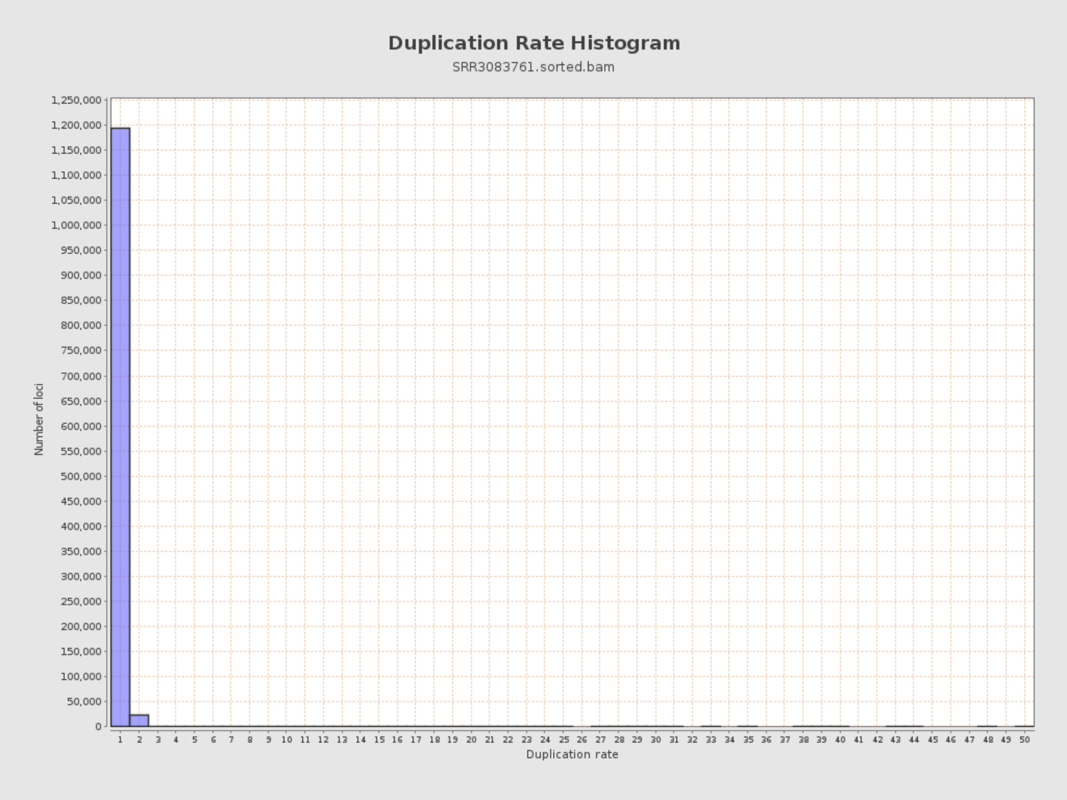
5. Results : Coverage Histogram (0-50X)



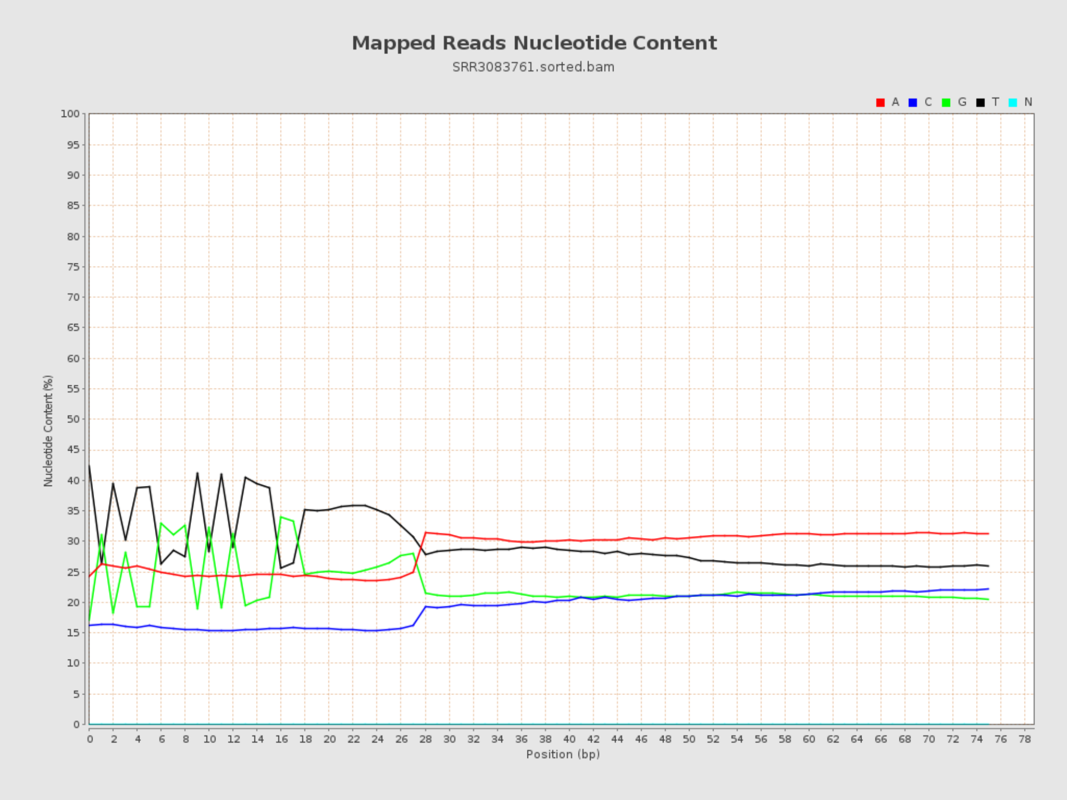
6. Results : Genome Fraction Coverage



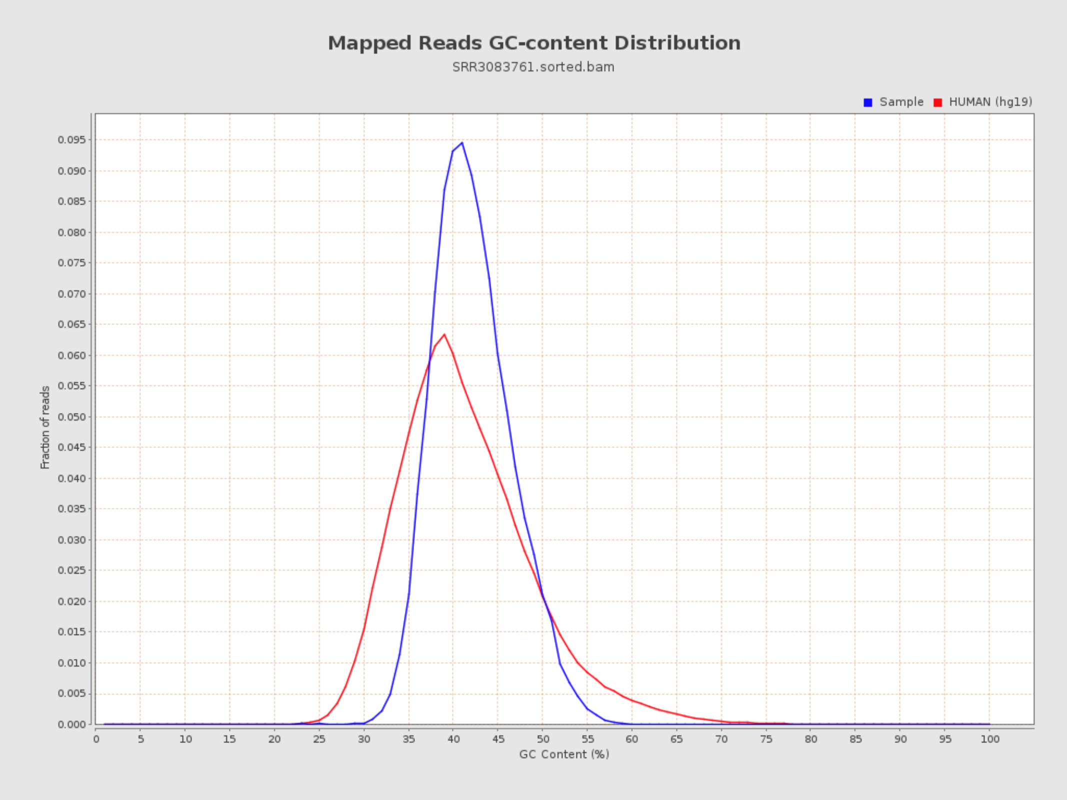
7. Results : Duplication Rate Histogram



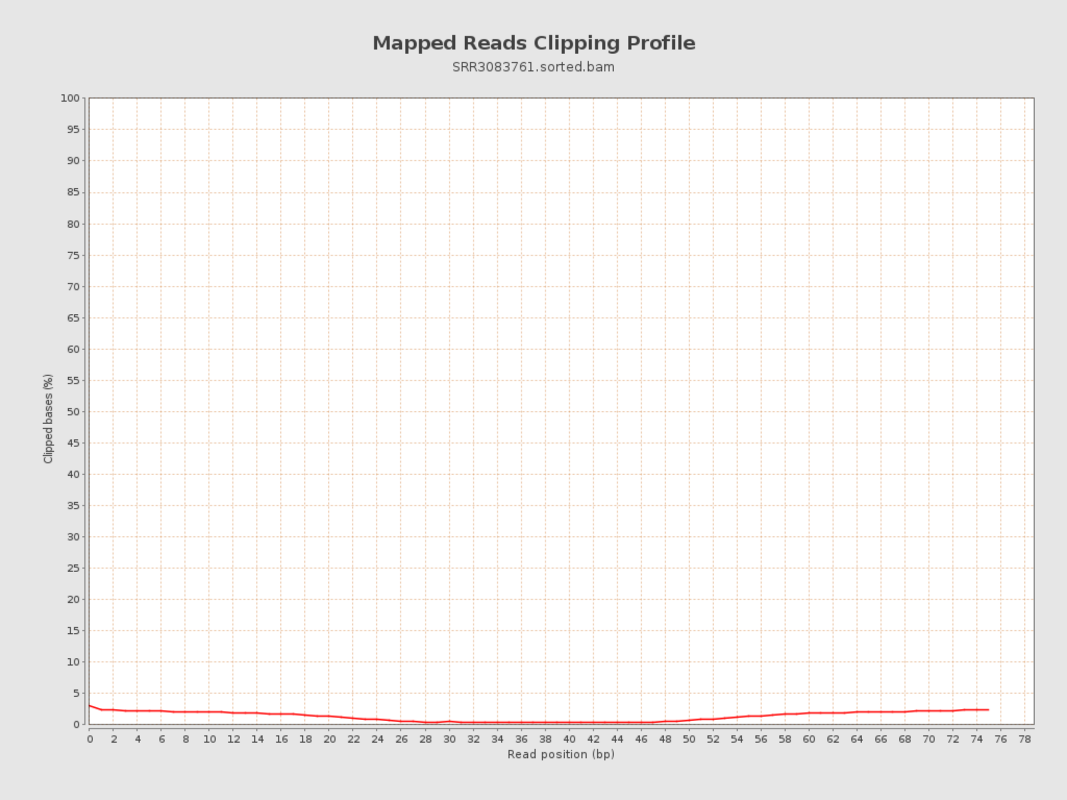
8. Results : Mapped Reads Nucleotide Content



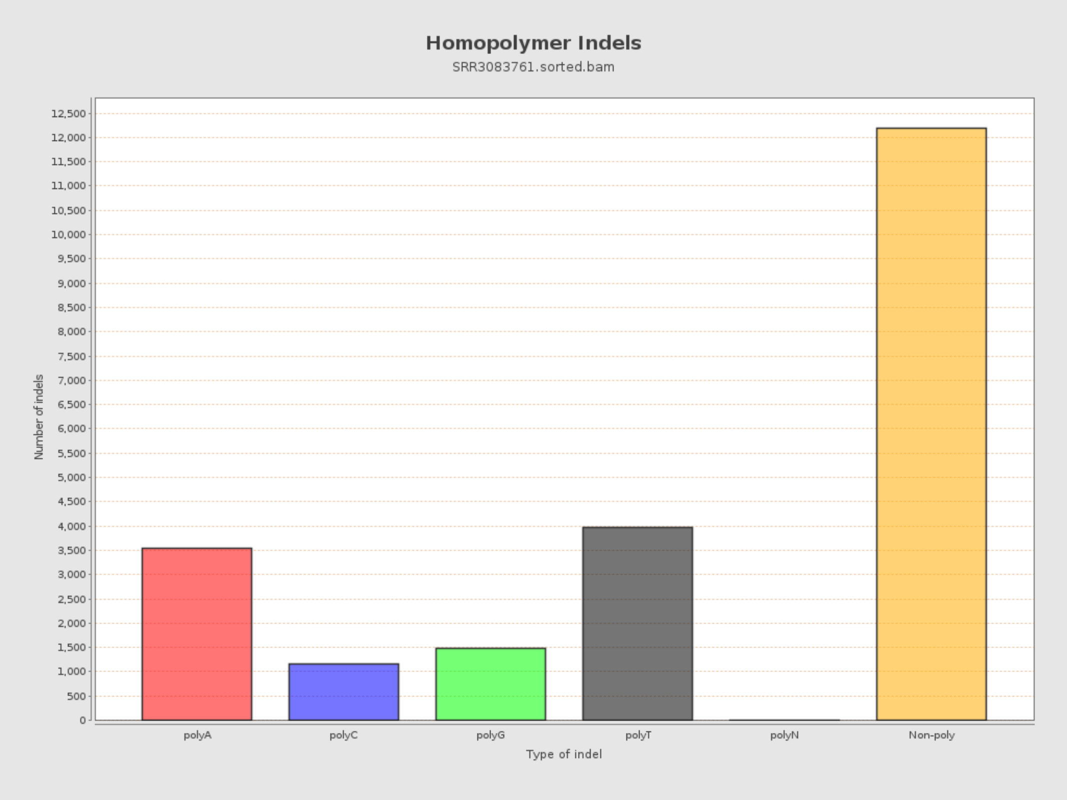
9. Results : Mapped Reads GC-content Distribution



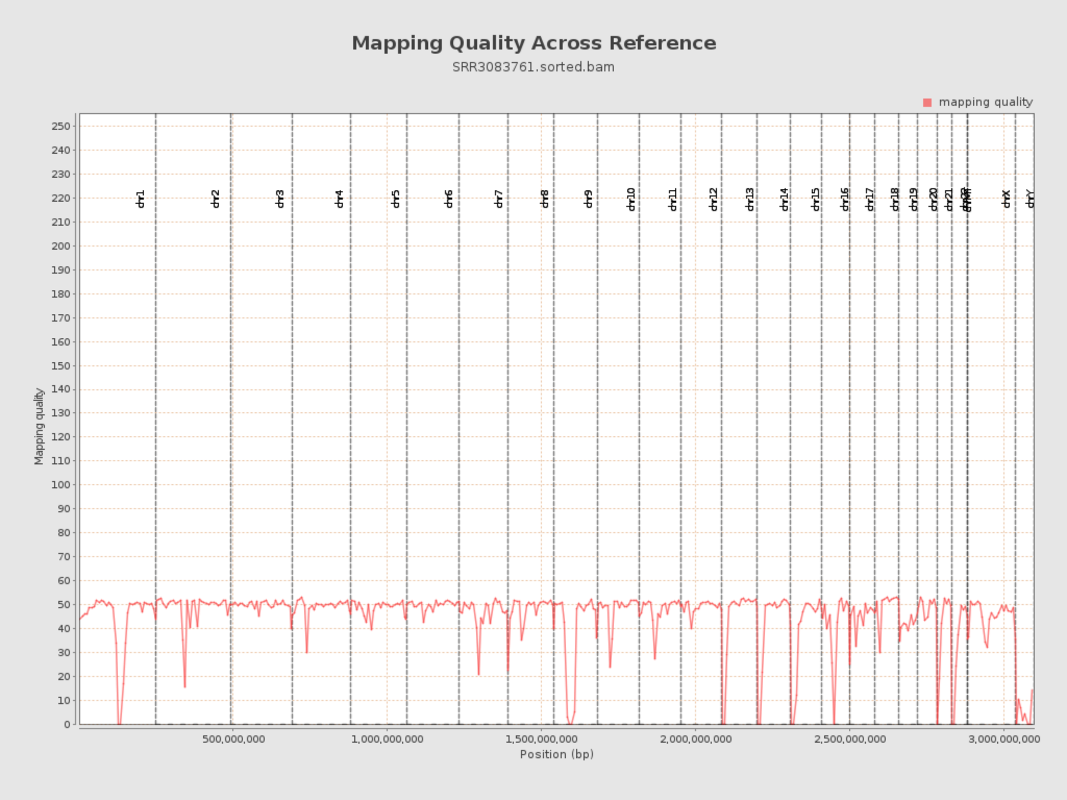
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram