Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 23:51:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524347.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_SRR10524347 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524347.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 23:51:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524347.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,138,188
Mapped reads	3,794,796 / 91.7%
Unmapped reads	343,392 / 8.3%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,743 / 0.43%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	277,913 / 6.72%
Duplication rate	5.4%
Clipped reads	3,803,952 / 91.92%

2.2. ACGT Content

Number/percentage of A's	55,396,562 / 25.1%
Number/percentage of C's	41,638,645 / 18.87%
Number/percentage of T's	70,767,110 / 32.07%
Number/percentage of G's	52,828,714 / 23.94%
Number/percentage of N's	32,245 / 0.01%
GC Percentage	42.81%

2.3. Coverage

Mean	0.0713

Standard Deviation	0.6019

2.4. Mapping Quality

Mean Mapping Quality	44.34

2.5. Mismatches and indels

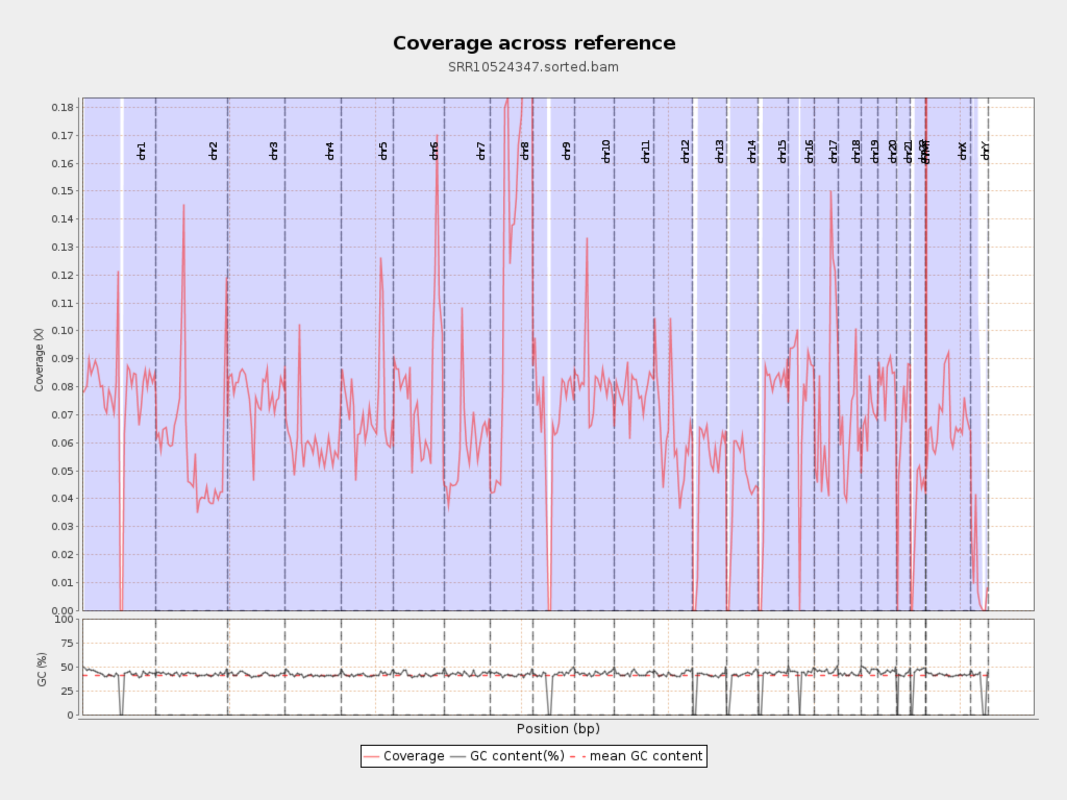
General error rate	0.52%
Mismatches	1,115,880
Insertions	15,761
Mapped reads with at least one insertion	0.41%
Deletions	38,181
Mapped reads with at least one deletion	1%
Homopolymer indels	41.94%

2.6. Chromosome stats

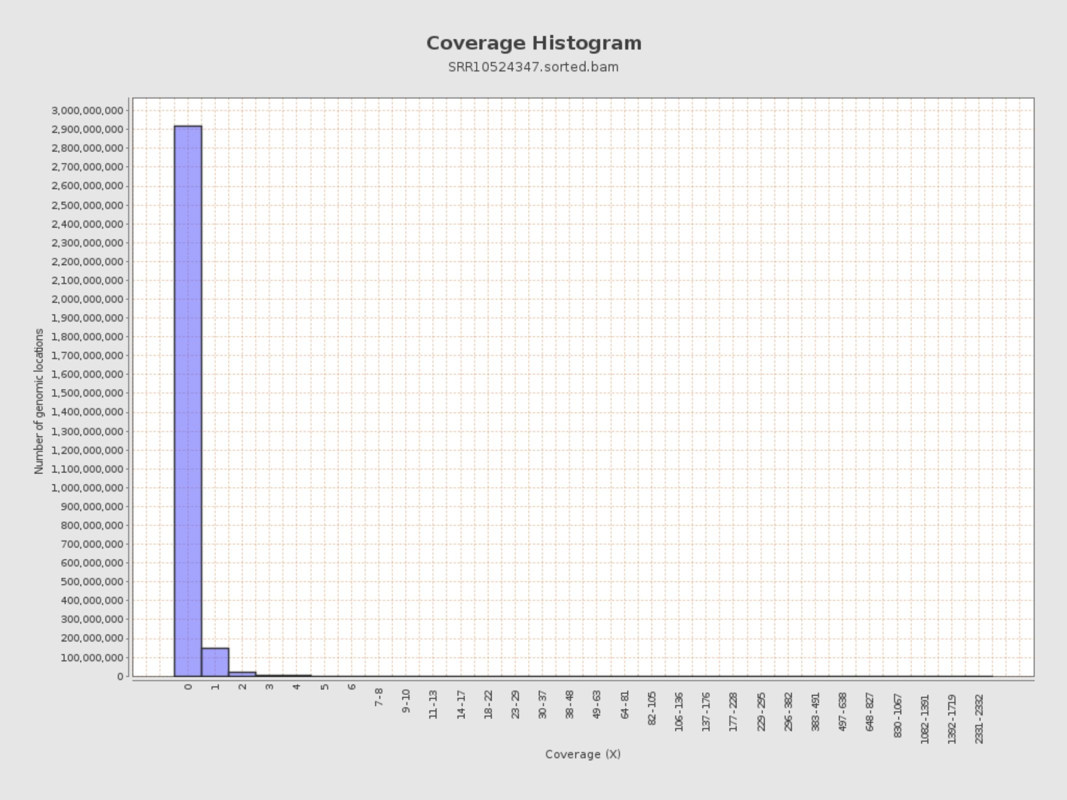
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	19114954	0.0767	1.1464
chr2	243199373	14243532	0.0586	0.9754
chr3	198022430	15353008	0.0775	0.3397
chr4	191154276	11456533	0.0599	0.3768
chr5	180915260	13147177	0.0727	0.3288
chr6	171115067	13913679	0.0813	0.3977
chr7	159138663	9375827	0.0589	0.7228

chr8	146364022	23022359	0.1573	0.7461
chr9	141213431	9390981	0.0665	0.4268
chr10	135534747	11123792	0.0821	0.5545
chr11	135006516	10590499	0.0784	0.4634
chr12	133851895	8604572	0.0643	0.317
chr13	115169878	5702118	0.0495	0.2705
chr14	107349540	4679136	0.0436	0.2757
chr15	102531392	6886514	0.0672	0.316
chr16	90354753	7097301	0.0785	0.374
chr17	81195210	6354073	0.0783	0.4025
chr18	78077248	5082152	0.0651	0.8369
chr19	59128983	4089977	0.0692	0.7644
chr20	63025520	5255623	0.0834	0.3653
chr21	48129895	3081864	0.064	0.362
chr22	51304566	1734748	0.0338	0.2272
chrMT	16571	171797	10.3673	6.7495
chrX	155270560	10591333	0.0682	0.3784
chrY	59373566	659924	0.0111	0.3165

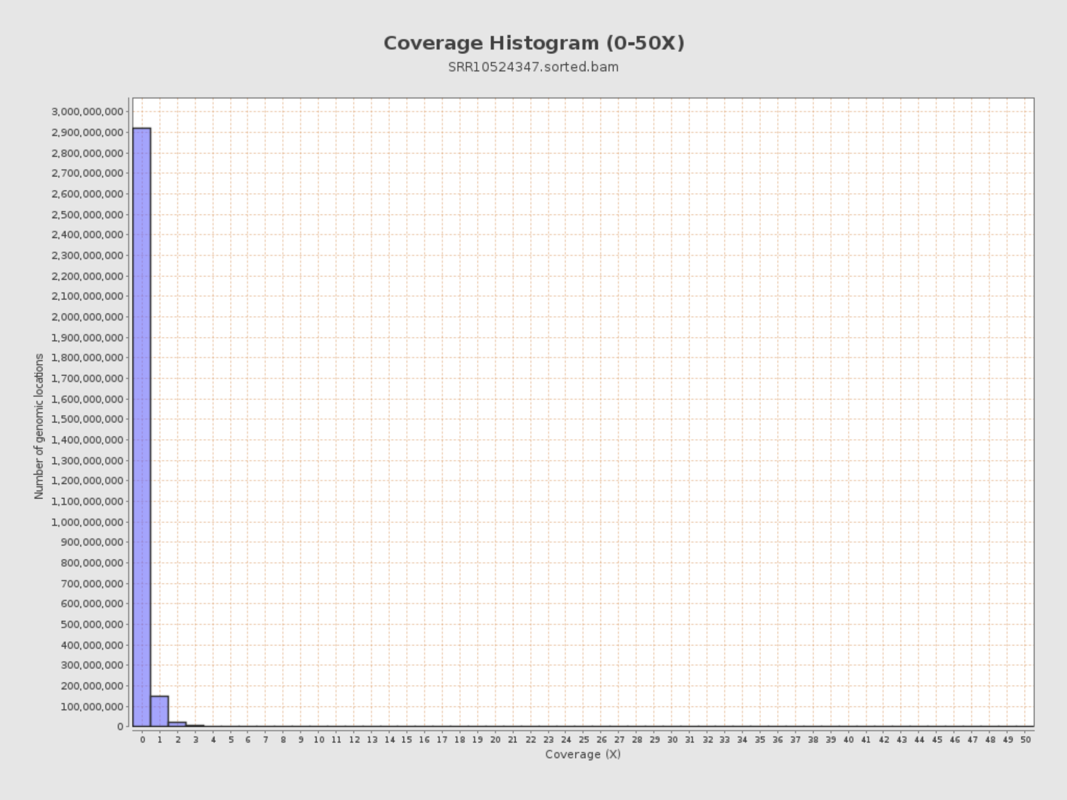
3. Results : Coverage across reference



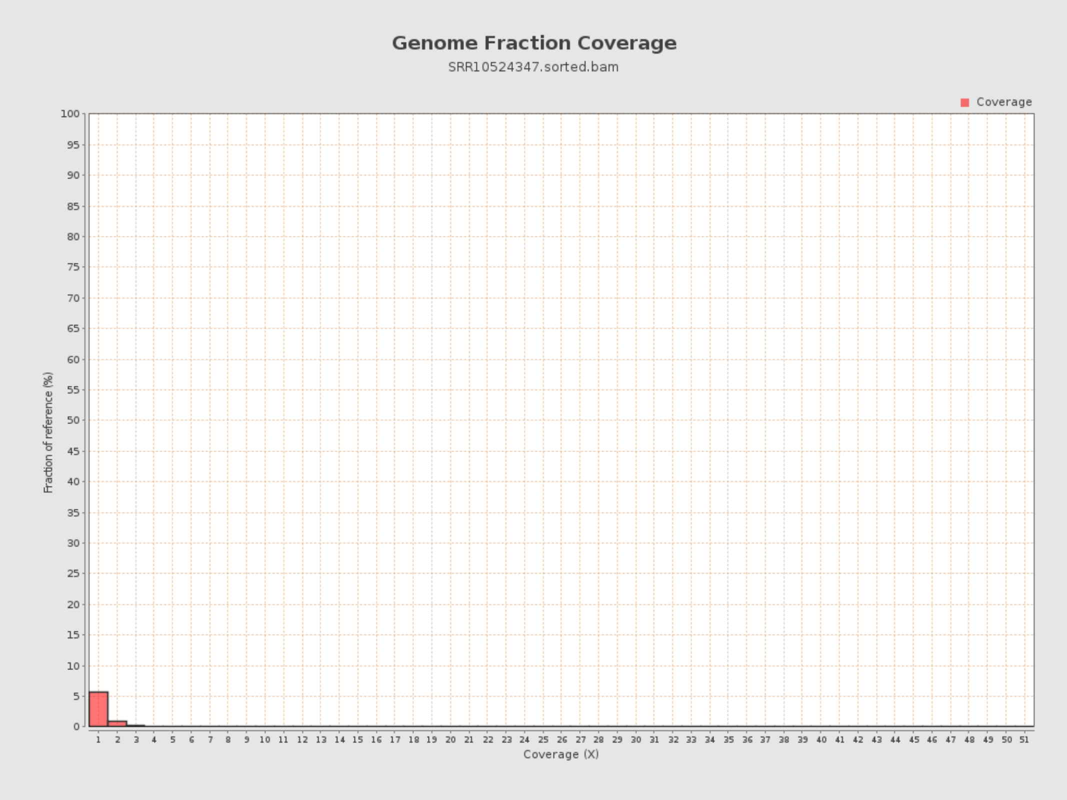
4. Results : Coverage Histogram



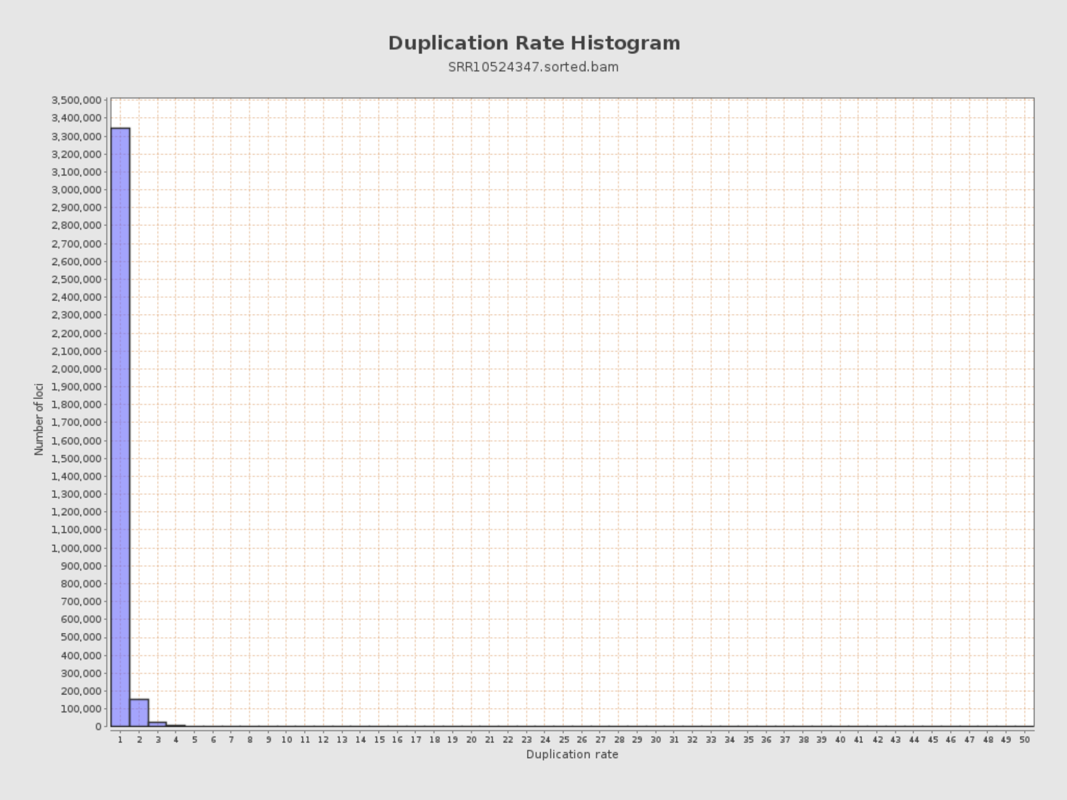
5. Results : Coverage Histogram (0-50X)



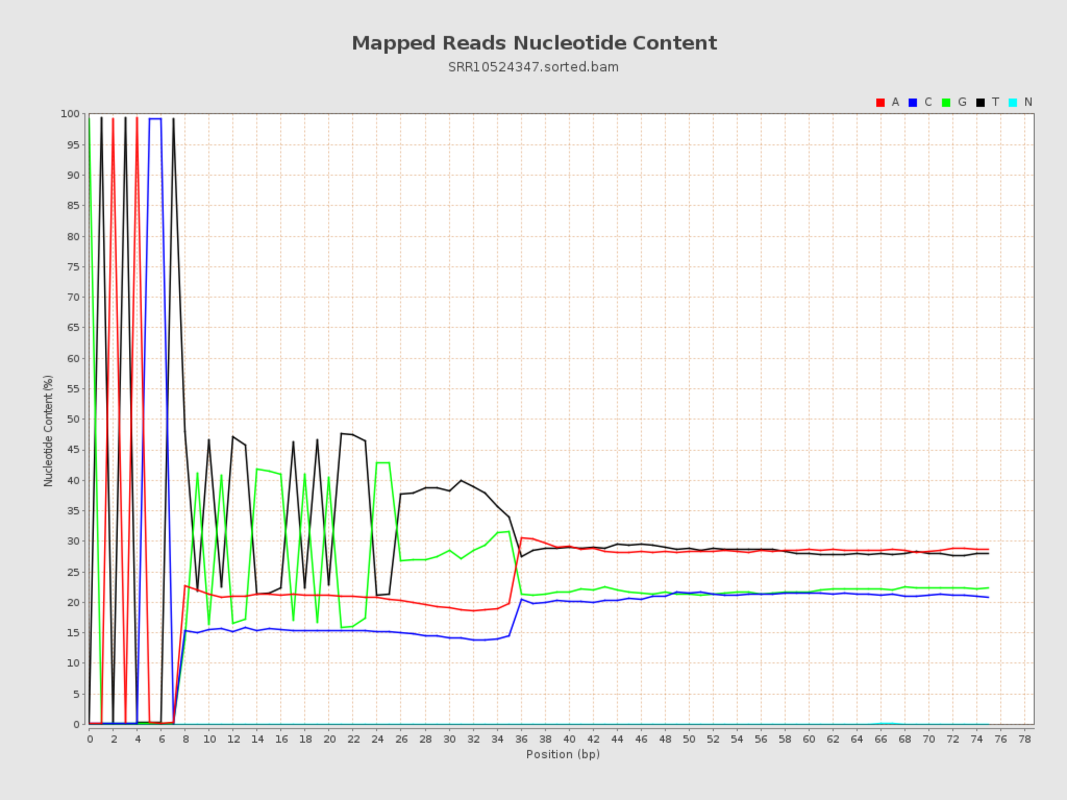
6. Results : Genome Fraction Coverage



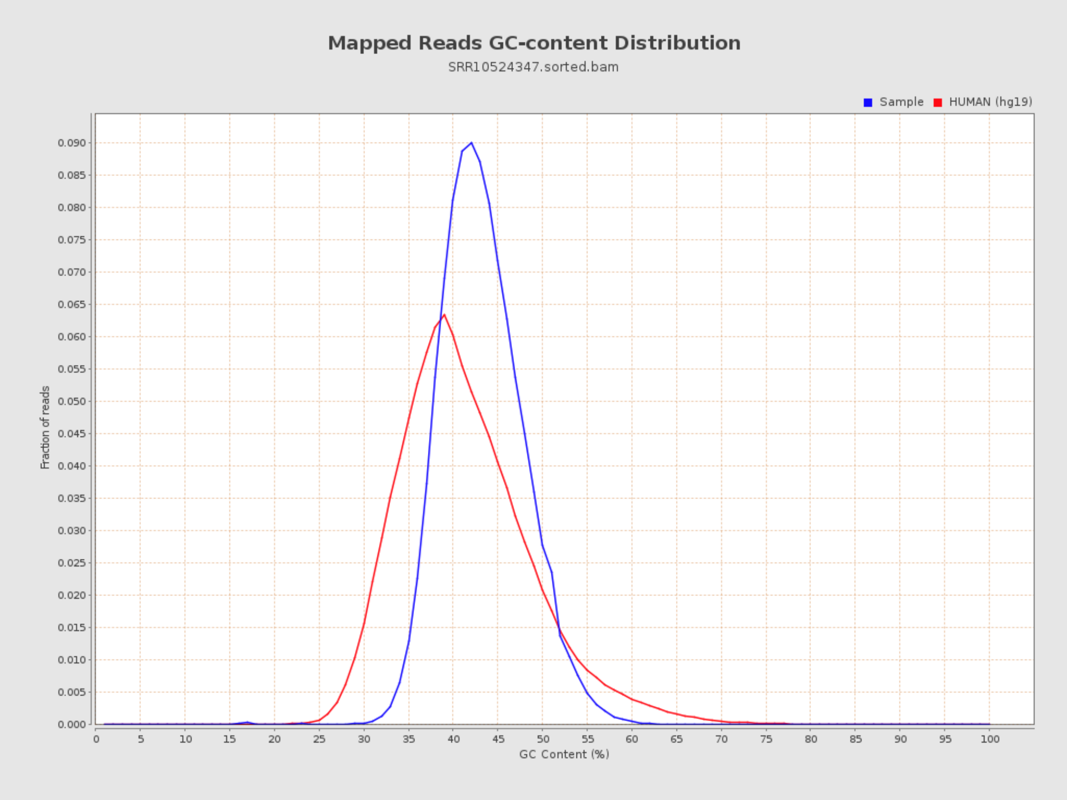
7. Results : Duplication Rate Histogram



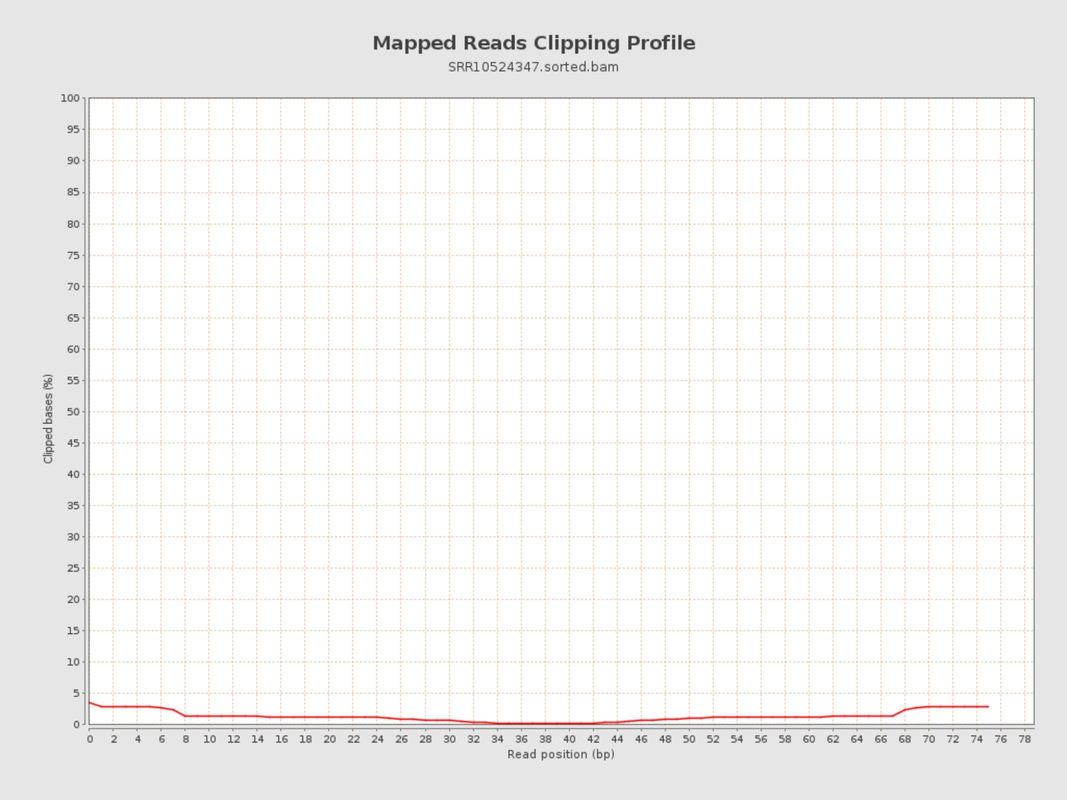
8. Results : Mapped Reads Nucleotide Content



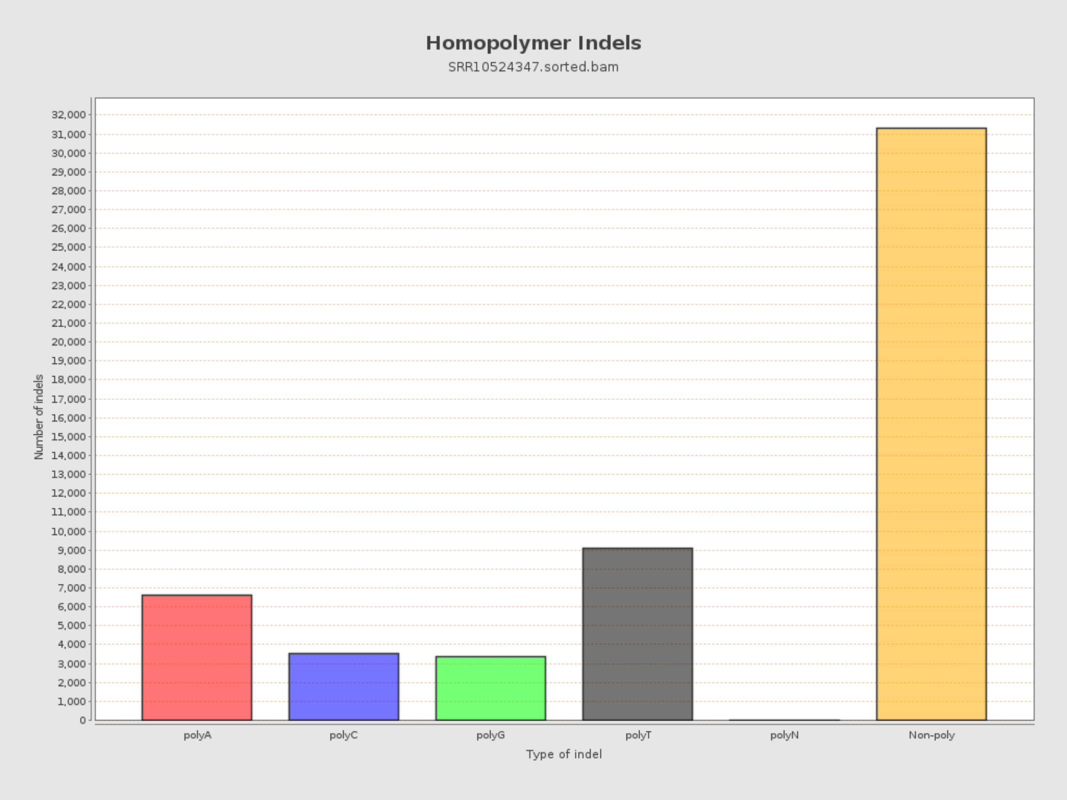
9. Results : Mapped Reads GC-content Distribution



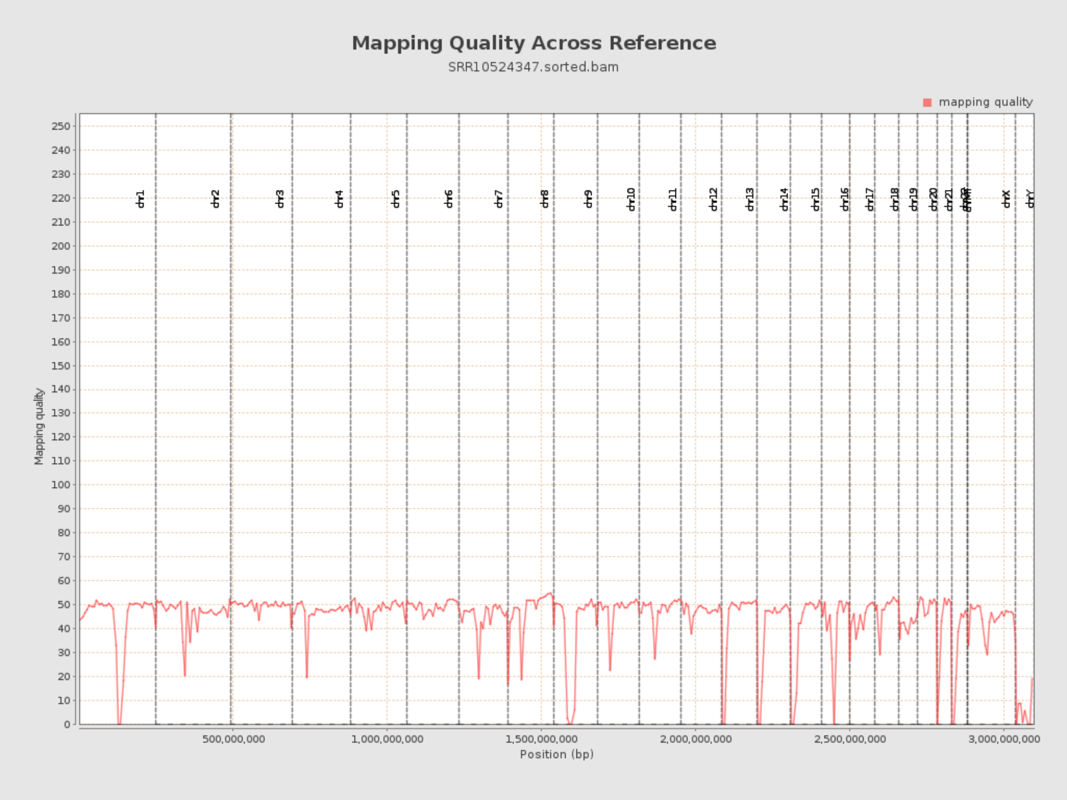
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram