Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 06:30:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080771.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_SRR3080771 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080771.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 06:30:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080771.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,142,107
Mapped reads	6,756,020 / 66.61%
Unmapped reads	3,386,087 / 33.39%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	45,369 / 0.45%
Read min/max/mean length	30 / 66 / 66.15
Duplicated reads (estimated)	748,592 / 7.38%
Duplication rate	8.37%
Clipped reads	1,100,043 / 10.85%

2.2. ACGT Content

Number/percentage of A's	131,337,441 / 30.61%
Number/percentage of C's	87,178,813 / 20.32%
Number/percentage of T's	113,136,130 / 26.37%
Number/percentage of G's	97,268,057 / 22.67%
Number/percentage of N's	138,141 / 0.03%
GC Percentage	42.99%

2.3. Coverage

Mean	0.1386

Standard Deviation	0.7947

2.4. Mapping Quality

Mean Mapping Quality	44.47

2.5. Mismatches and indels

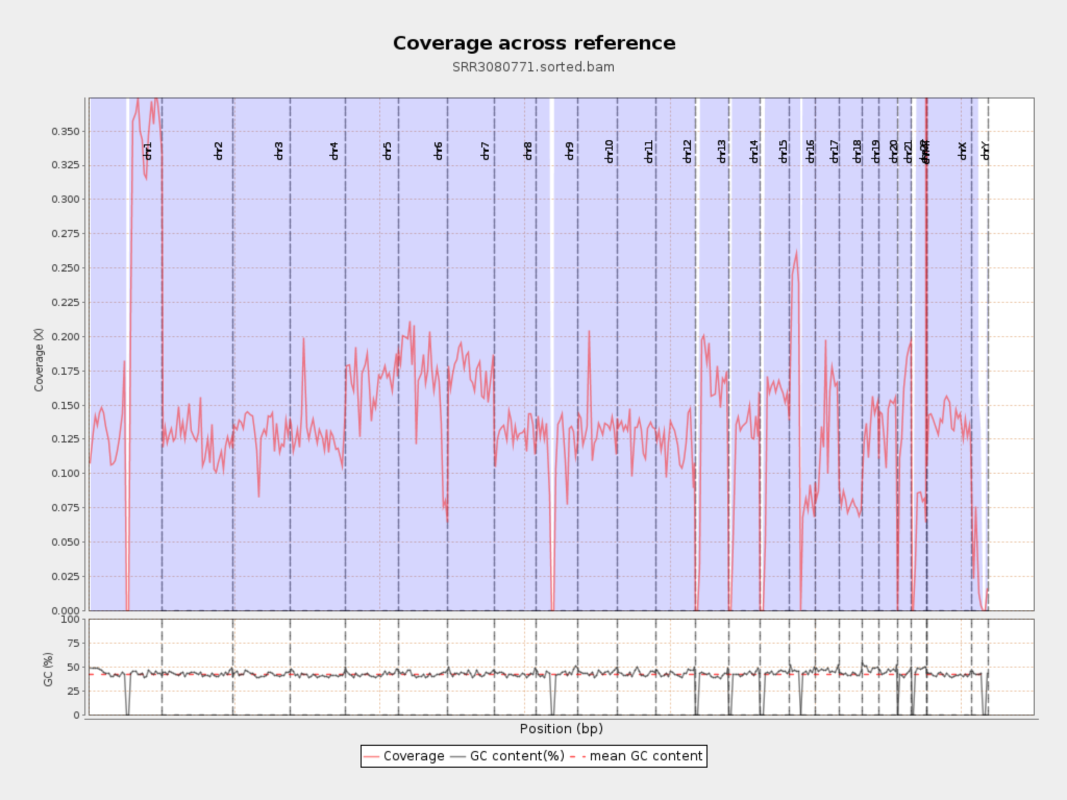
General error rate	0.84%
Mismatches	3,542,090
Insertions	31,014
Mapped reads with at least one insertion	0.46%
Deletions	78,956
Mapped reads with at least one deletion	1.16%
Homopolymer indels	42.89%

2.6. Chromosome stats

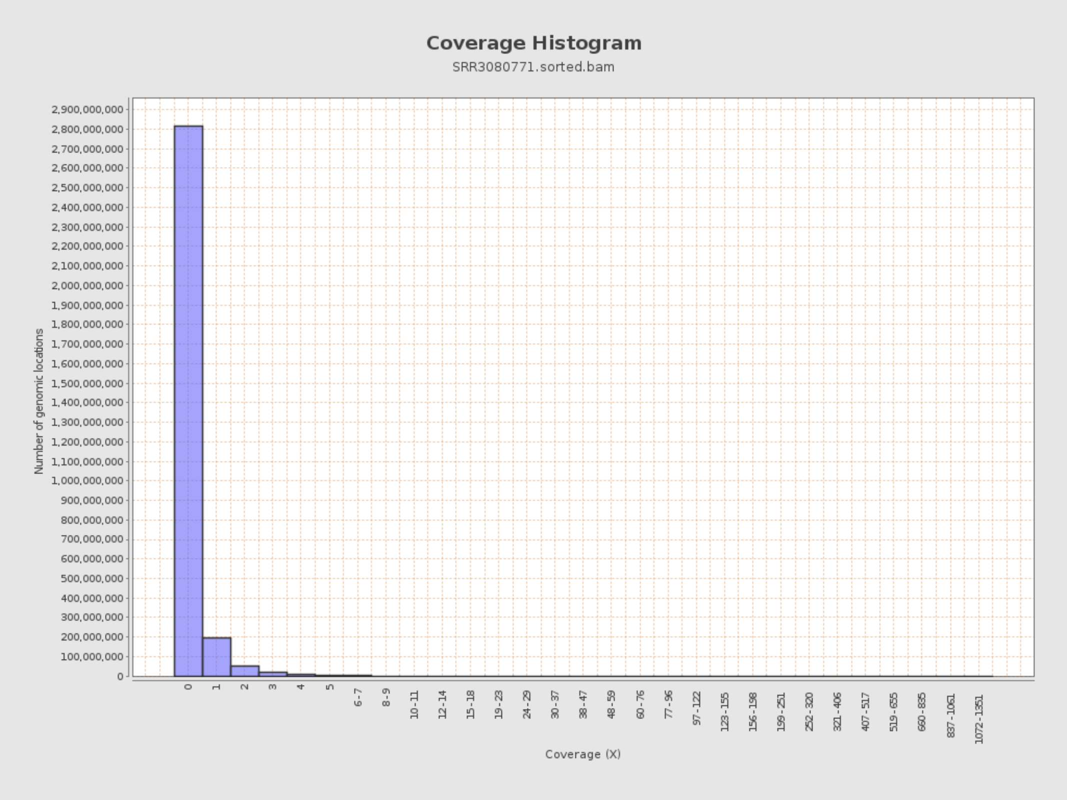
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	54067853	0.2169	1.2452
chr2	243199373	30314557	0.1246	0.7286
chr3	198022430	25890219	0.1307	0.53
chr4	191154276	24612989	0.1288	0.6561
chr5	180915260	30430838	0.1682	0.6057
chr6	171115067	28684676	0.1676	0.9354
chr7	159138663	27713823	0.1741	1.169

chr8	146364022	18999625	0.1298	1.0459
chr9	141213431	15520974	0.1099	0.6068
chr10	135534747	18246366	0.1346	0.8816
chr11	135006516	17643842	0.1307	0.6884
chr12	133851895	16268321	0.1215	0.583
chr13	115169878	16593559	0.1441	0.5579
chr14	107349540	12027013	0.112	0.5727
chr15	102531392	13324653	0.13	0.5452
chr16	90354753	12206049	0.1351	0.6344
chr17	81195210	11255665	0.1386	0.5874
chr18	78077248	6063321	0.0777	0.8838
chr19	59128983	7949938	0.1345	1.1802
chr20	63025520	8721498	0.1384	0.5822
chr21	48129895	6980218	0.145	0.7027
chr22	51304566	2967604	0.0578	0.3524
chrMT	16571	53798	3.2465	3.4922
chrX	155270560	21403588	0.1378	0.579
chrY	59373566	1264279	0.0213	0.6357

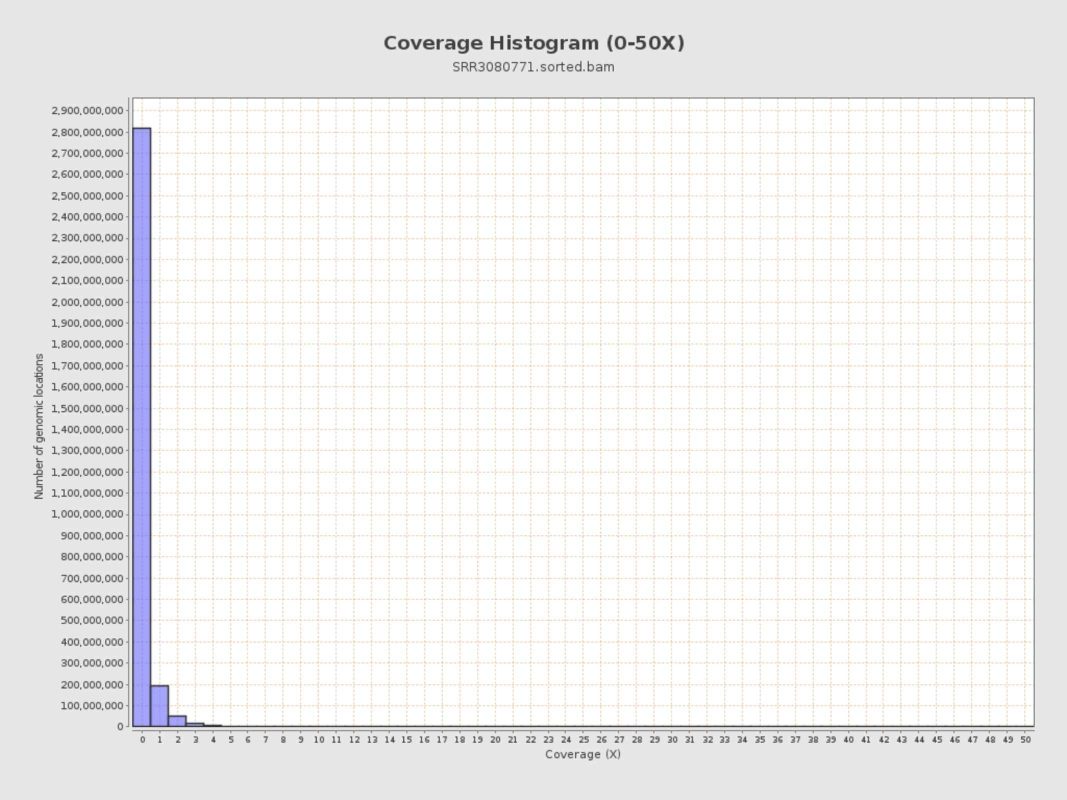
3. Results : Coverage across reference



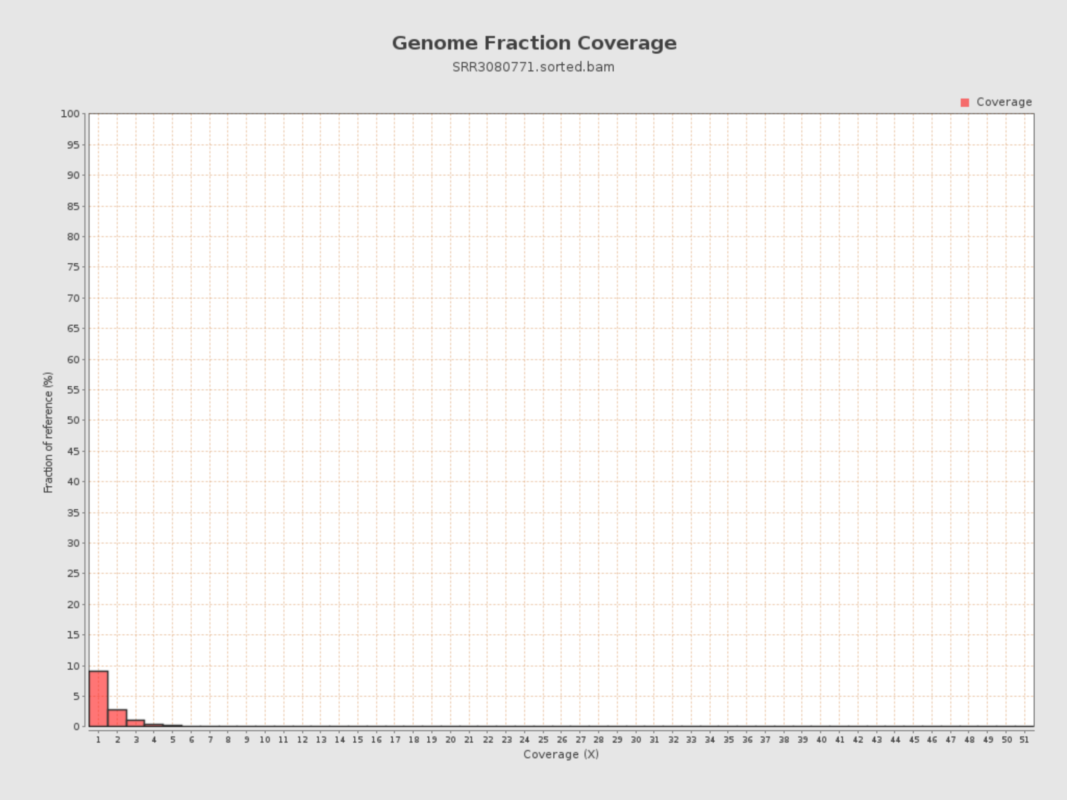
4. Results : Coverage Histogram



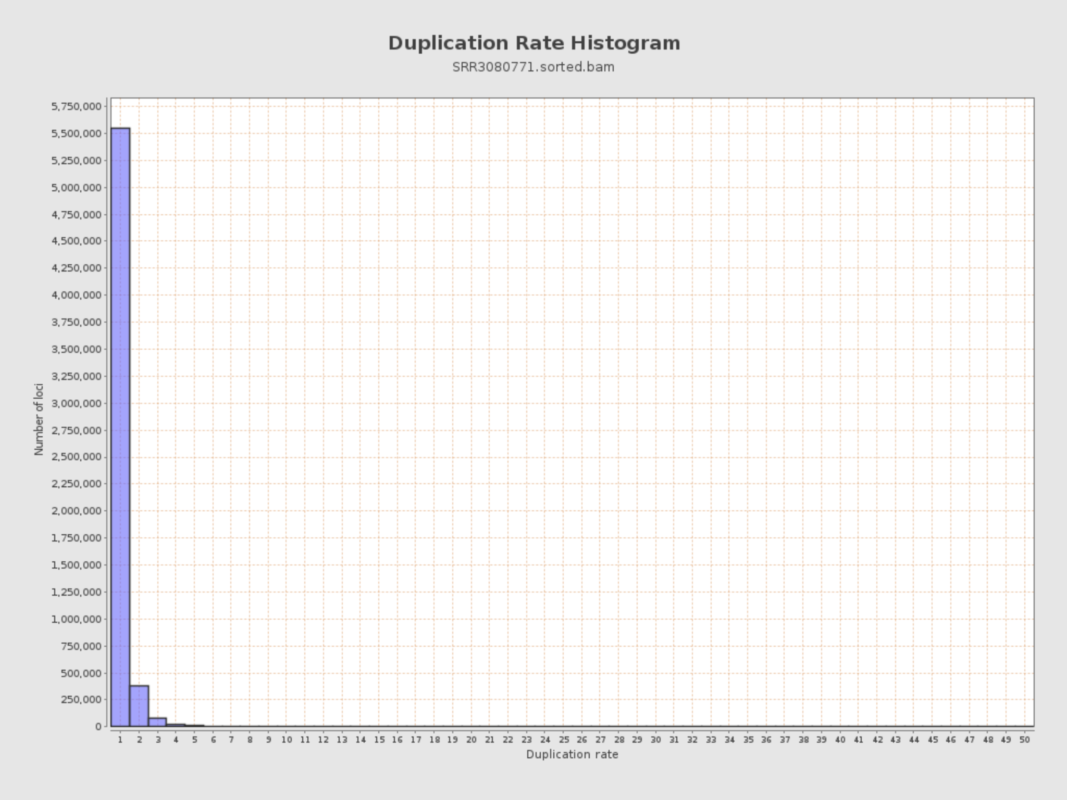
5. Results : Coverage Histogram (0-50X)



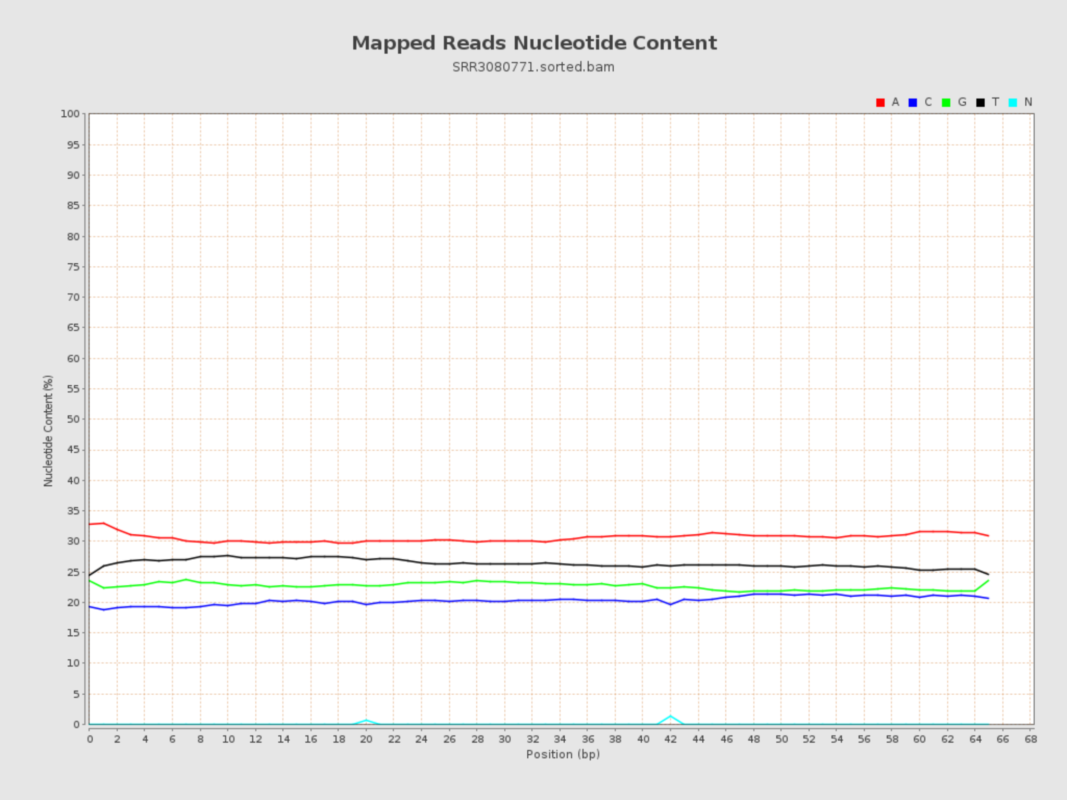
6. Results : Genome Fraction Coverage



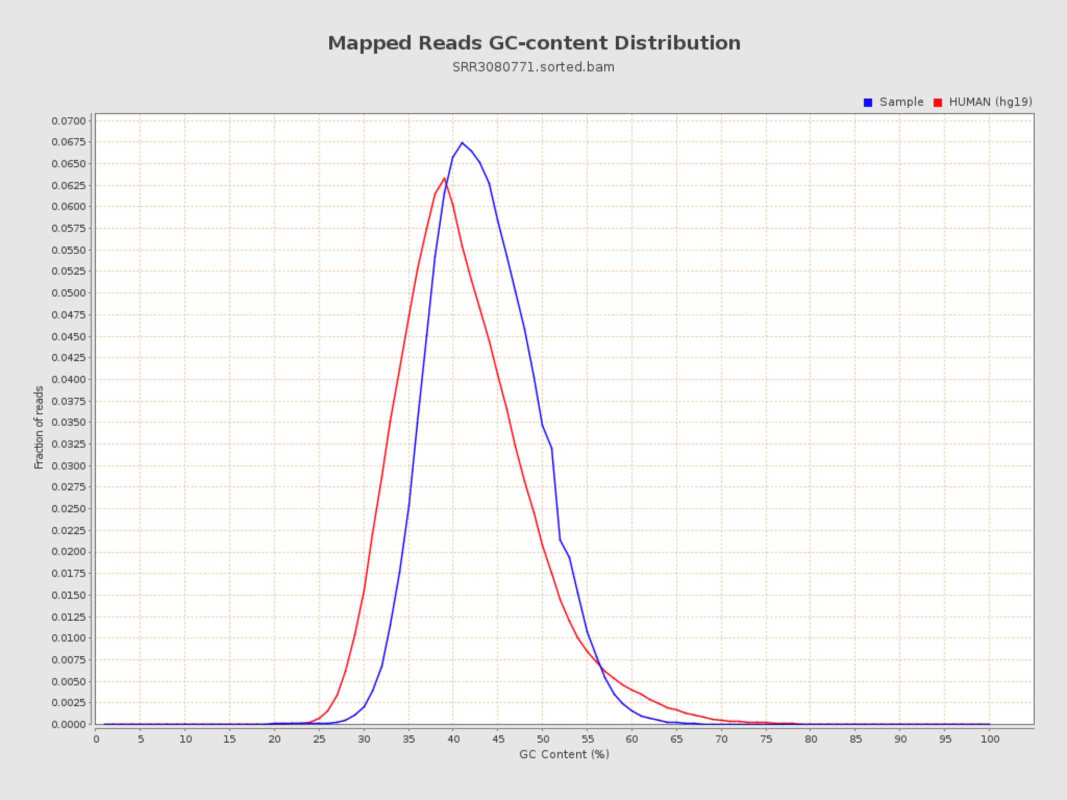
7. Results : Duplication Rate Histogram



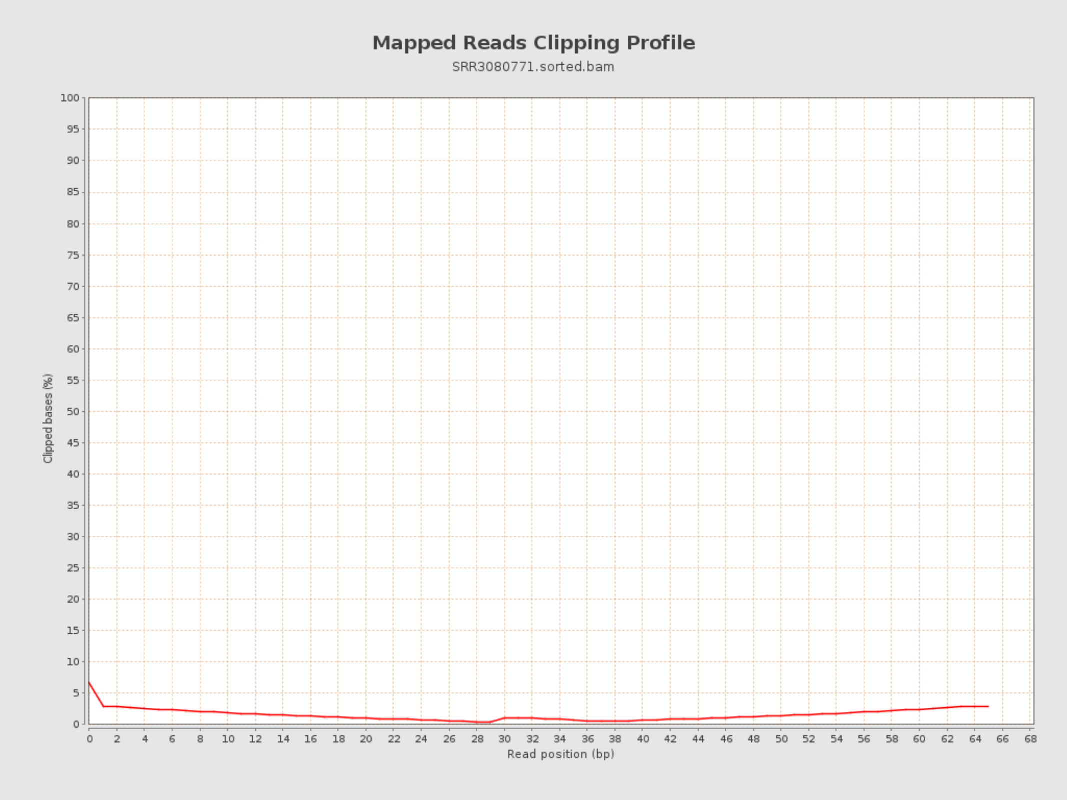
8. Results : Mapped Reads Nucleotide Content



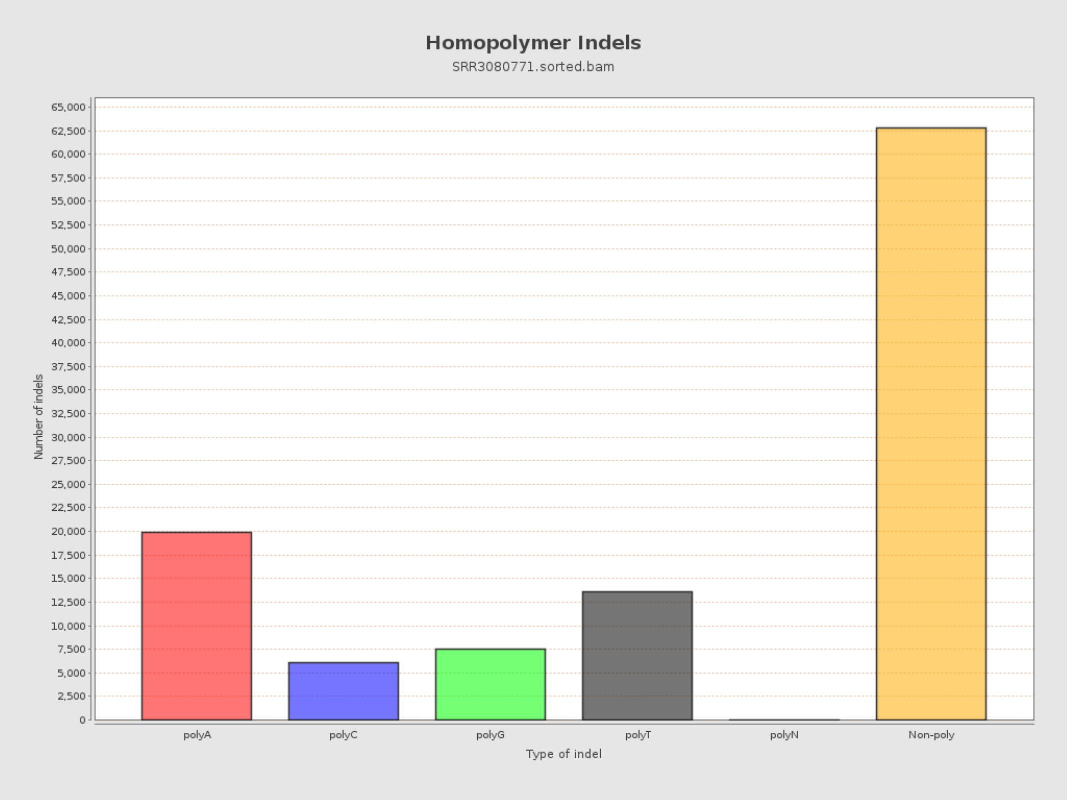
9. Results : Mapped Reads GC-content Distribution



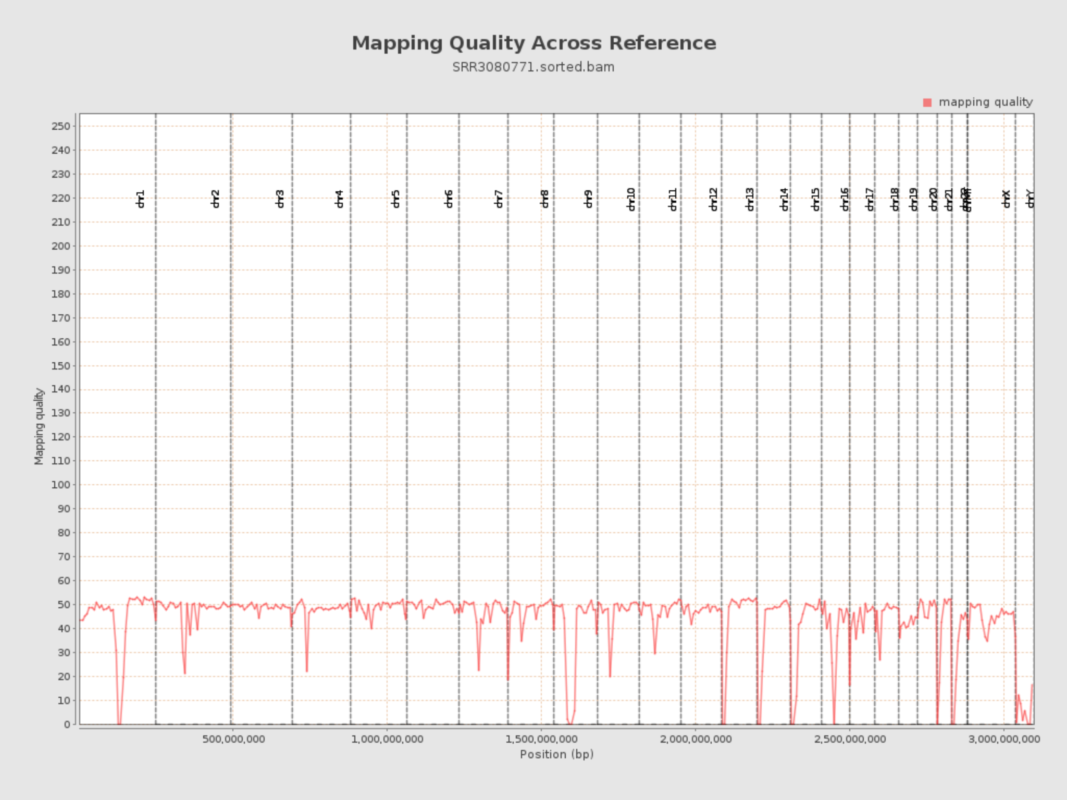
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram