Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 04:49:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080759.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_SRR3080759 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080759.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 04:49:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080759.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,658,864
Mapped reads	3,425,381 / 73.52%
Unmapped reads	1,233,483 / 26.48%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	23,388 / 0.5%
Read min/max/mean length	30 / 66 / 66.17
Duplicated reads (estimated)	543,262 / 11.66%
Duplication rate	11.97%
Clipped reads	498,524 / 10.7%

2.2. ACGT Content

Number/percentage of A's	64,052,708 / 29.27%
Number/percentage of C's	45,199,510 / 20.65%
Number/percentage of T's	60,550,090 / 27.67%
Number/percentage of G's	48,978,263 / 22.38%
Number/percentage of N's	68,632 / 0.03%
GC Percentage	43.03%

2.3. Coverage

Mean	0.0707

Standard Deviation	0.5188

2.4. Mapping Quality

Mean Mapping Quality	44.98

2.5. Mismatches and indels

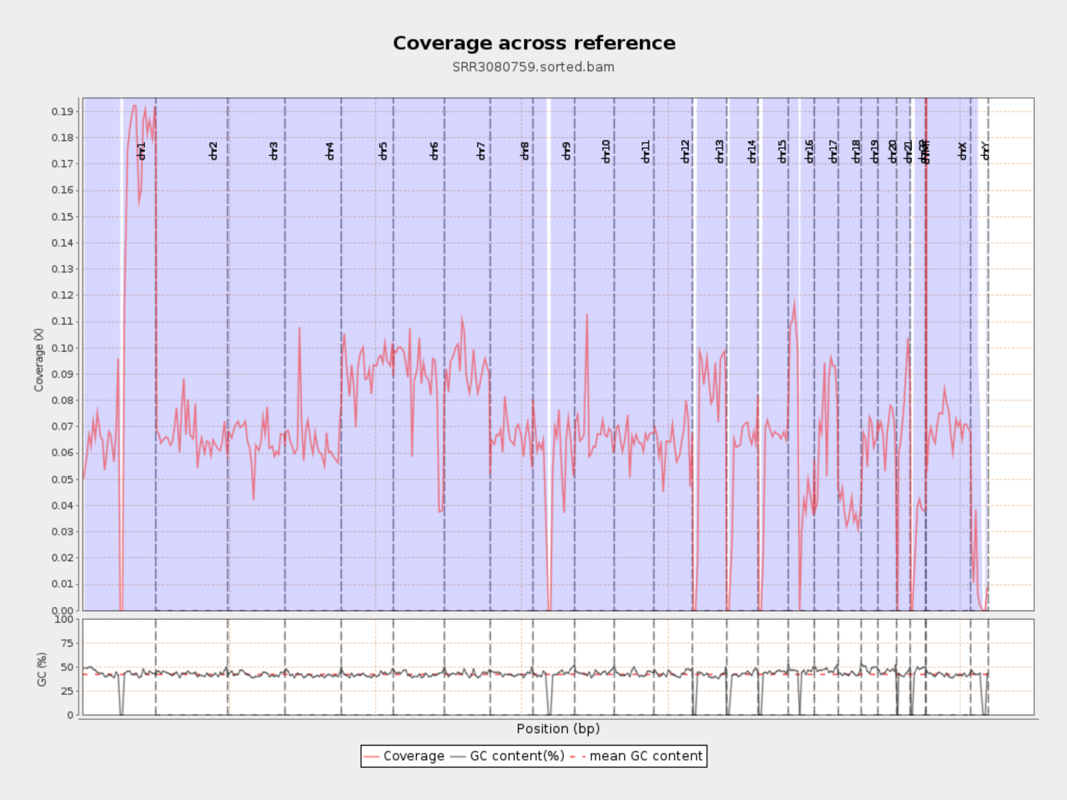
General error rate	0.83%
Mismatches	1,776,017
Insertions	15,397
Mapped reads with at least one insertion	0.45%
Deletions	38,191
Mapped reads with at least one deletion	1.1%
Homopolymer indels	43.55%

2.6. Chromosome stats

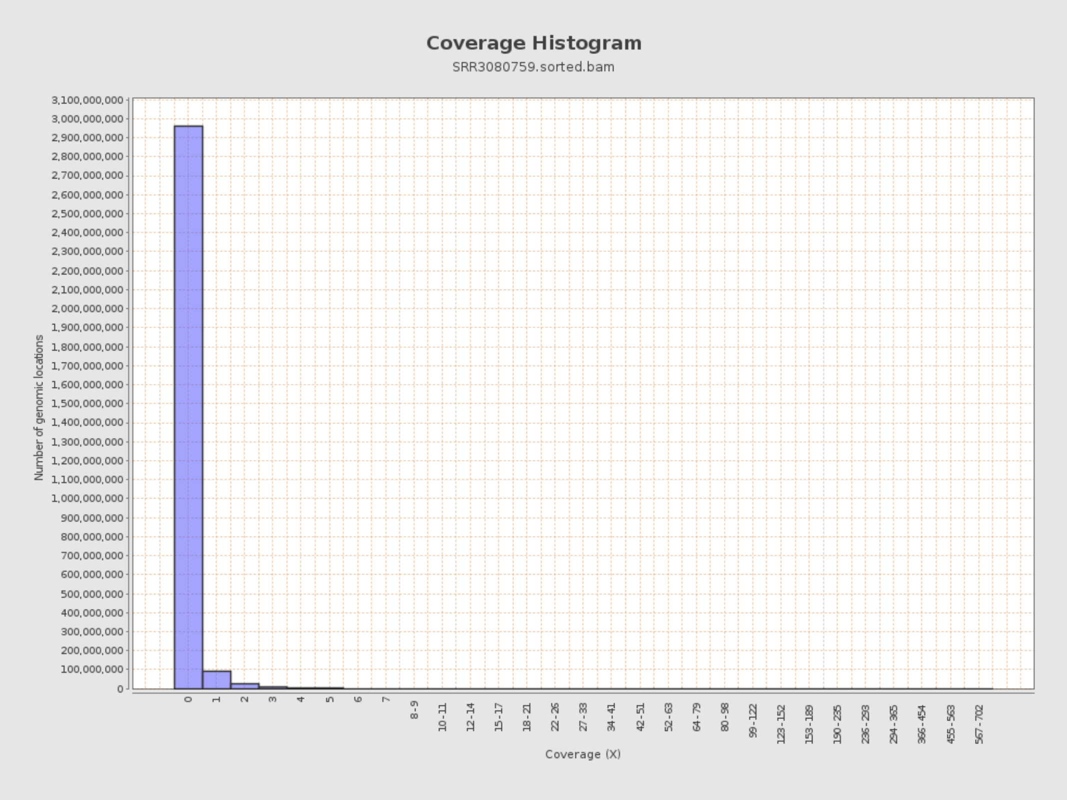
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	27649099	0.1109	0.7866
chr2	243199373	16212356	0.0667	0.4749
chr3	198022430	12869051	0.065	0.3841
chr4	191154276	12429018	0.065	0.4361
chr5	180915260	16781298	0.0928	0.4671
chr6	171115067	14768209	0.0863	0.5616
chr7	159138663	14802260	0.093	0.7912

chr8	146364022	9704342	0.0663	0.547
chr9	141213431	7645377	0.0541	0.4178
chr10	135534747	9337310	0.0689	0.5571
chr11	135006516	8783783	0.0651	0.4681
chr12	133851895	8524323	0.0637	0.3942
chr13	115169878	8678632	0.0754	0.422
chr14	107349540	5898796	0.0549	0.4141
chr15	102531392	5612037	0.0547	0.3616
chr16	90354753	5609267	0.0621	0.4204
chr17	81195210	6017150	0.0741	0.4528
chr18	78077248	2962276	0.0379	0.5984
chr19	59128983	3849013	0.0651	0.6648
chr20	63025520	4325817	0.0686	0.4522
chr21	48129895	3496514	0.0726	0.4974
chr22	51304566	1419890	0.0277	0.2748
chrMT	16571	34407	2.0763	2.4921
chrX	155270560	10874560	0.07	0.4344
chrY	59373566	634320	0.0107	0.3255

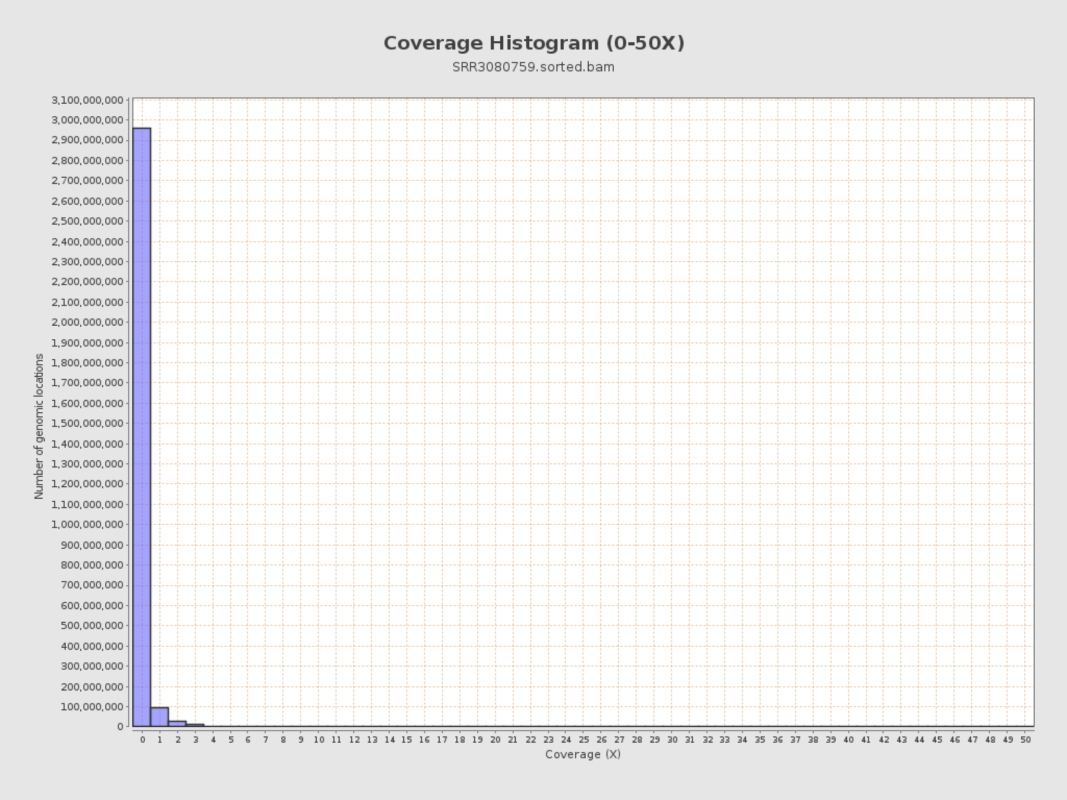
3. Results : Coverage across reference



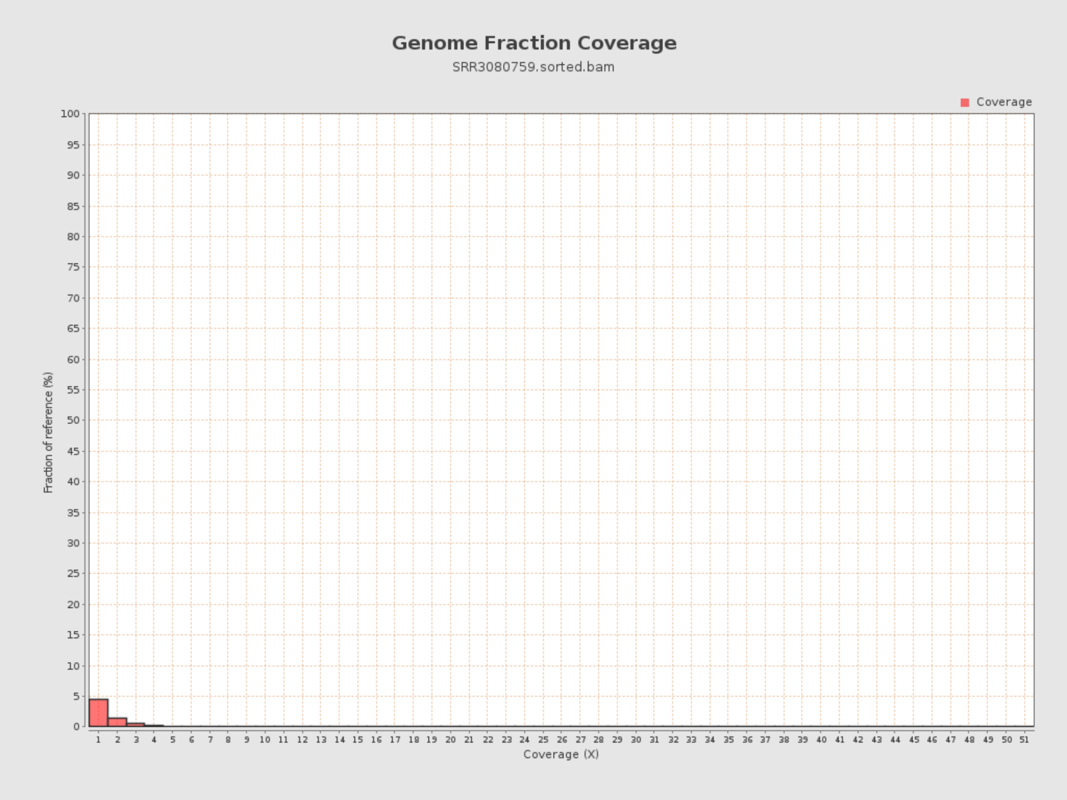
4. Results : Coverage Histogram



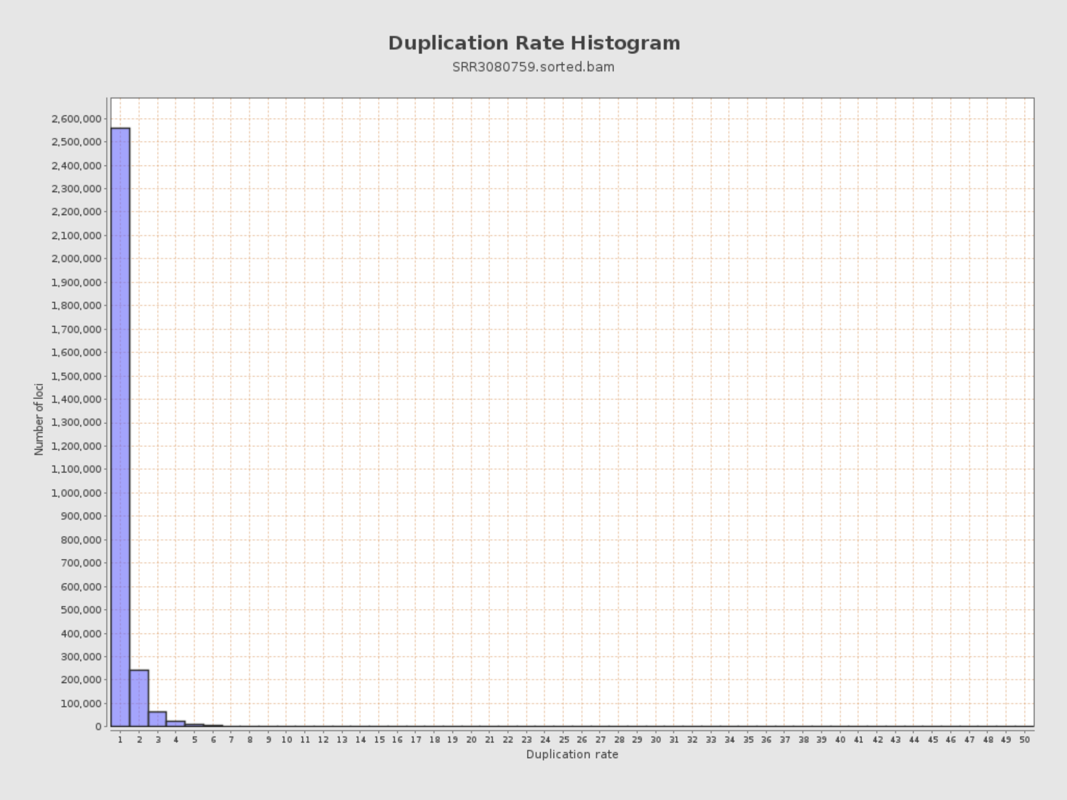
5. Results : Coverage Histogram (0-50X)



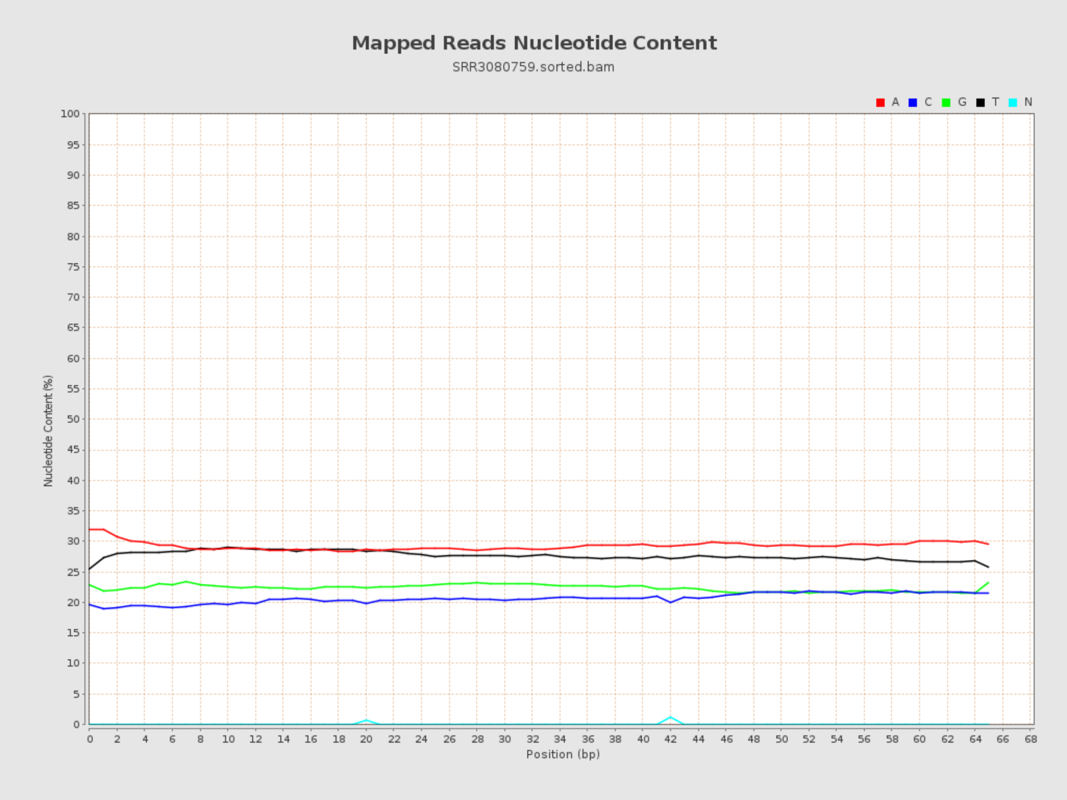
6. Results : Genome Fraction Coverage



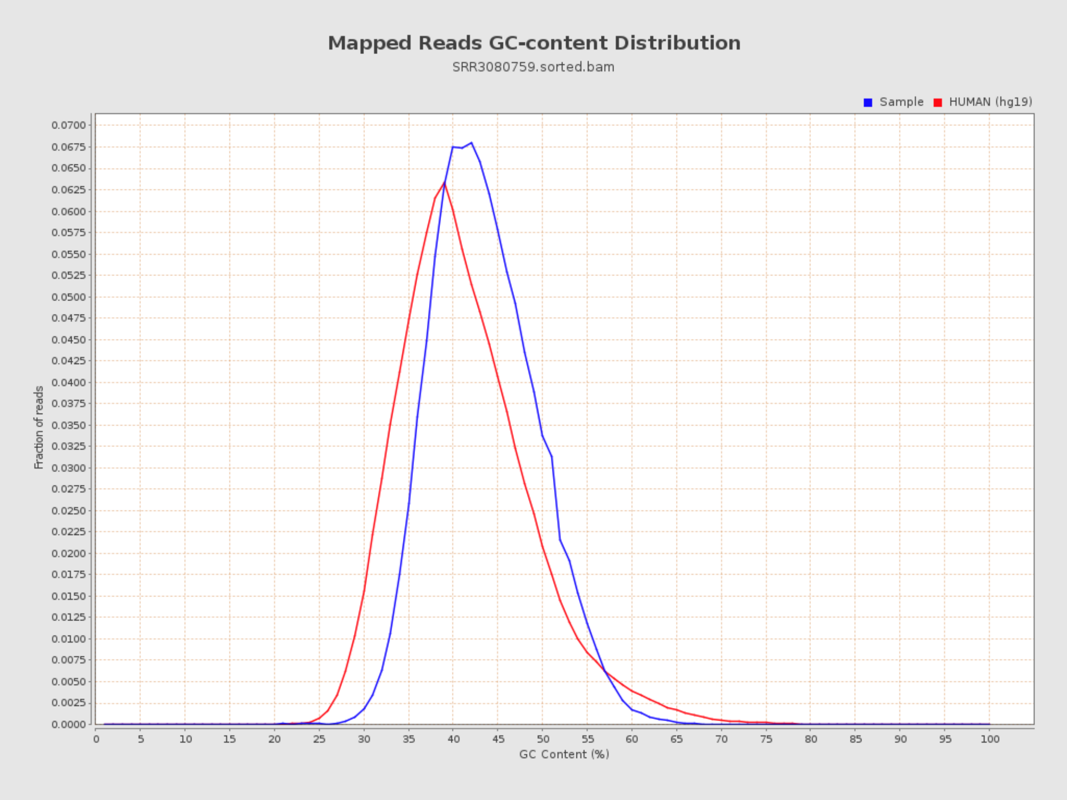
7. Results : Duplication Rate Histogram



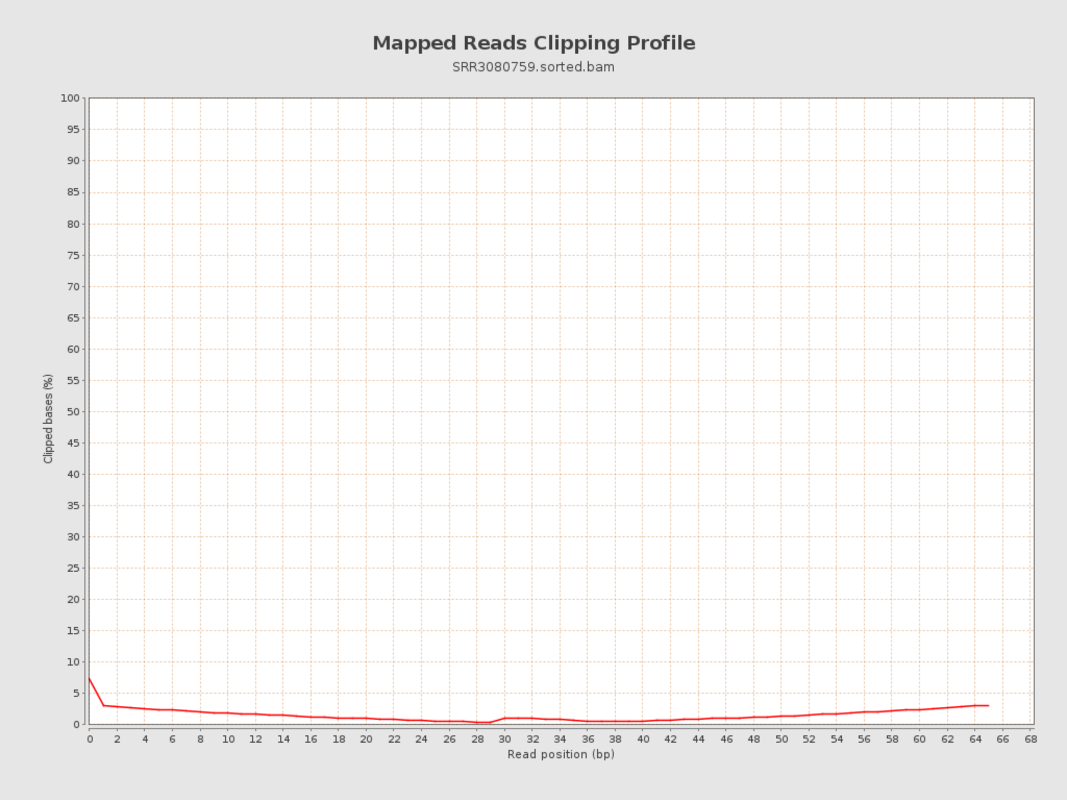
8. Results : Mapped Reads Nucleotide Content



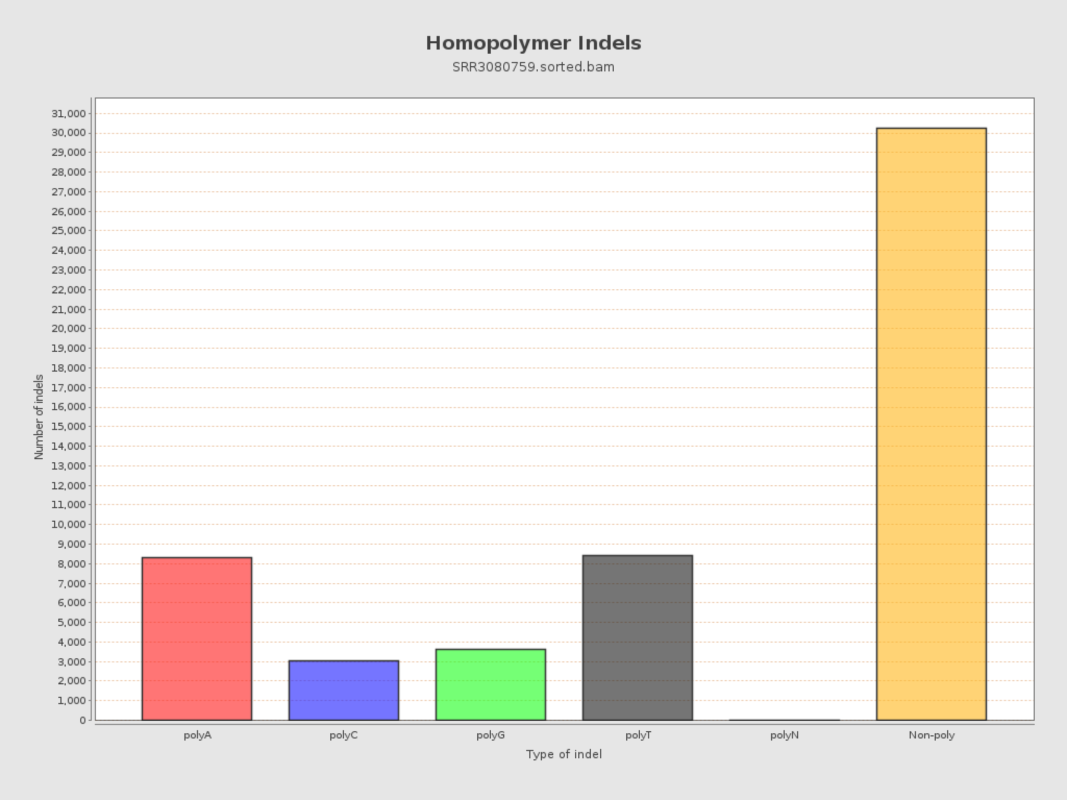
9. Results : Mapped Reads GC-content Distribution



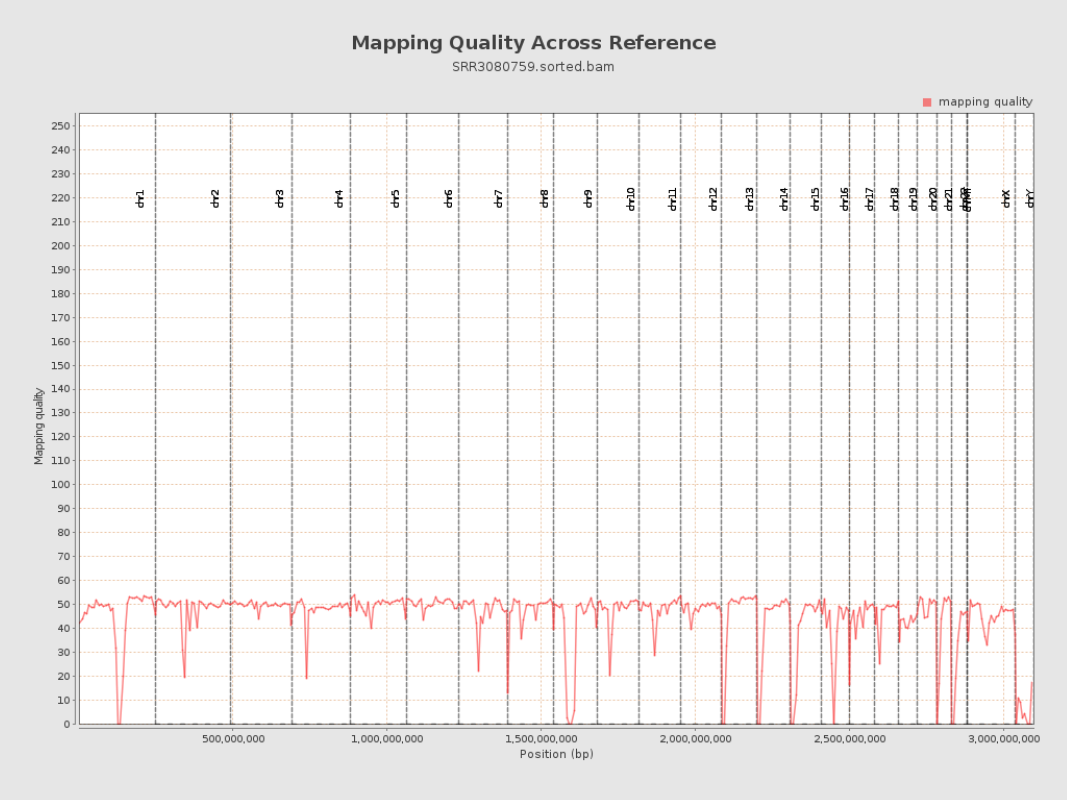
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram