Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 03:52:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524427.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_SRR10524427 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524427.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 03:52:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524427.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,181,017
Mapped reads	2,921,186 / 91.83%
Unmapped reads	259,831 / 8.17%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,204 / 0.45%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	219,745 / 6.91%
Duplication rate	5.51%
Clipped reads	2,927,098 / 92.02%

2.2. ACGT Content

Number/percentage of A's	43,008,379 / 25.07%
Number/percentage of C's	34,733,994 / 20.25%
Number/percentage of T's	52,691,542 / 30.72%
Number/percentage of G's	41,097,040 / 23.96%
Number/percentage of N's	17,227 / 0.01%
GC Percentage	44.2%

2.3. Coverage

Mean	0.0554

Standard Deviation	0.5151

2.4. Mapping Quality

Mean Mapping Quality	45.01

2.5. Mismatches and indels

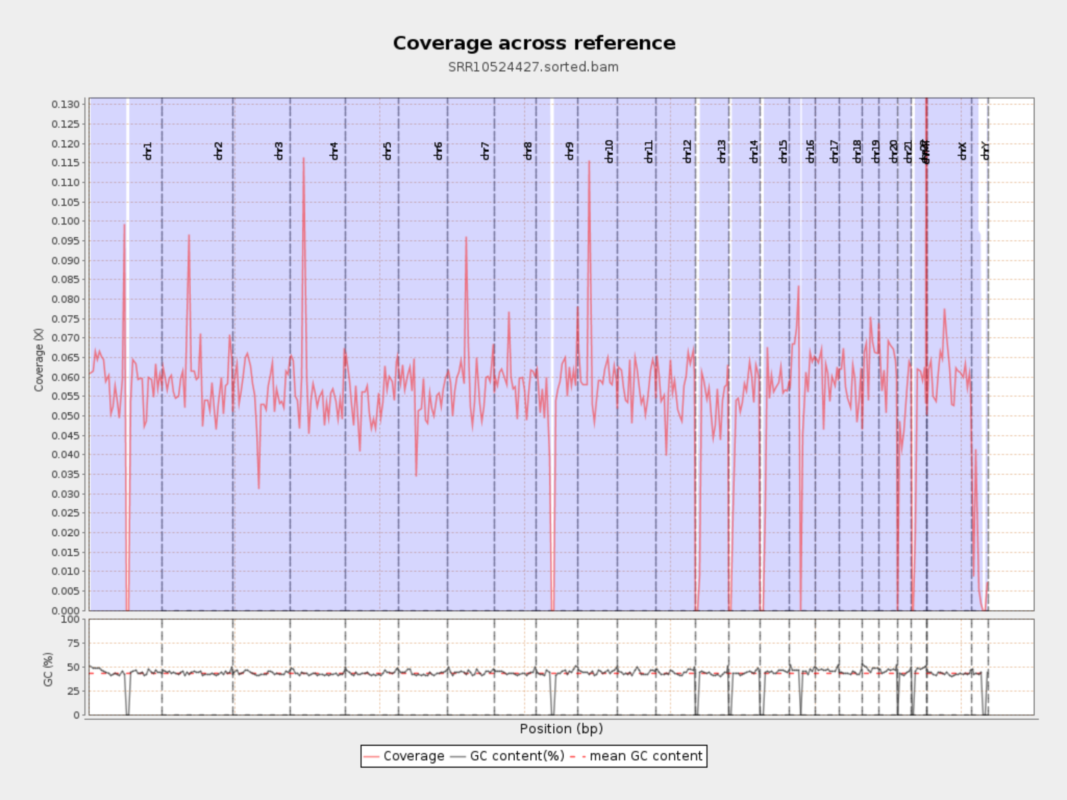
General error rate	0.53%
Mismatches	870,781
Insertions	13,543
Mapped reads with at least one insertion	0.46%
Deletions	28,640
Mapped reads with at least one deletion	0.97%
Homopolymer indels	39.7%

2.6. Chromosome stats

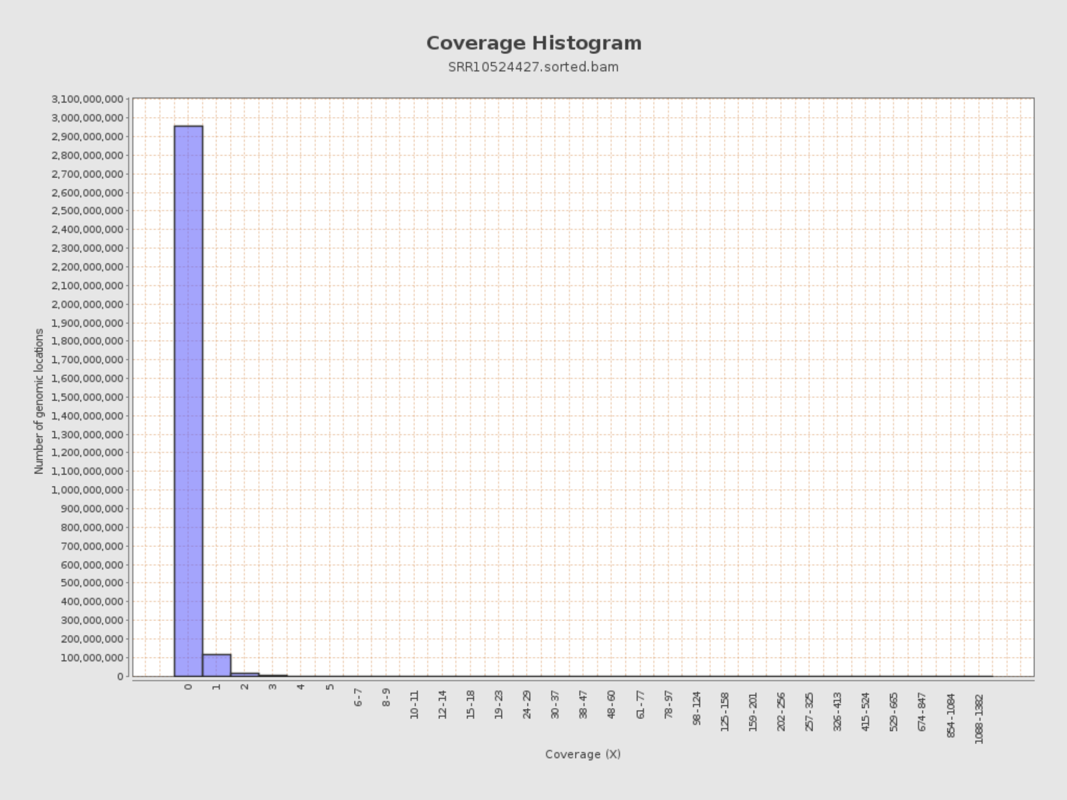
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14053579	0.0564	1.0675
chr2	243199373	14445900	0.0594	0.6895
chr3	198022430	11140941	0.0563	0.2848
chr4	191154276	10964406	0.0574	0.4166
chr5	180915260	9883533	0.0546	0.2817
chr6	171115067	9473068	0.0554	0.3161
chr7	159138663	9502356	0.0597	0.6719

chr8	146364022	8663370	0.0592	0.3947
chr9	141213431	7165928	0.0507	0.3635
chr10	135534747	8389445	0.0619	0.5714
chr11	135006516	7822035	0.0579	0.4087
chr12	133851895	7682949	0.0574	0.2979
chr13	115169878	5183320	0.045	0.2554
chr14	107349540	5118646	0.0477	0.2773
chr15	102531392	4905512	0.0478	0.2645
chr16	90354753	5347272	0.0592	0.3242
chr17	81195210	4868134	0.06	0.3294
chr18	78077248	4538165	0.0581	0.7098
chr19	59128983	3896785	0.0659	0.6547
chr20	63025520	3954390	0.0627	0.3312
chr21	48129895	2299630	0.0478	0.3726
chr22	51304566	2157530	0.0421	0.2528
chrMT	16571	7886	0.4759	0.9113
chrX	155270560	9489114	0.0611	0.34
chrY	59373566	640938	0.0108	0.3688

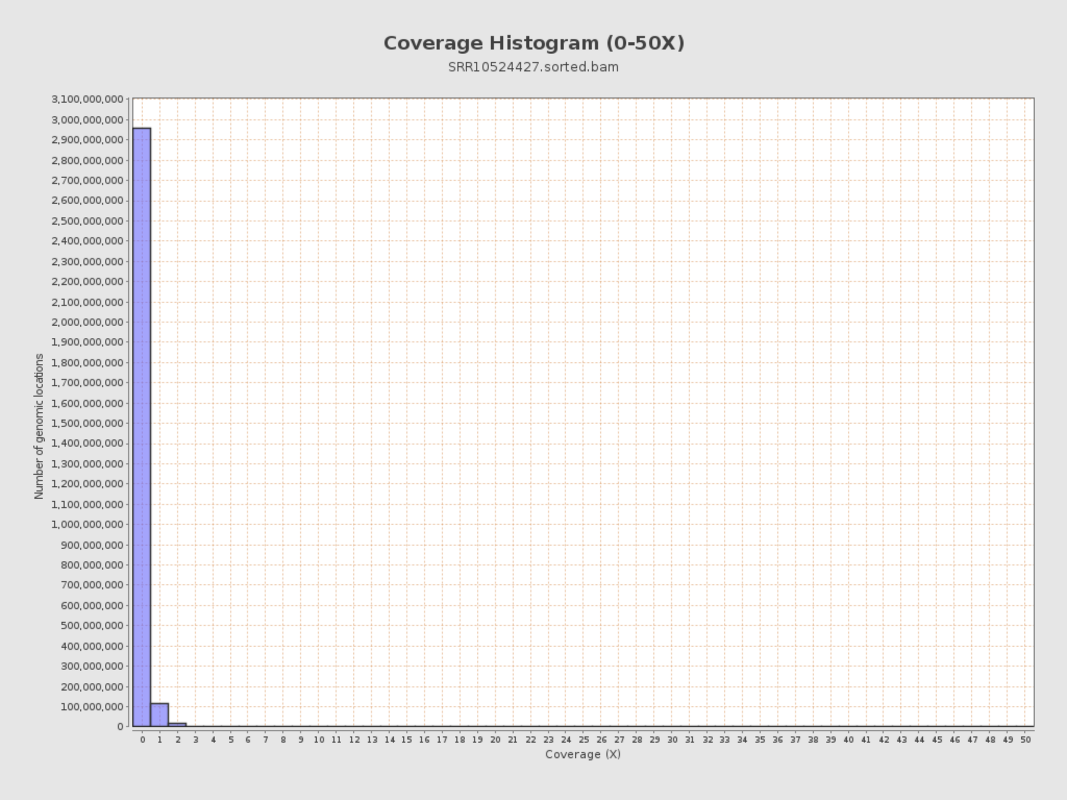
3. Results : Coverage across reference



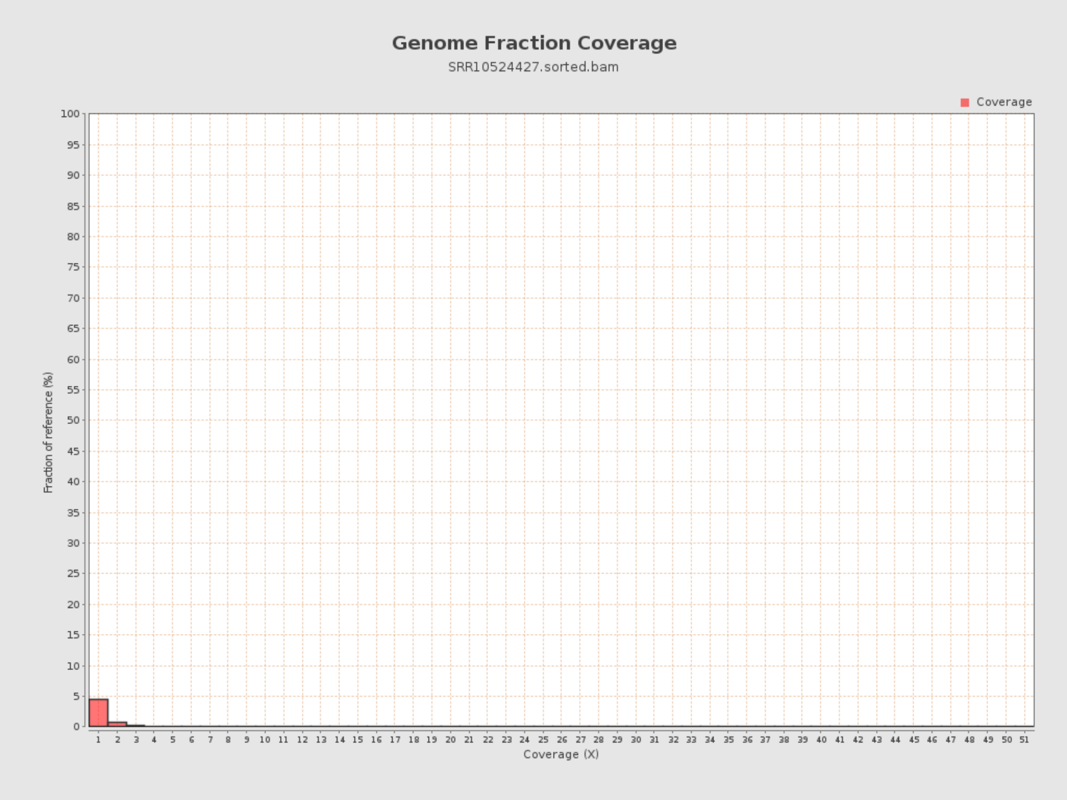
4. Results : Coverage Histogram



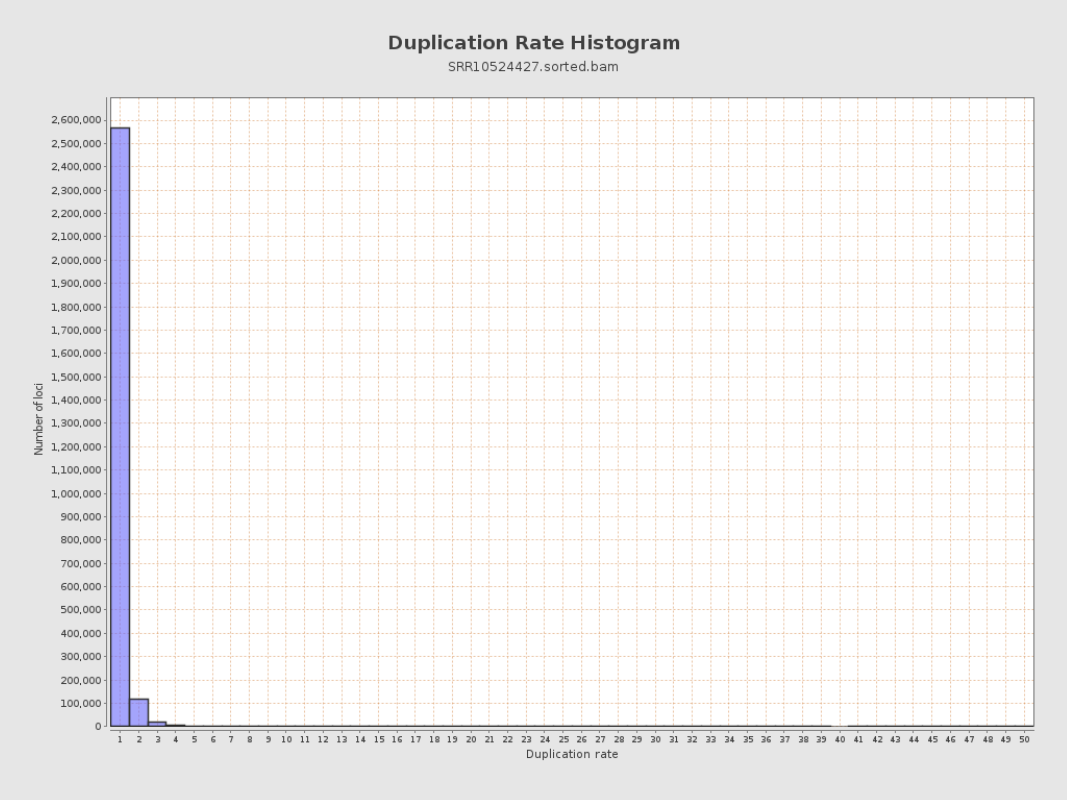
5. Results : Coverage Histogram (0-50X)



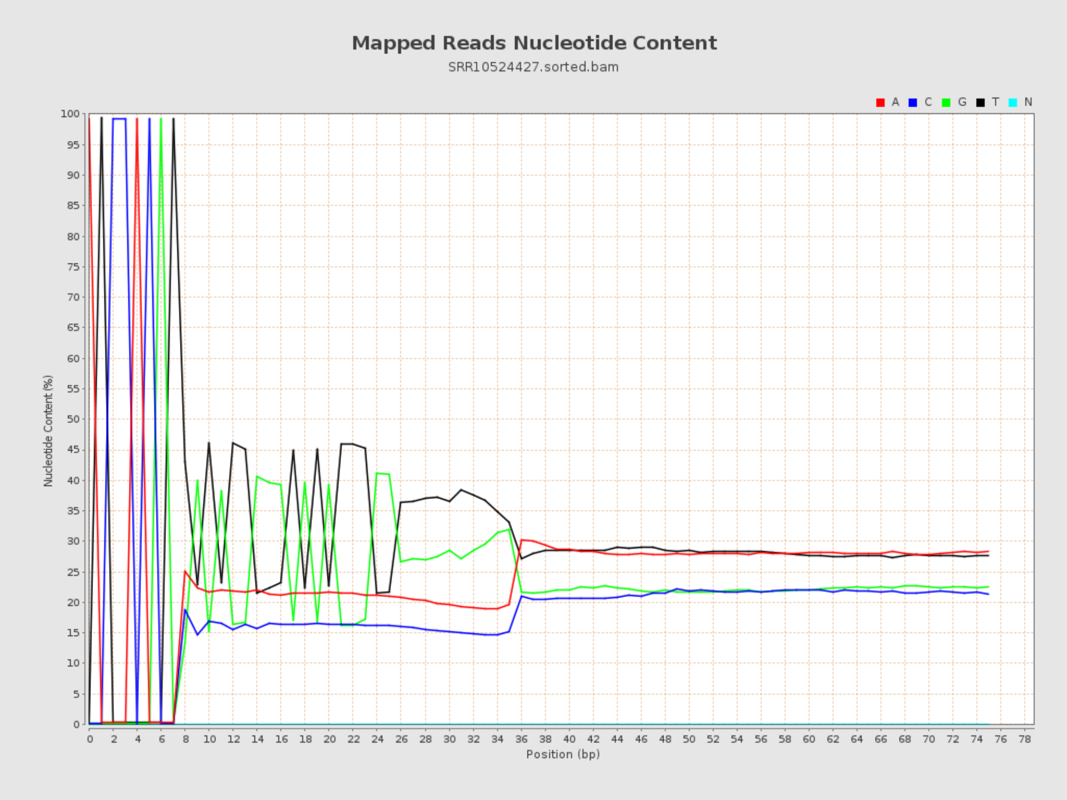
6. Results : Genome Fraction Coverage



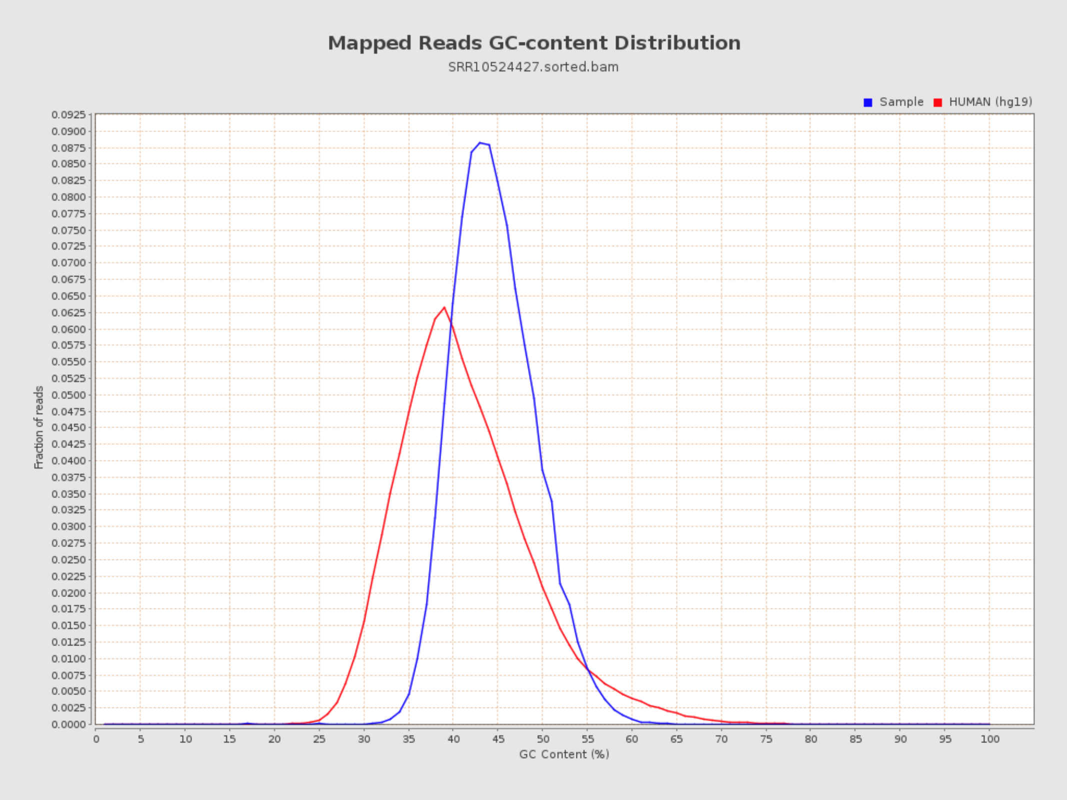
7. Results : Duplication Rate Histogram



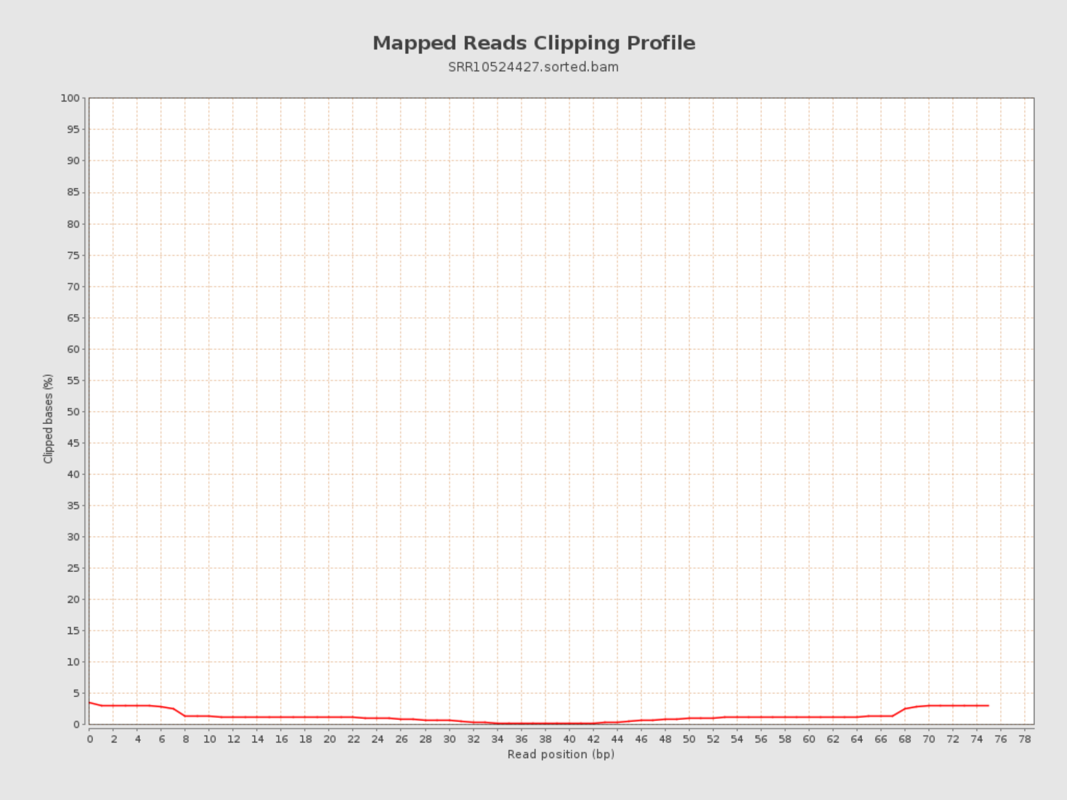
8. Results : Mapped Reads Nucleotide Content



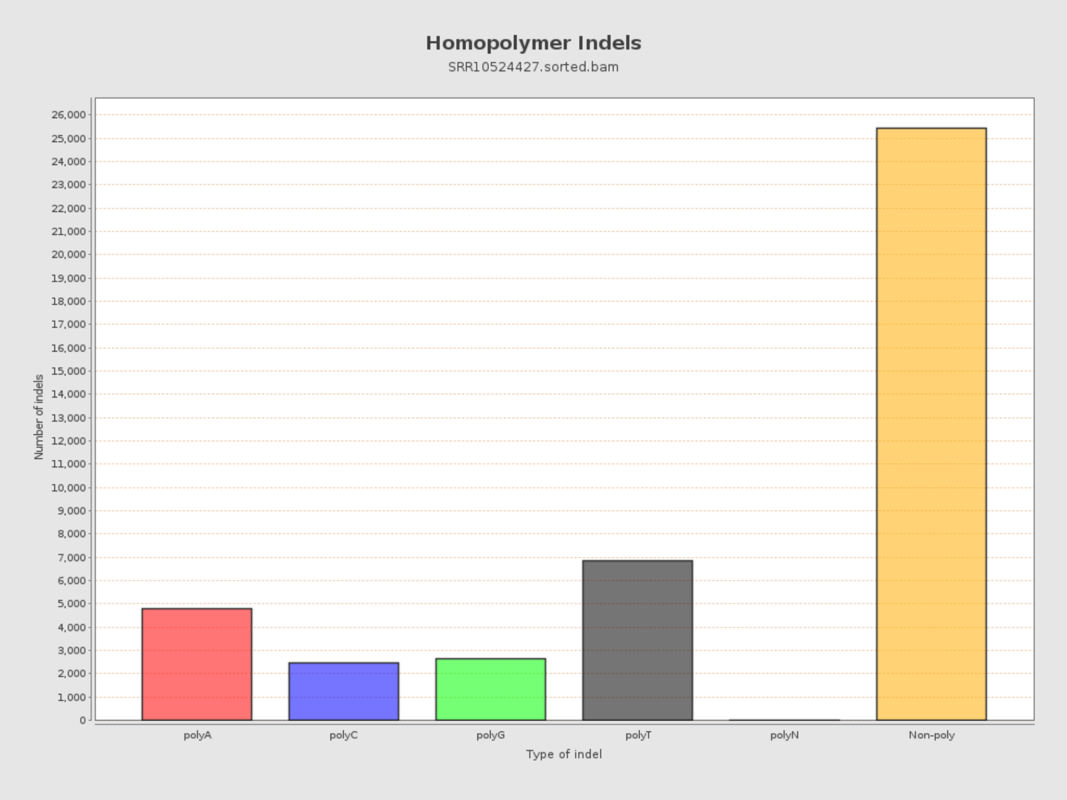
9. Results : Mapped Reads GC-content Distribution



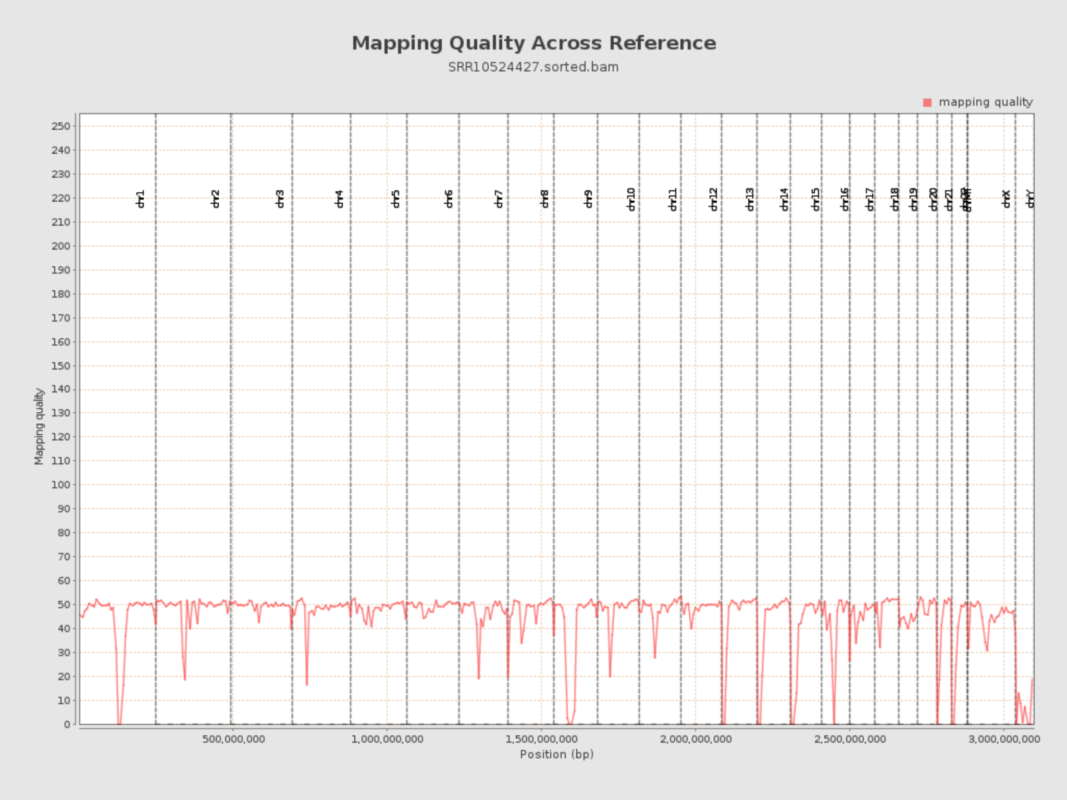
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram