Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 05:05:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081247.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_SRR3081247 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081247.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 05:05:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081247.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,791,190
Mapped reads	3,123,012 / 82.38%
Unmapped reads	668,178 / 17.62%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	26,469 / 0.7%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	199,199 / 5.25%
Duplication rate	5.16%
Clipped reads	1,273,207 / 33.58%

2.2. ACGT Content

Number/percentage of A's	58,561,344 / 27.83%
Number/percentage of C's	37,985,854 / 18.05%
Number/percentage of T's	67,899,248 / 32.26%
Number/percentage of G's	45,960,334 / 21.84%
Number/percentage of N's	55,694 / 0.03%
GC Percentage	39.89%

2.3. Coverage

Mean	0.068

Standard Deviation	0.5588

2.4. Mapping Quality

Mean Mapping Quality	47.11

2.5. Mismatches and indels

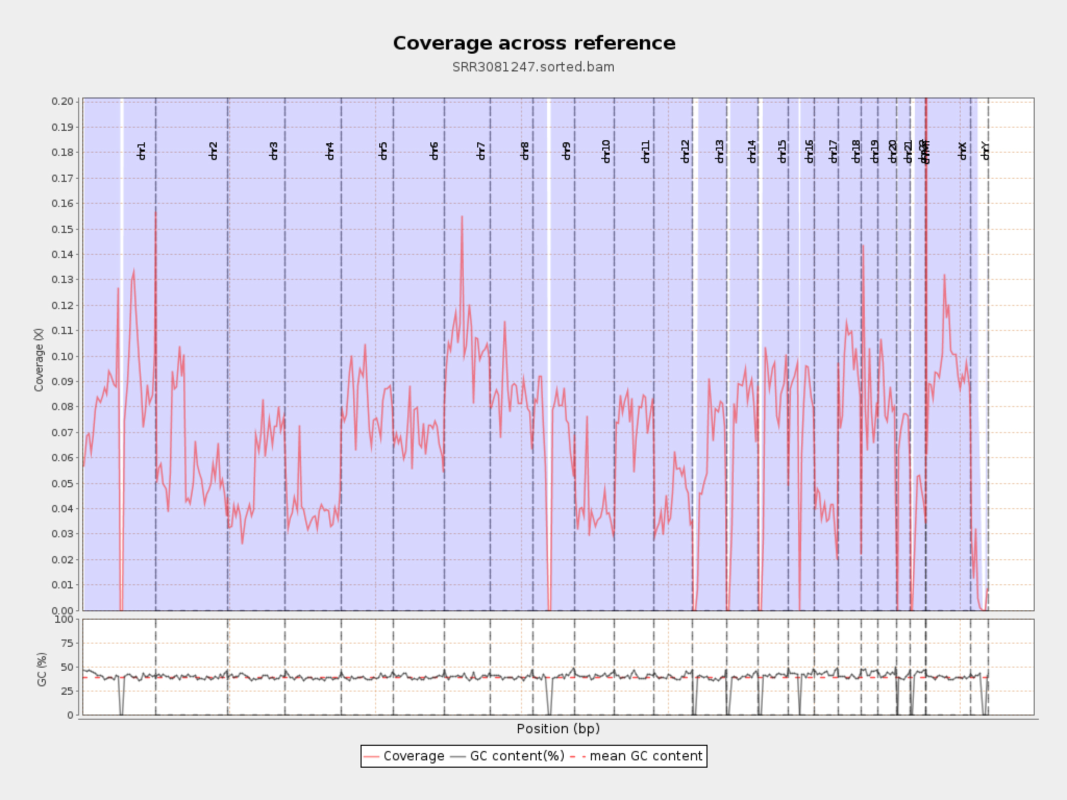
General error rate	0.87%
Mismatches	1,808,806
Insertions	17,255
Mapped reads with at least one insertion	0.55%
Deletions	53,910
Mapped reads with at least one deletion	1.71%
Homopolymer indels	49.69%

2.6. Chromosome stats

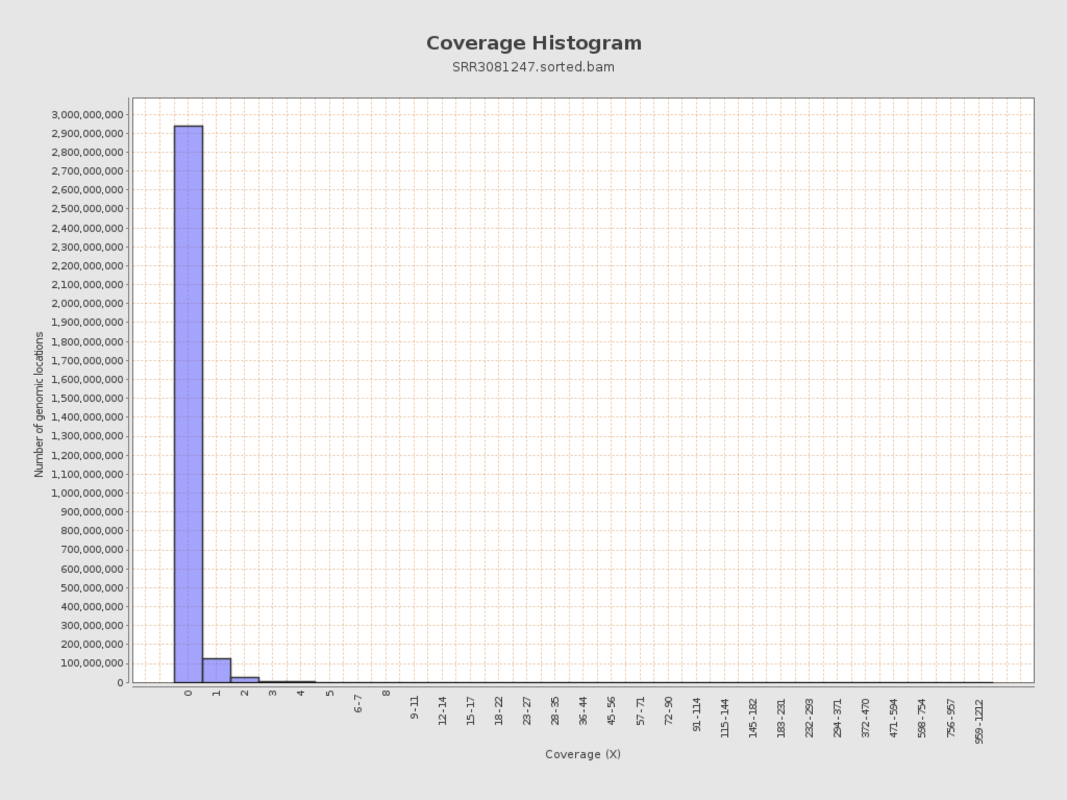
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	20859097	0.0837	1.0859
chr2	243199373	14298308	0.0588	0.5146
chr3	198022430	10808975	0.0546	0.2963
chr4	191154276	7583031	0.0397	0.2838
chr5	180915260	14841287	0.082	0.3632
chr6	171115067	11803983	0.069	0.3872
chr7	159138663	16926957	0.1064	0.9551

chr8	146364022	12346605	0.0844	0.818
chr9	141213431	9716128	0.0688	0.4821
chr10	135534747	5354631	0.0395	0.3875
chr11	135006516	10305835	0.0763	0.4747
chr12	133851895	5799845	0.0433	0.2667
chr13	115169878	6573865	0.0571	0.2992
chr14	107349540	7497931	0.0698	0.3484
chr15	102531392	7474045	0.0729	0.3389
chr16	90354753	6965094	0.0771	0.3719
chr17	81195210	3143082	0.0387	0.2802
chr18	78077248	7493850	0.096	0.7689
chr19	59128983	4977704	0.0842	0.798
chr20	63025520	5316530	0.0844	0.3734
chr21	48129895	3099266	0.0644	0.3603
chr22	51304566	1743994	0.034	0.2251
chrMT	16571	99213	5.9871	4.1417
chrX	155270560	14920575	0.0961	0.4315
chrY	59373566	603562	0.0102	0.2355

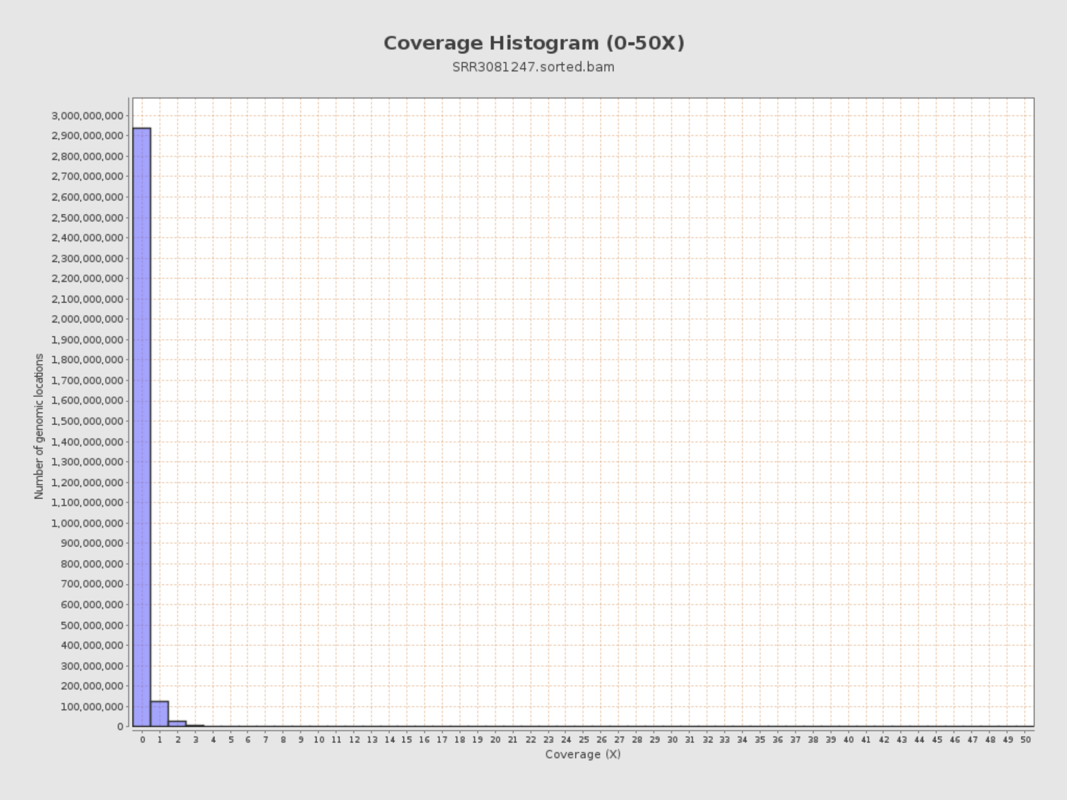
3. Results : Coverage across reference



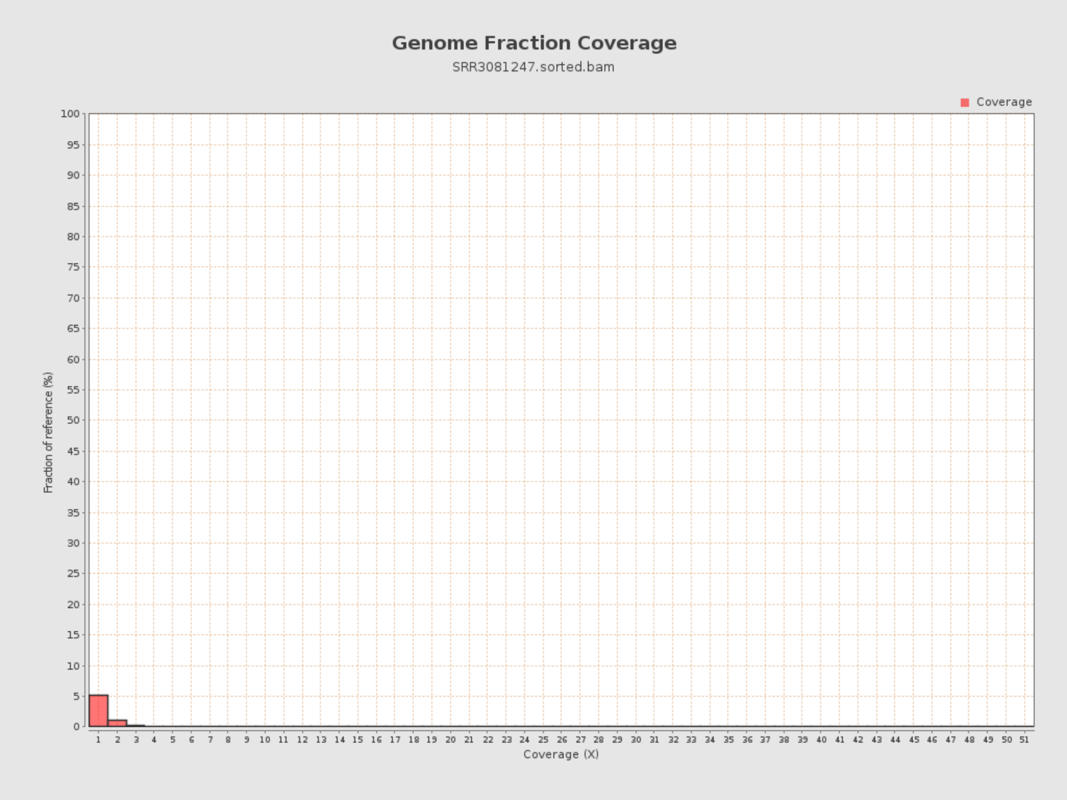
4. Results : Coverage Histogram



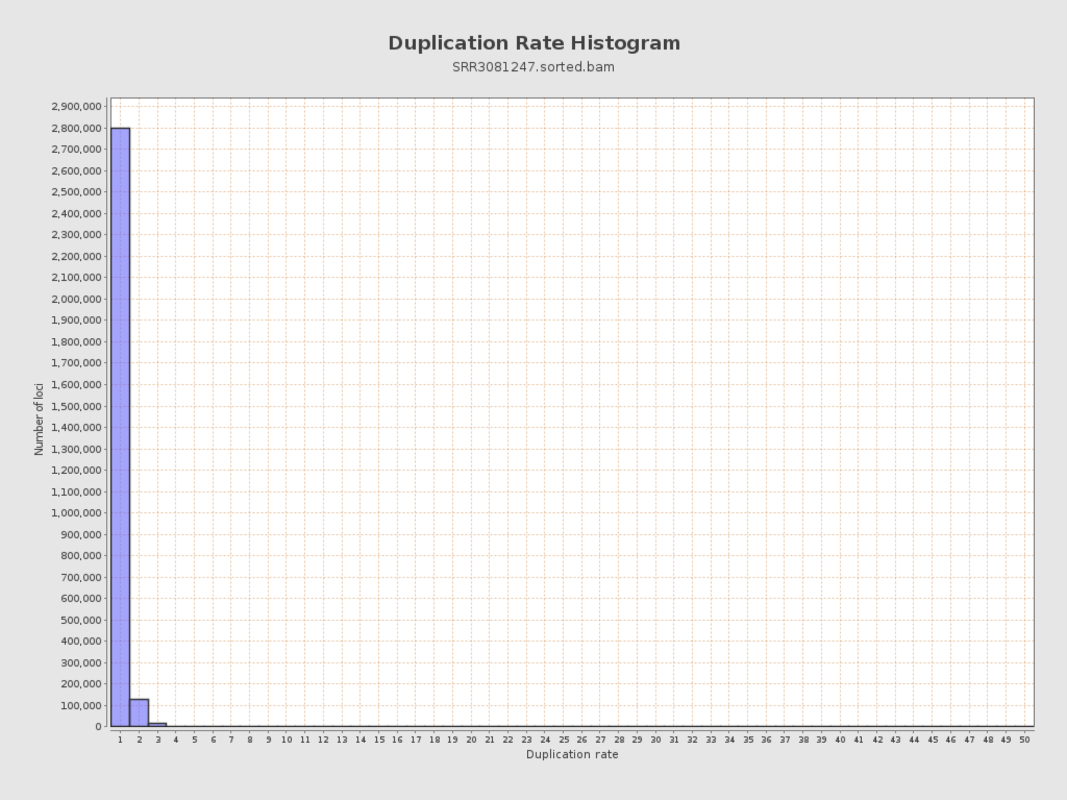
5. Results : Coverage Histogram (0-50X)



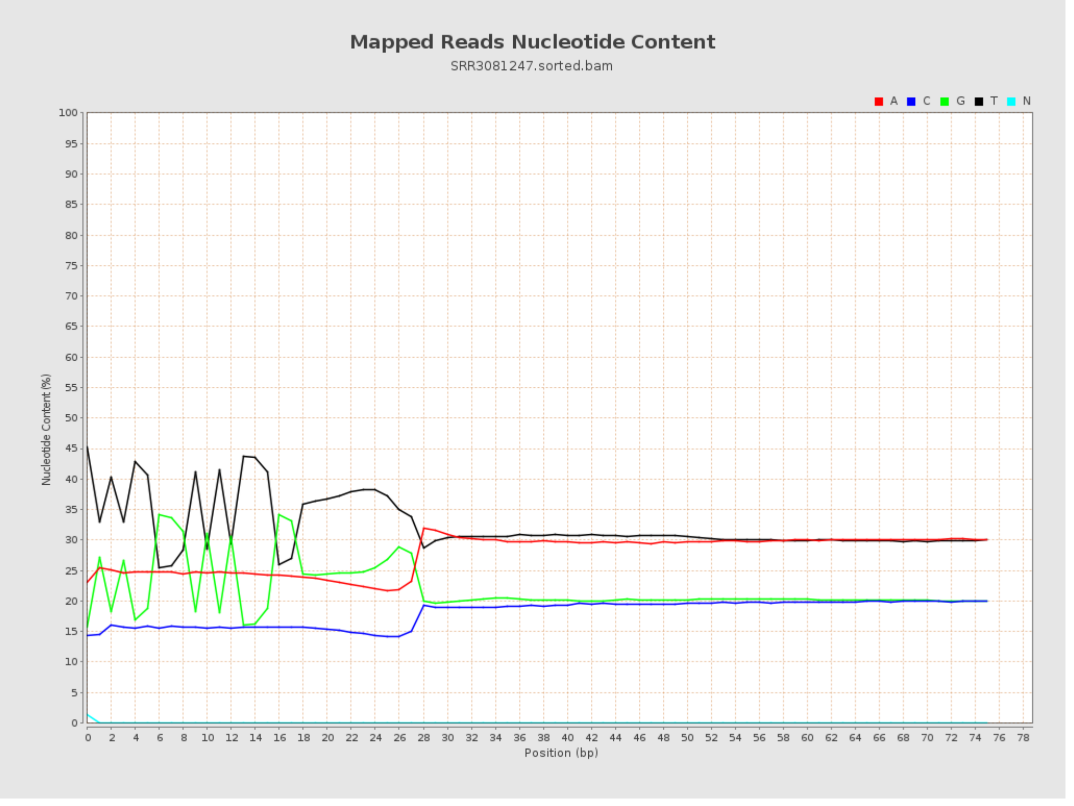
6. Results : Genome Fraction Coverage



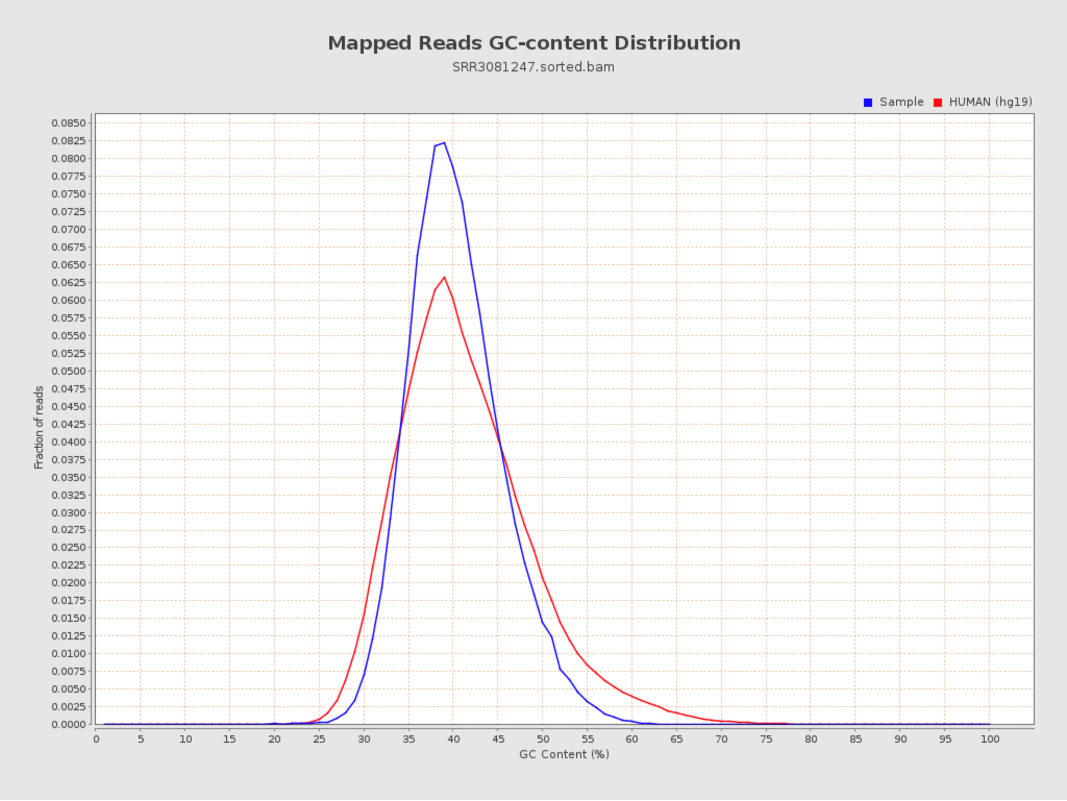
7. Results : Duplication Rate Histogram



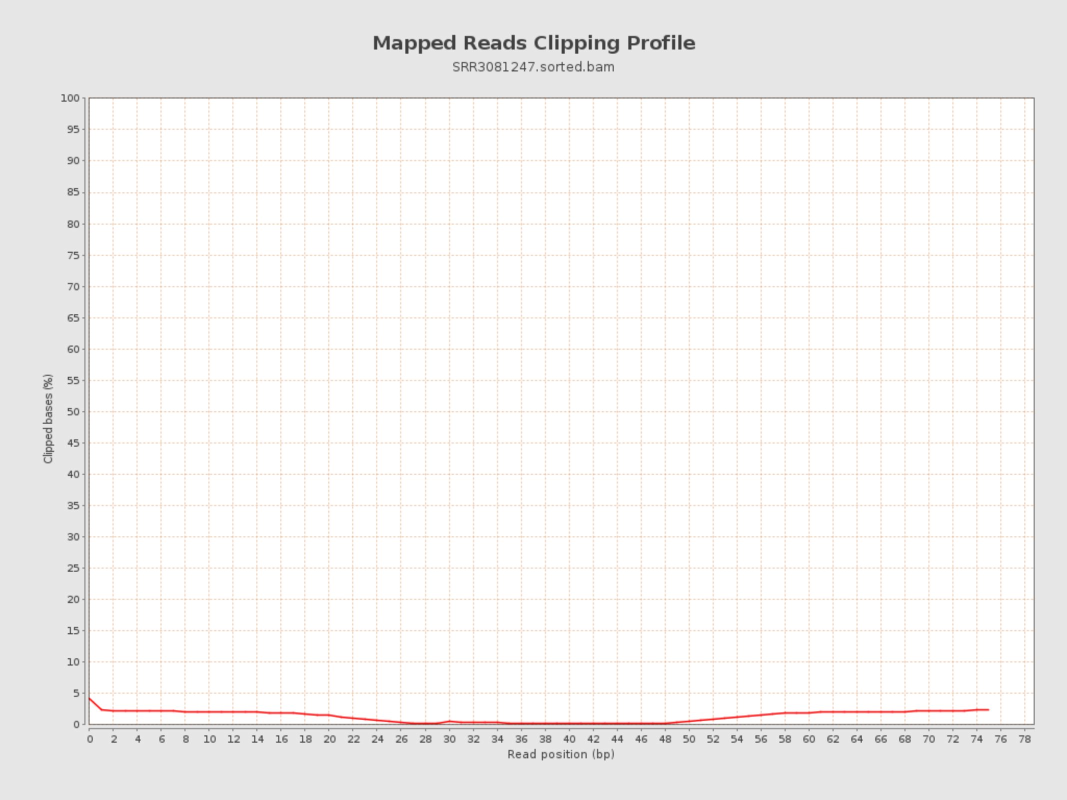
8. Results : Mapped Reads Nucleotide Content



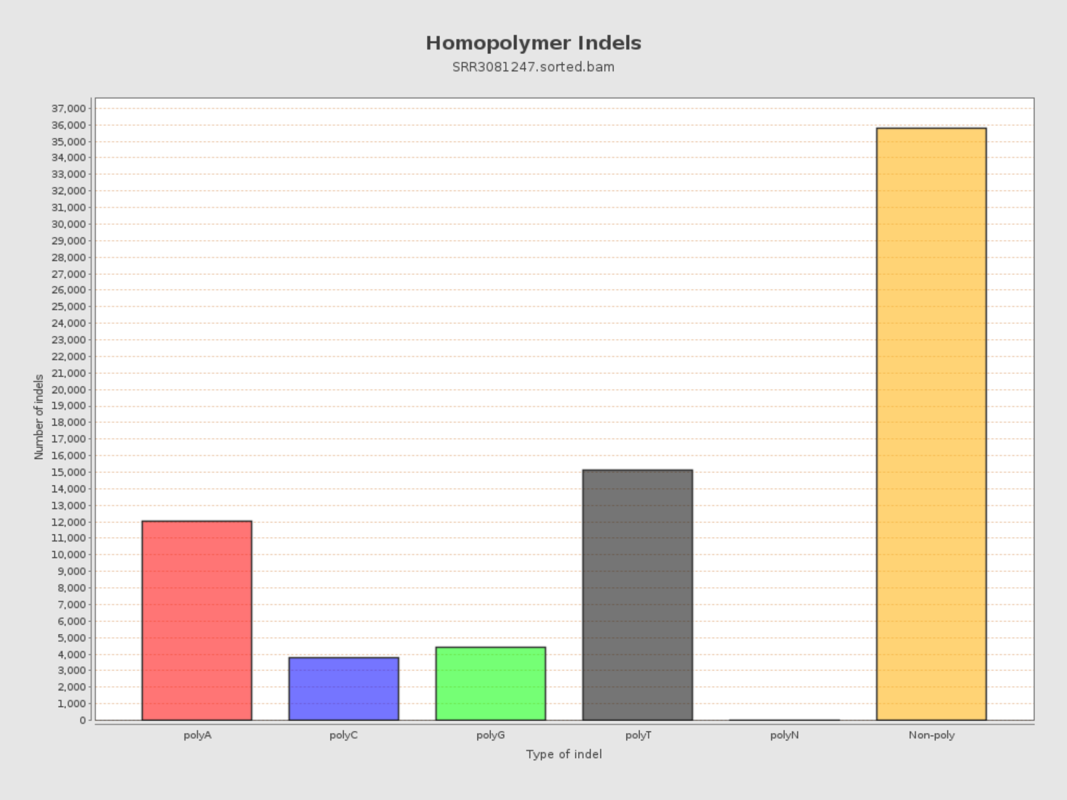
9. Results : Mapped Reads GC-content Distribution



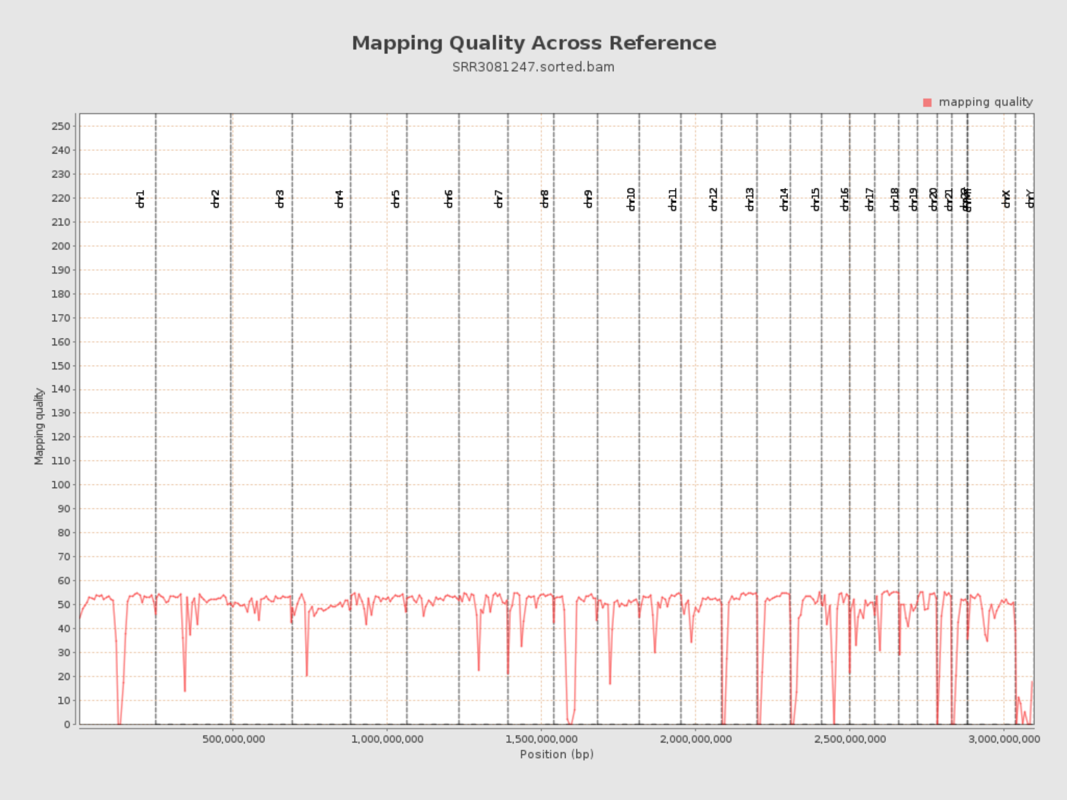
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram