Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 04:05:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080756.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_SRR3080756 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080756.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 04:05:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080756.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,004,039
Mapped reads	7,963,109 / 79.6%
Unmapped reads	2,040,930 / 20.4%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	34,094 / 0.34%
Read min/max/mean length	30 / 66 / 66.11
Duplicated reads (estimated)	1,231,026 / 12.31%
Duplication rate	11.8%
Clipped reads	1,008,630 / 10.08%

2.2. ACGT Content

Number/percentage of A's	158,280,559 / 31%
Number/percentage of C's	102,695,263 / 20.11%
Number/percentage of T's	131,346,674 / 25.72%
Number/percentage of G's	117,155,860 / 22.94%
Number/percentage of N's	1,175,874 / 0.23%
GC Percentage	43.05%

2.3. Coverage

Mean	0.165

Standard Deviation	0.9506

2.4. Mapping Quality

Mean Mapping Quality	44.97

2.5. Mismatches and indels

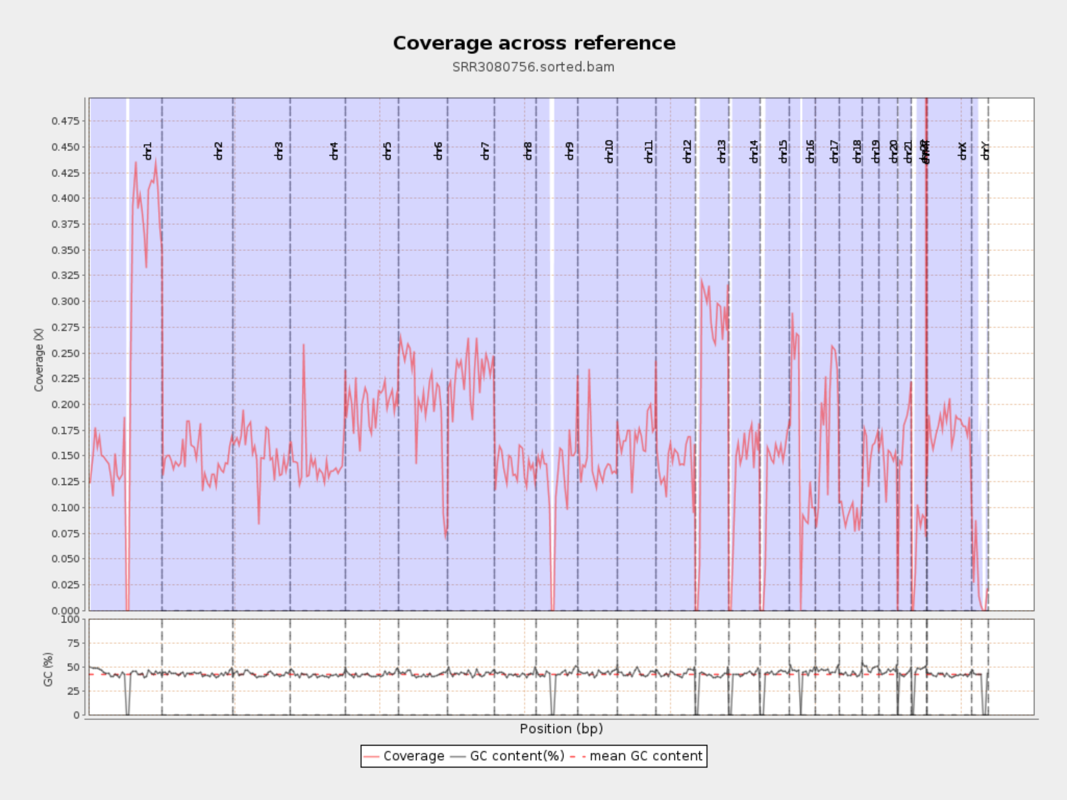
General error rate	1.03%
Mismatches	5,168,247
Insertions	36,006
Mapped reads with at least one insertion	0.45%
Deletions	85,354
Mapped reads with at least one deletion	1.06%
Homopolymer indels	42.44%

2.6. Chromosome stats

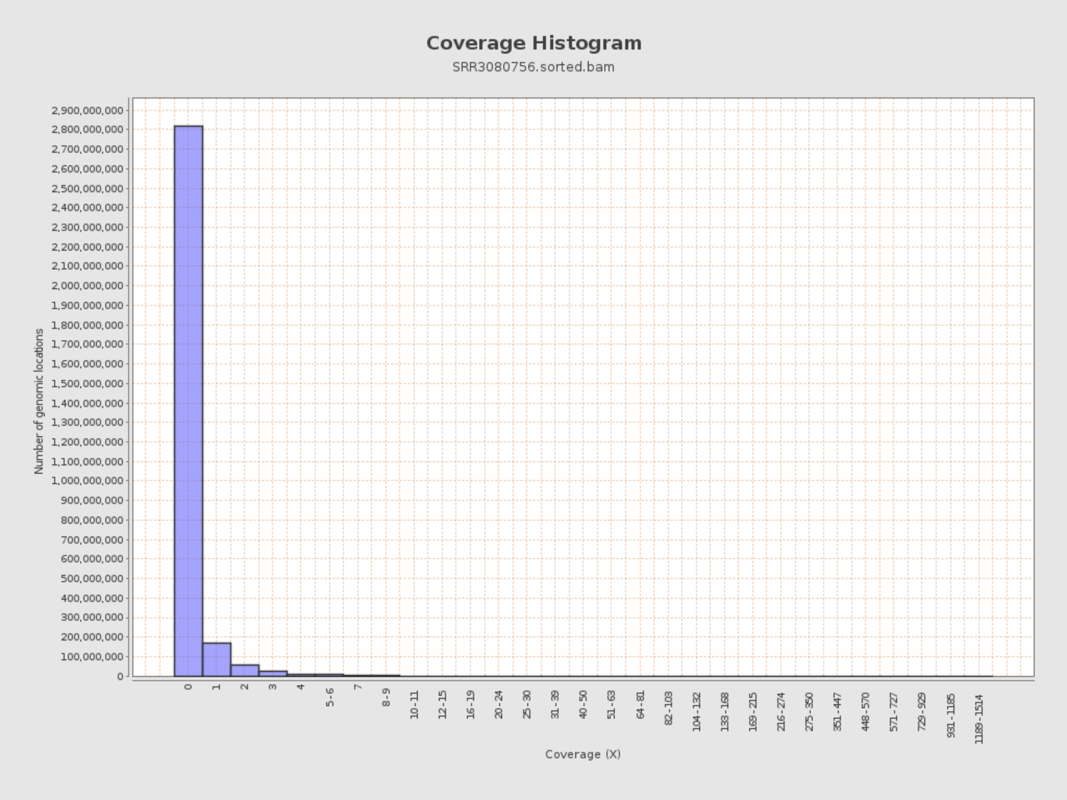
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	60543444	0.2429	1.3414
chr2	243199373	35526982	0.1461	0.8822
chr3	198022430	30435481	0.1537	0.668
chr4	191154276	27470889	0.1437	0.8362
chr5	180915260	36029168	0.1991	0.7668
chr6	171115067	35274899	0.2061	1.0543
chr7	159138663	36589309	0.2299	1.5316

chr8	146364022	20383110	0.1393	1.1657
chr9	141213431	17618591	0.1248	0.7031
chr10	135534747	19184330	0.1415	1.0837
chr11	135006516	22788679	0.1688	0.9131
chr12	133851895	19241015	0.1437	0.6748
chr13	115169878	27823337	0.2416	0.8828
chr14	107349540	14113596	0.1315	0.6799
chr15	102531392	12852727	0.1254	0.6179
chr16	90354753	13747137	0.1521	0.7964
chr17	81195210	15174649	0.1869	0.8315
chr18	78077248	7272578	0.0931	1.0104
chr19	59128983	9253012	0.1565	1.1571
chr20	63025520	9310778	0.1477	0.7169
chr21	48129895	7717140	0.1603	0.926
chr22	51304566	3268991	0.0637	0.4298
chrMT	16571	102009	6.1559	5.4164
chrX	155270560	27570634	0.1776	0.7601
chrY	59373566	1522348	0.0256	0.7697

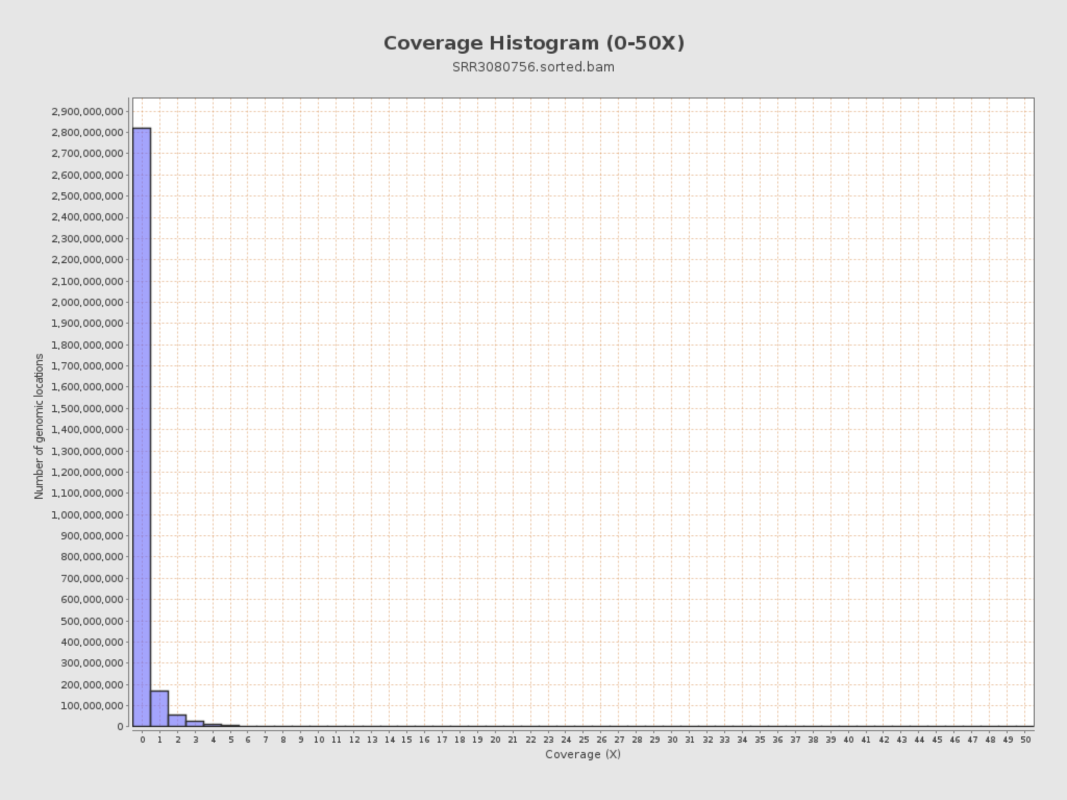
3. Results : Coverage across reference



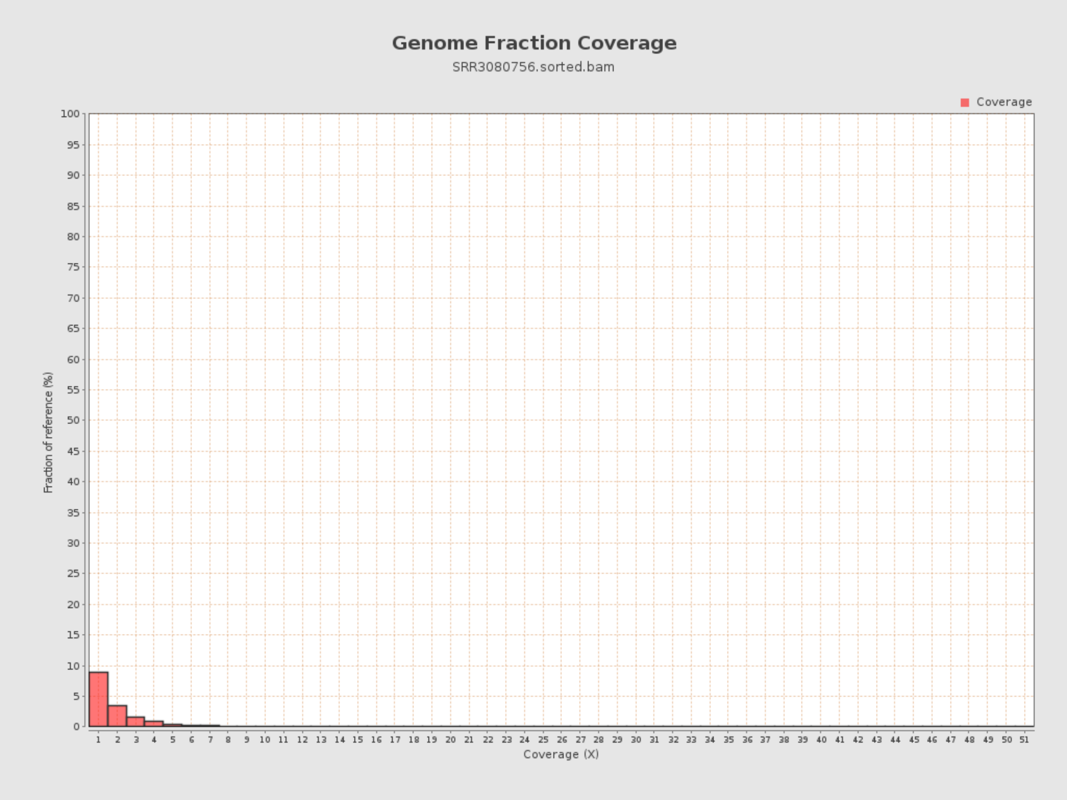
4. Results : Coverage Histogram



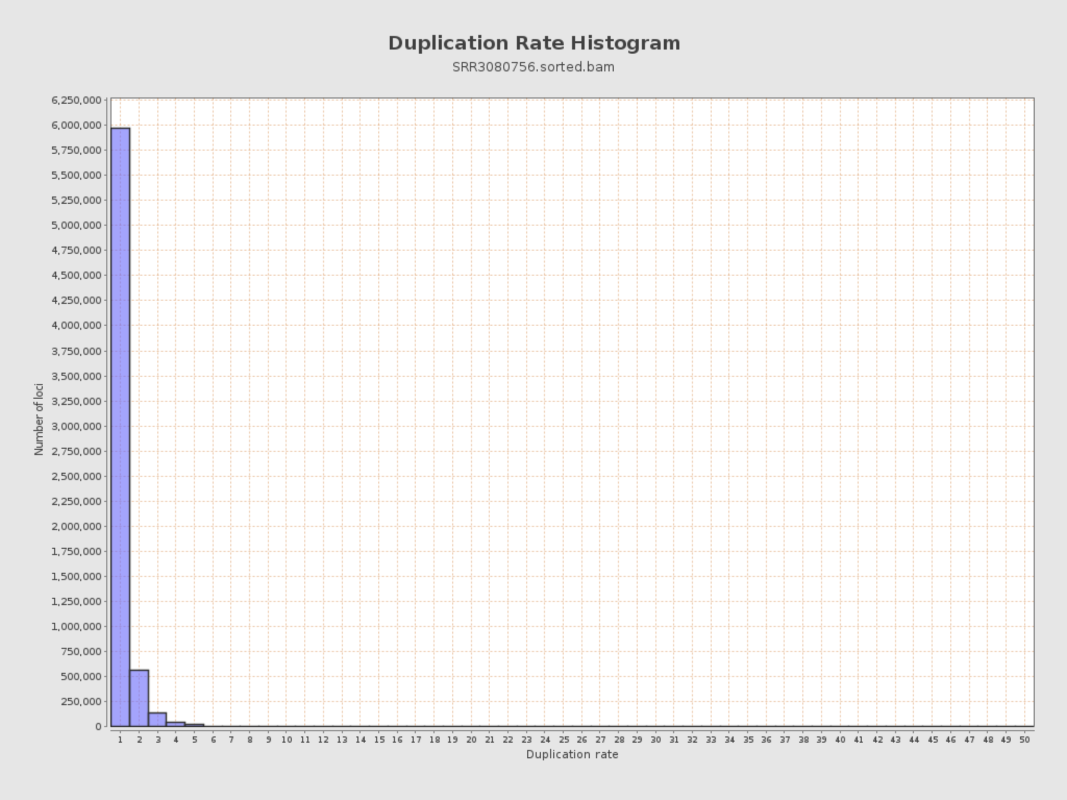
5. Results : Coverage Histogram (0-50X)



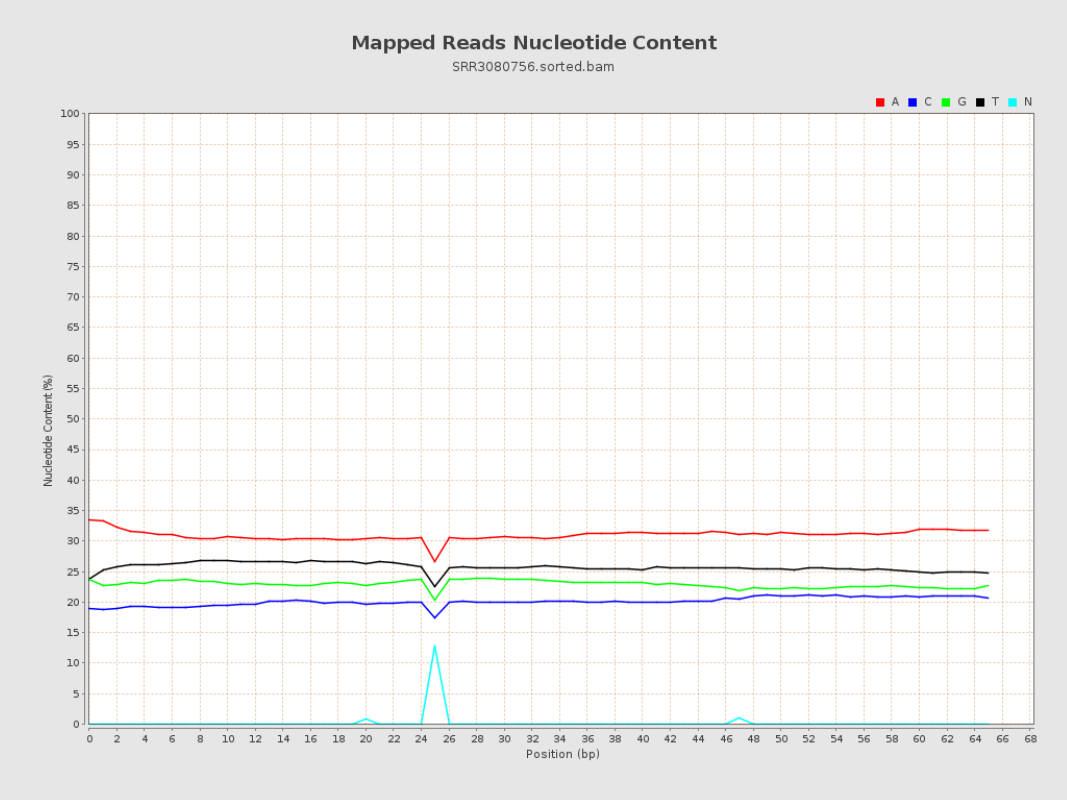
6. Results : Genome Fraction Coverage



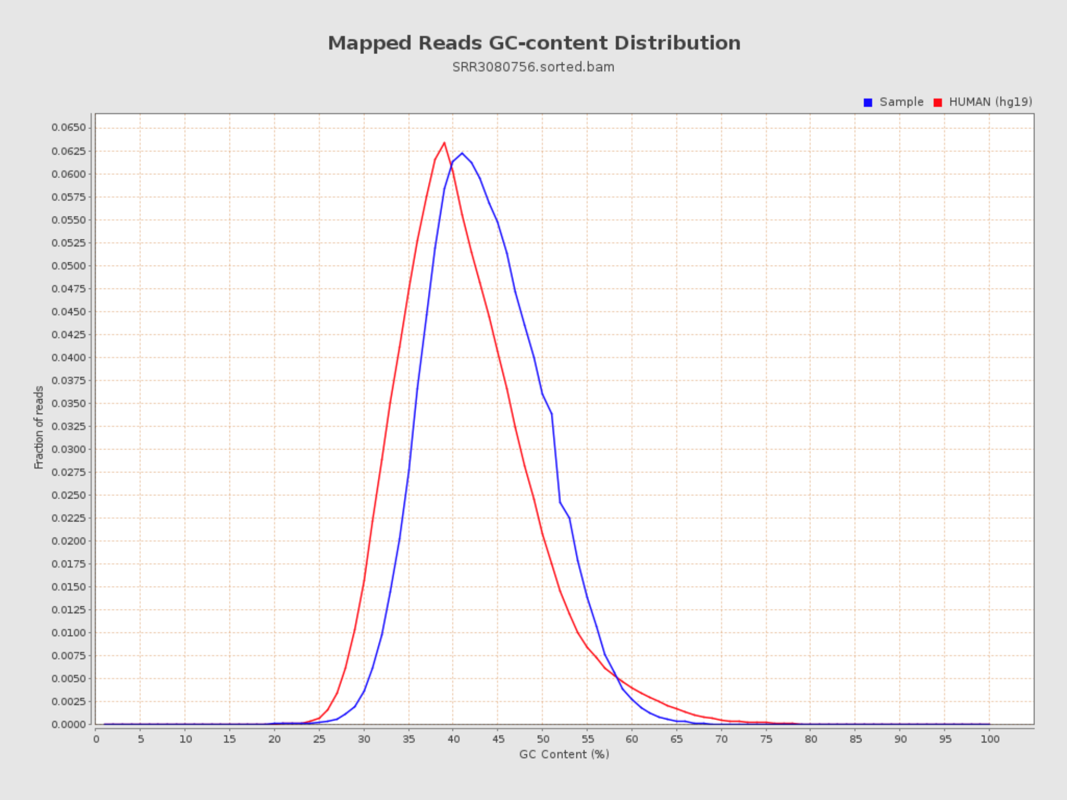
7. Results : Duplication Rate Histogram



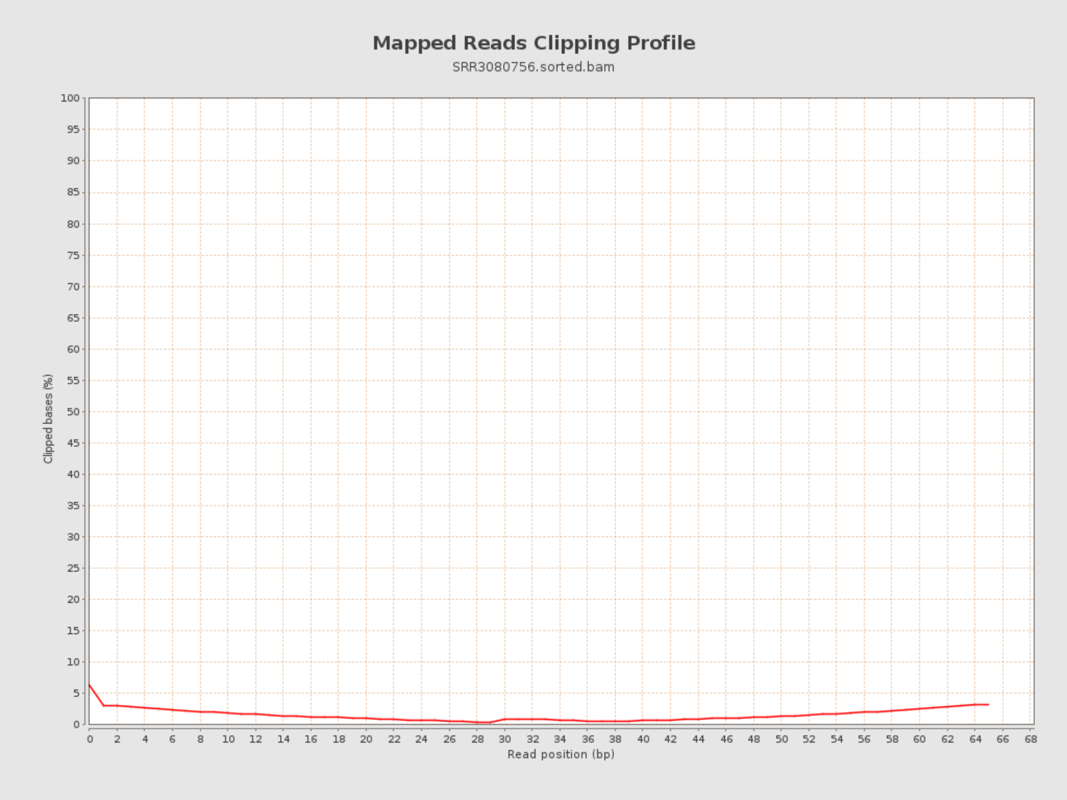
8. Results : Mapped Reads Nucleotide Content



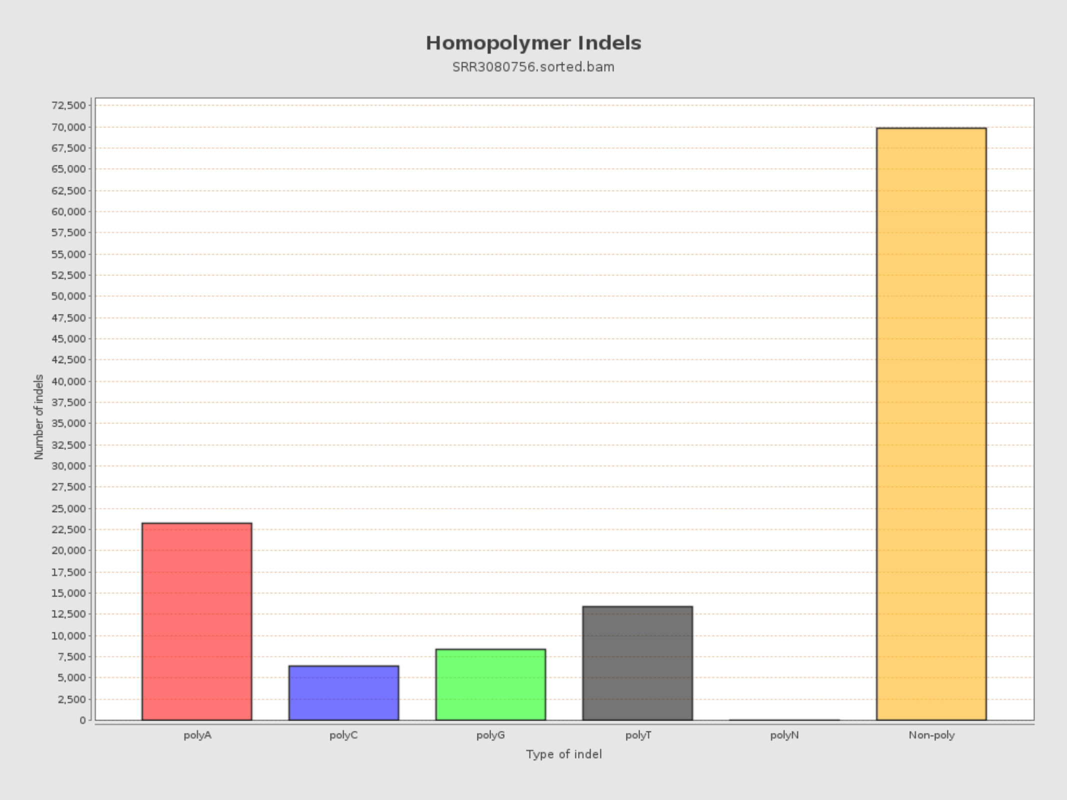
9. Results : Mapped Reads GC-content Distribution



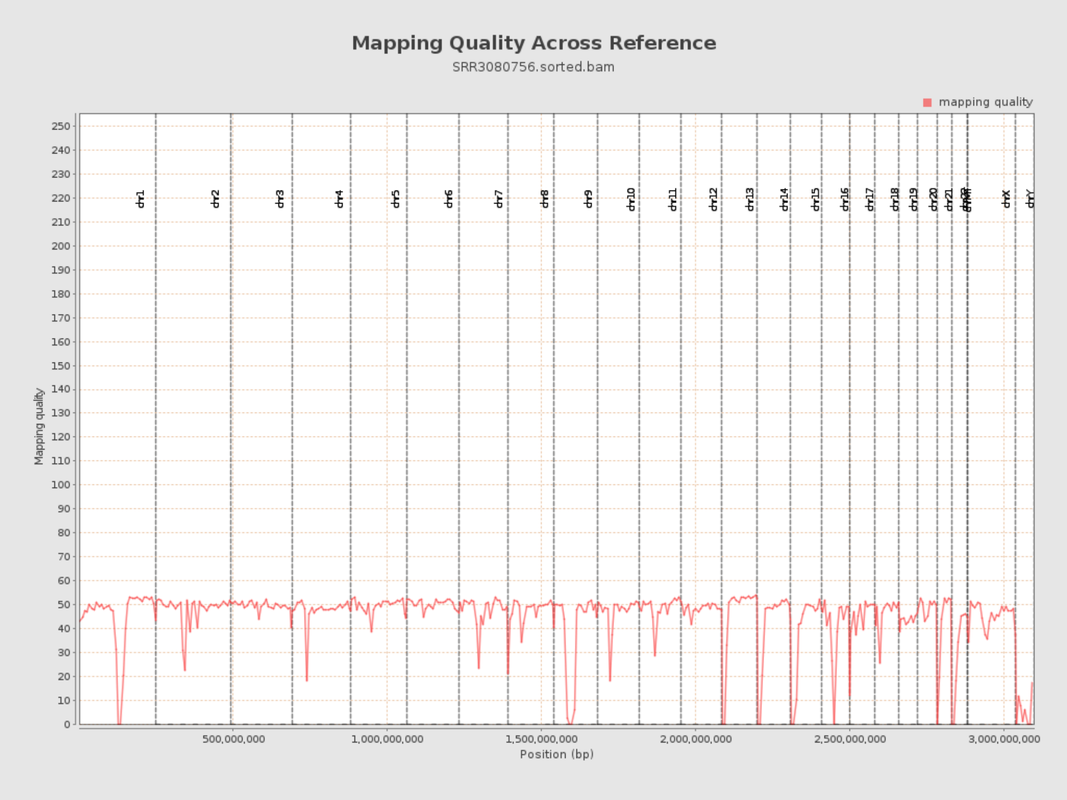
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram