Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 11:53:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081955.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_SRR3081955 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081955.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 11:53:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081955.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,941,741
Mapped reads	2,747,877 / 93.41%
Unmapped reads	193,864 / 6.59%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,653 / 0.63%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	129,687 / 4.41%
Duplication rate	3.52%
Clipped reads	948,009 / 32.23%

2.2. ACGT Content

Number/percentage of A's	54,012,143 / 28.51%
Number/percentage of C's	35,421,194 / 18.7%
Number/percentage of T's	59,600,058 / 31.46%
Number/percentage of G's	40,366,664 / 21.31%
Number/percentage of N's	24,937 / 0.01%
GC Percentage	40.01%

2.3. Coverage

Mean	0.0612

Standard Deviation	0.5289

2.4. Mapping Quality

Mean Mapping Quality	46.76

2.5. Mismatches and indels

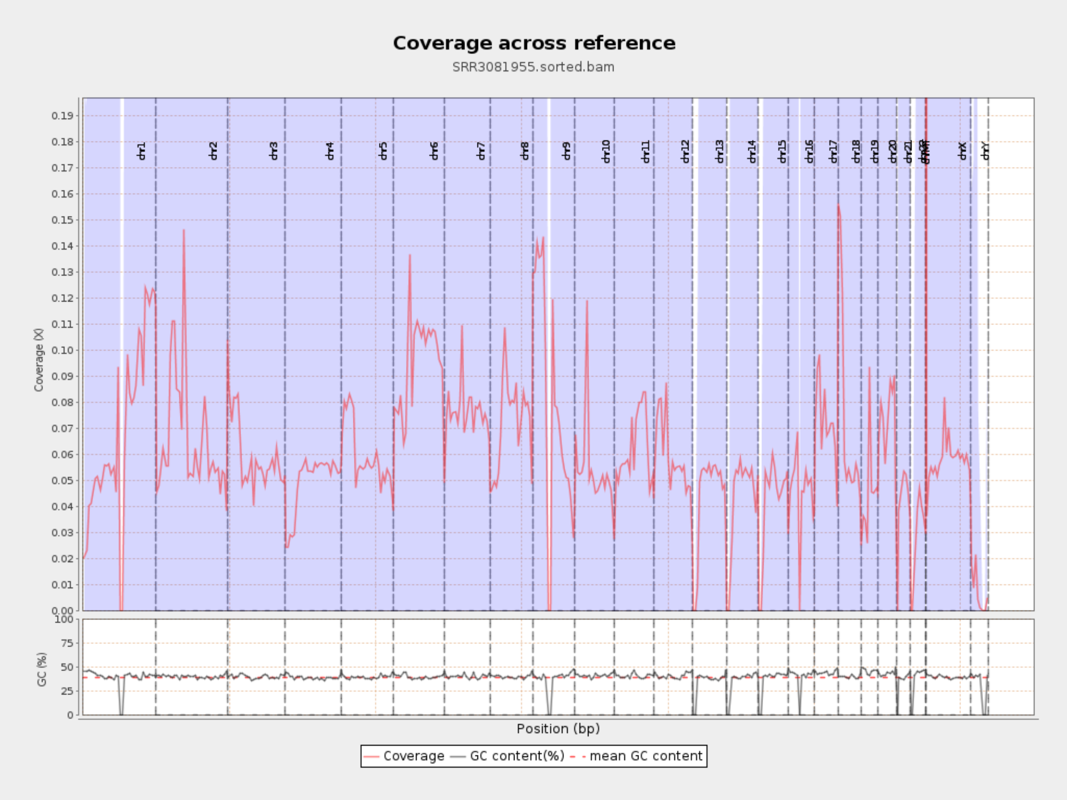
General error rate	0.76%
Mismatches	1,416,401
Insertions	13,580
Mapped reads with at least one insertion	0.49%
Deletions	38,091
Mapped reads with at least one deletion	1.37%
Homopolymer indels	48.06%

2.6. Chromosome stats

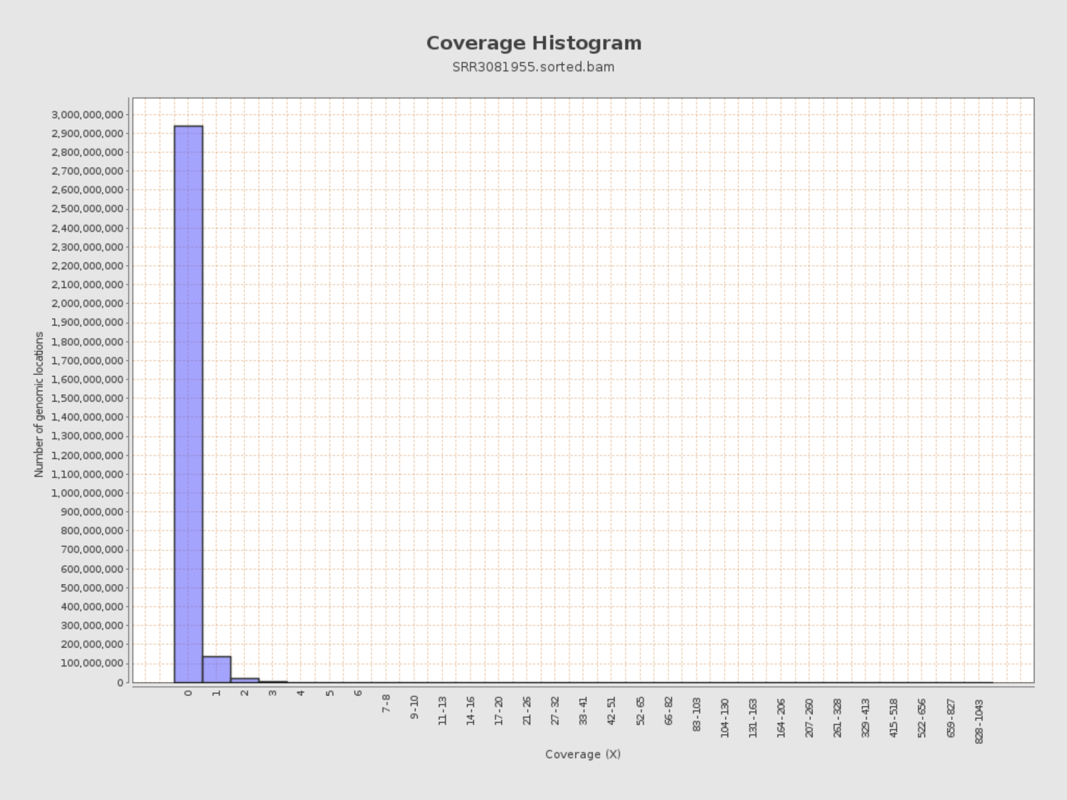
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	17070513	0.0685	0.8885
chr2	243199373	16273409	0.0669	0.7225
chr3	198022430	11843299	0.0598	0.2841
chr4	191154276	9434822	0.0494	0.2821
chr5	180915260	10749019	0.0594	0.2826
chr6	171115067	16516334	0.0965	0.4755
chr7	159138663	12135580	0.0763	0.6883

chr8	146364022	10621903	0.0726	0.7555
chr9	141213431	11175692	0.0791	0.6204
chr10	135534747	7419483	0.0547	0.5388
chr11	135006516	8397388	0.0622	0.4114
chr12	133851895	7890035	0.0589	0.298
chr13	115169878	5015967	0.0436	0.2362
chr14	107349540	4621039	0.043	0.2944
chr15	102531392	4198489	0.0409	0.2351
chr16	90354753	4033275	0.0446	0.3075
chr17	81195210	5970272	0.0735	0.3634
chr18	78077248	5743580	0.0736	0.9159
chr19	59128983	2711619	0.0459	0.7267
chr20	63025520	4718129	0.0749	0.3204
chr21	48129895	1990859	0.0414	0.2865
chr22	51304566	1435387	0.028	0.1871
chrMT	16571	128313	7.7432	4.383
chrX	155270560	8996919	0.0579	0.3322
chrY	59373566	400842	0.0068	0.1764

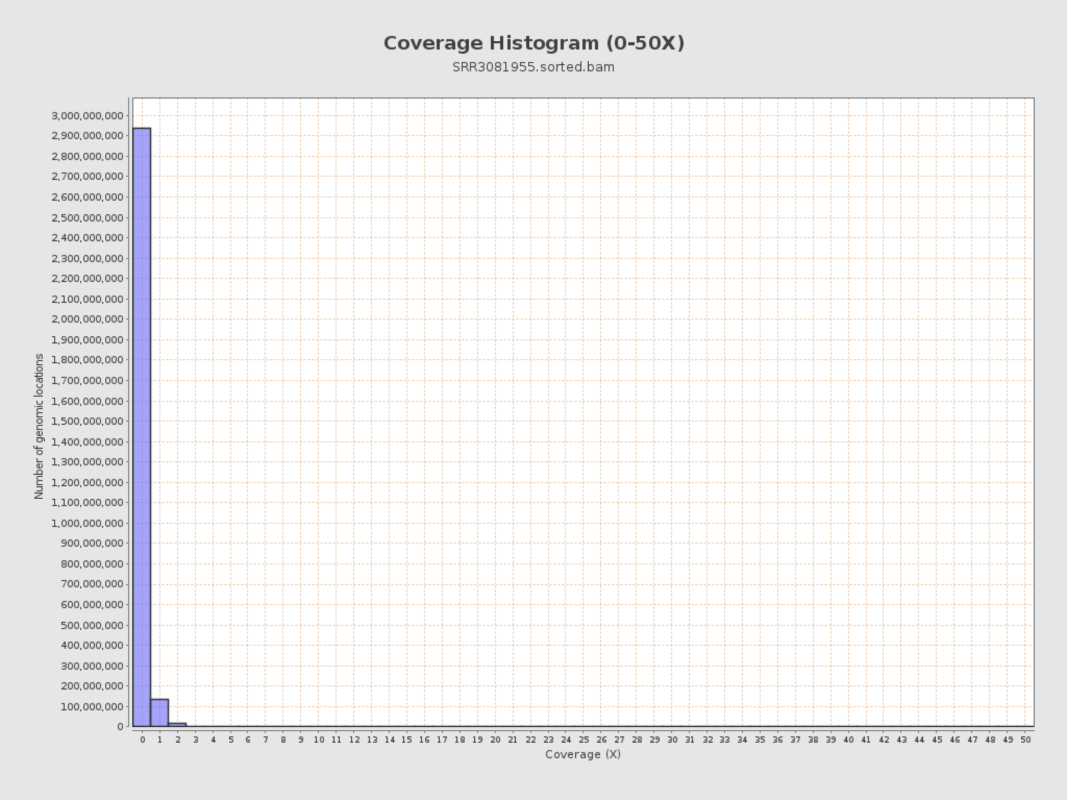
3. Results : Coverage across reference



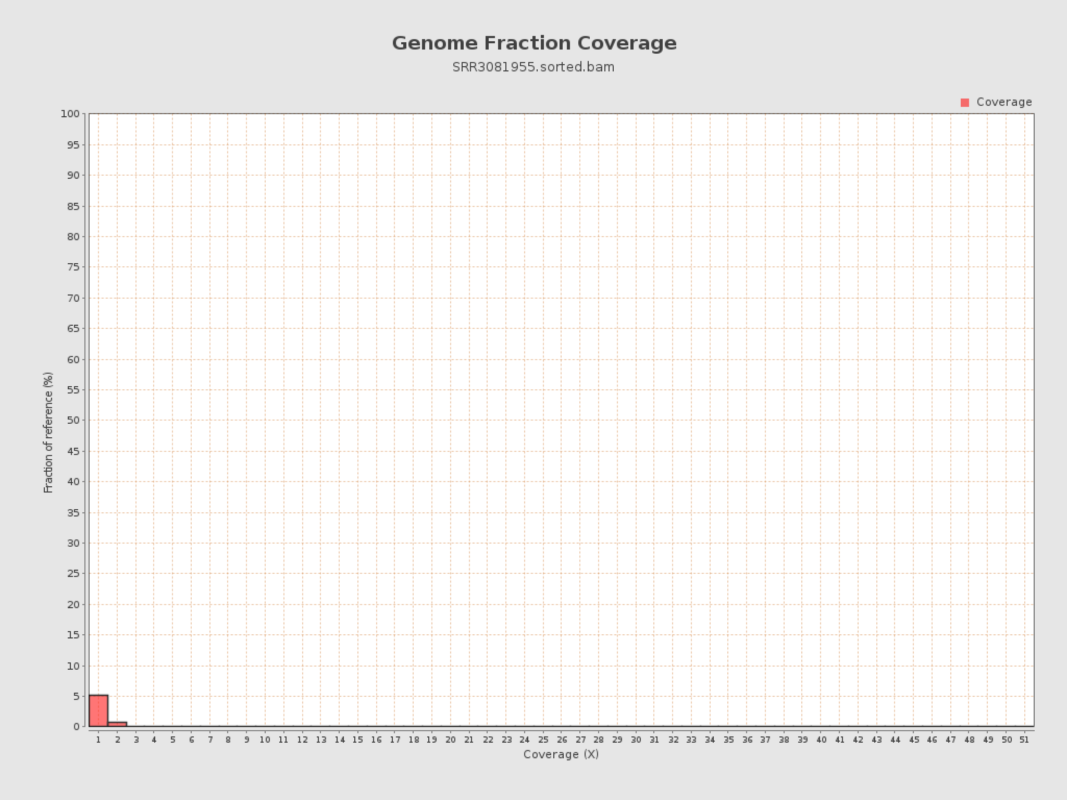
4. Results : Coverage Histogram



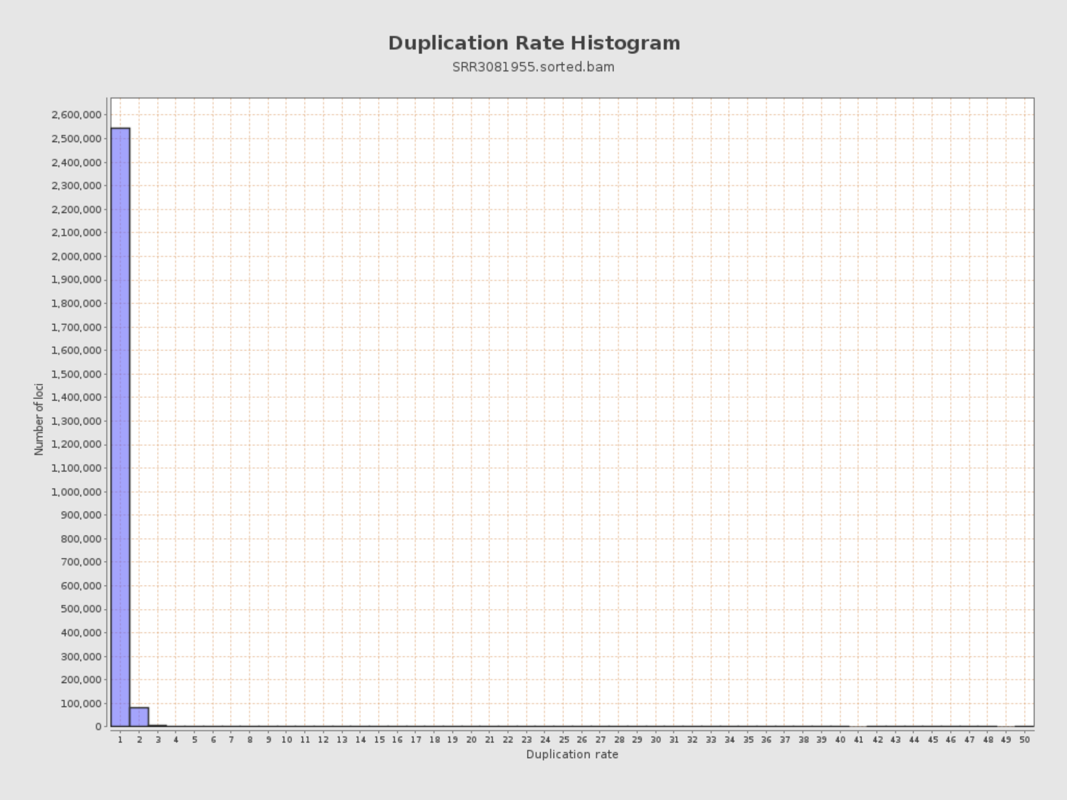
5. Results : Coverage Histogram (0-50X)



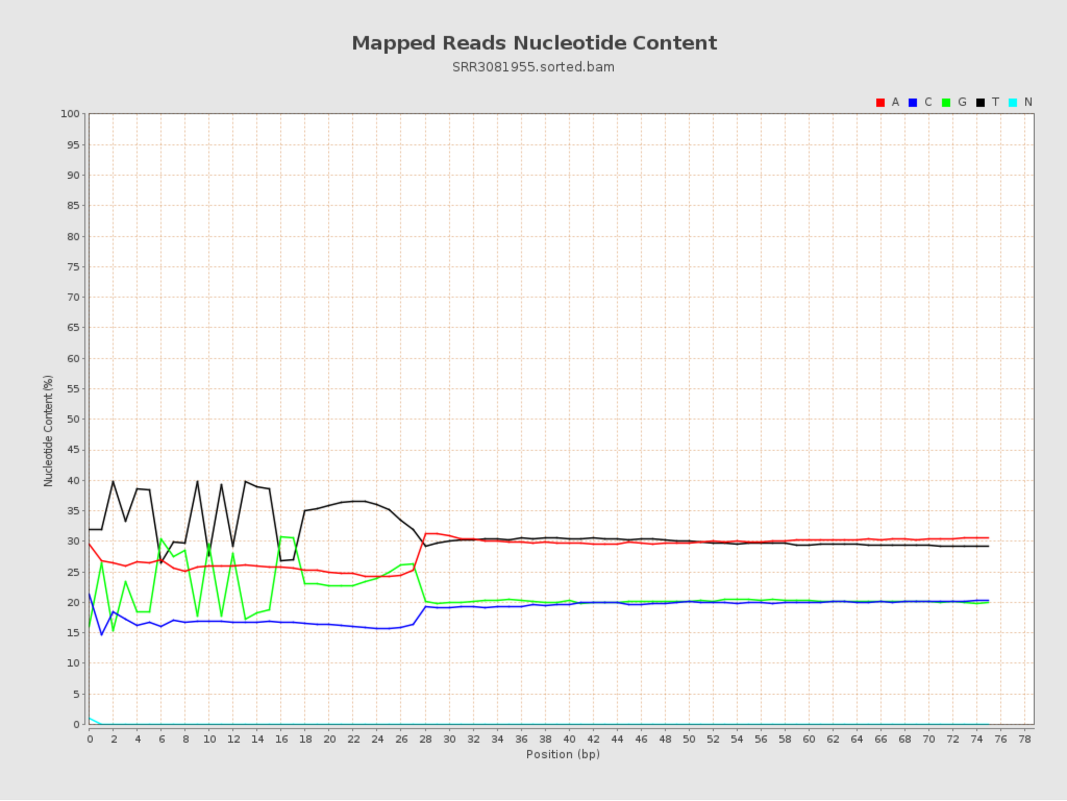
6. Results : Genome Fraction Coverage



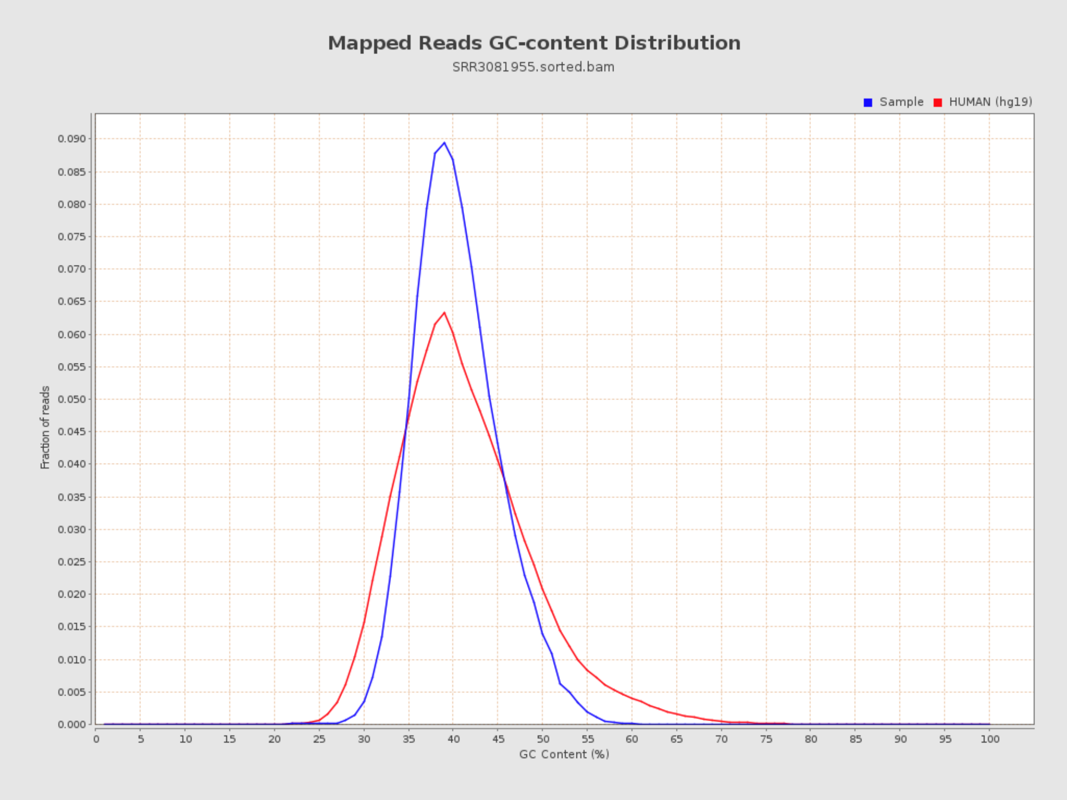
7. Results : Duplication Rate Histogram



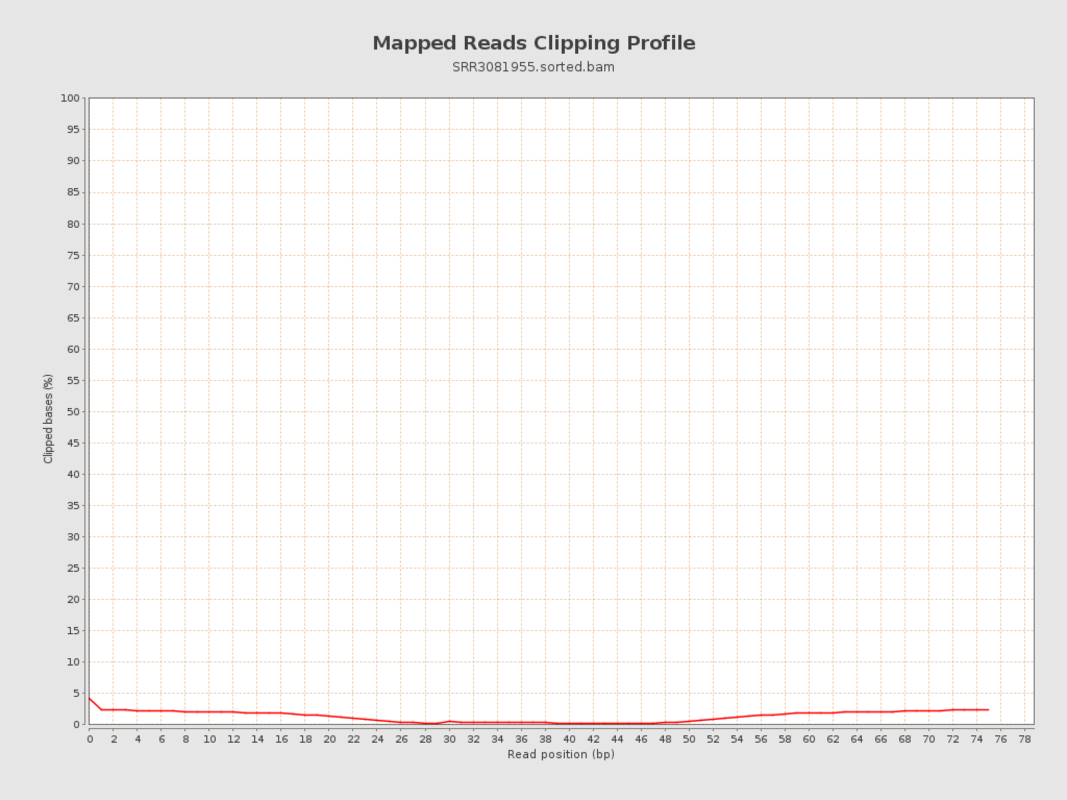
8. Results : Mapped Reads Nucleotide Content



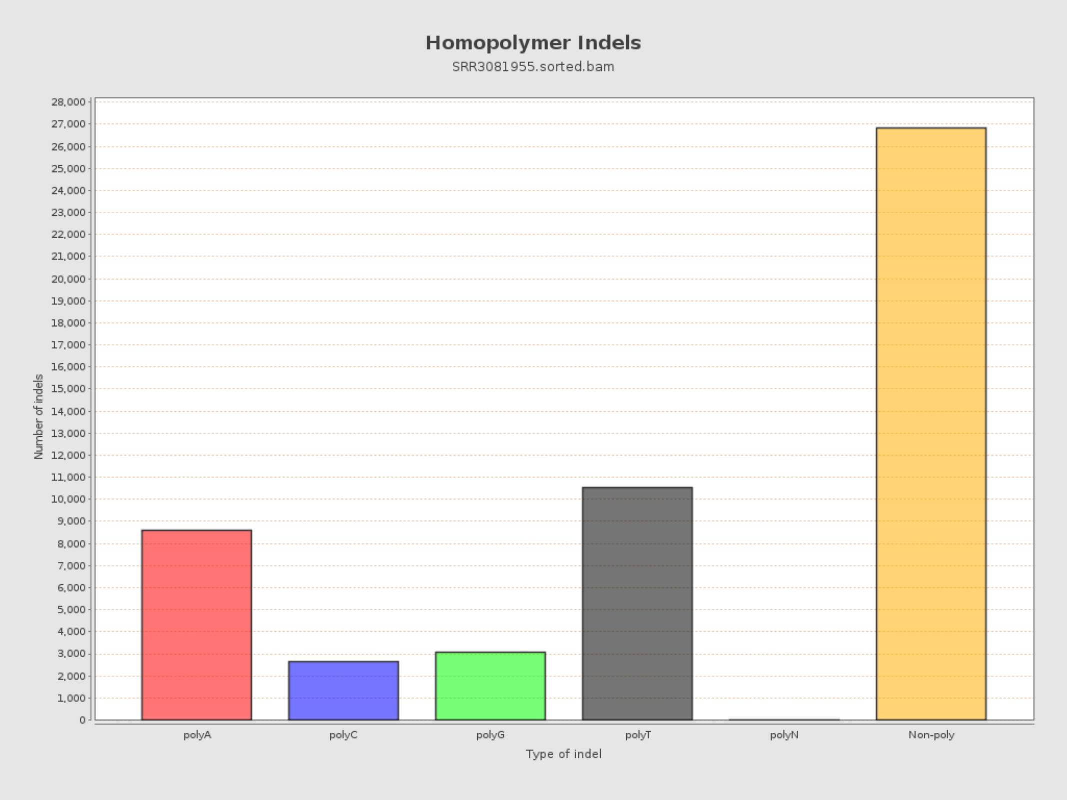
9. Results : Mapped Reads GC-content Distribution



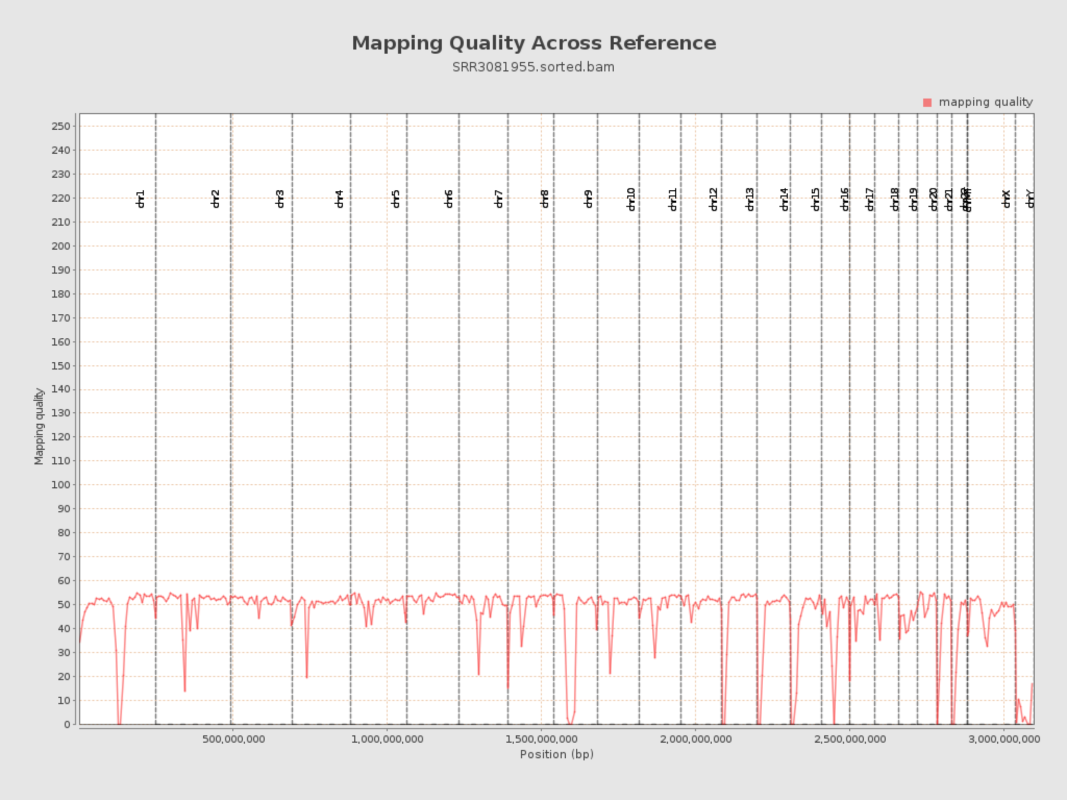
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram