Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/01 19:17:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524502.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_SRR10524502 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524502.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 01 19:17:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524502.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	440,336
Mapped reads	402,414 / 91.39%
Unmapped reads	37,922 / 8.61%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	911 / 0.21%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	8,367 / 1.9%
Duplication rate	1.65%
Clipped reads	402,074 / 91.31%

2.2. ACGT Content

Number/percentage of A's	5,739,112 / 24.68%
Number/percentage of C's	4,462,576 / 19.19%
Number/percentage of T's	7,720,591 / 33.19%
Number/percentage of G's	5,335,555 / 22.94%
Number/percentage of N's	505 / 0%
GC Percentage	42.13%

2.3. Coverage

Mean	0.0075

Standard Deviation	0.1037

2.4. Mapping Quality

Mean Mapping Quality	45.08

2.5. Mismatches and indels

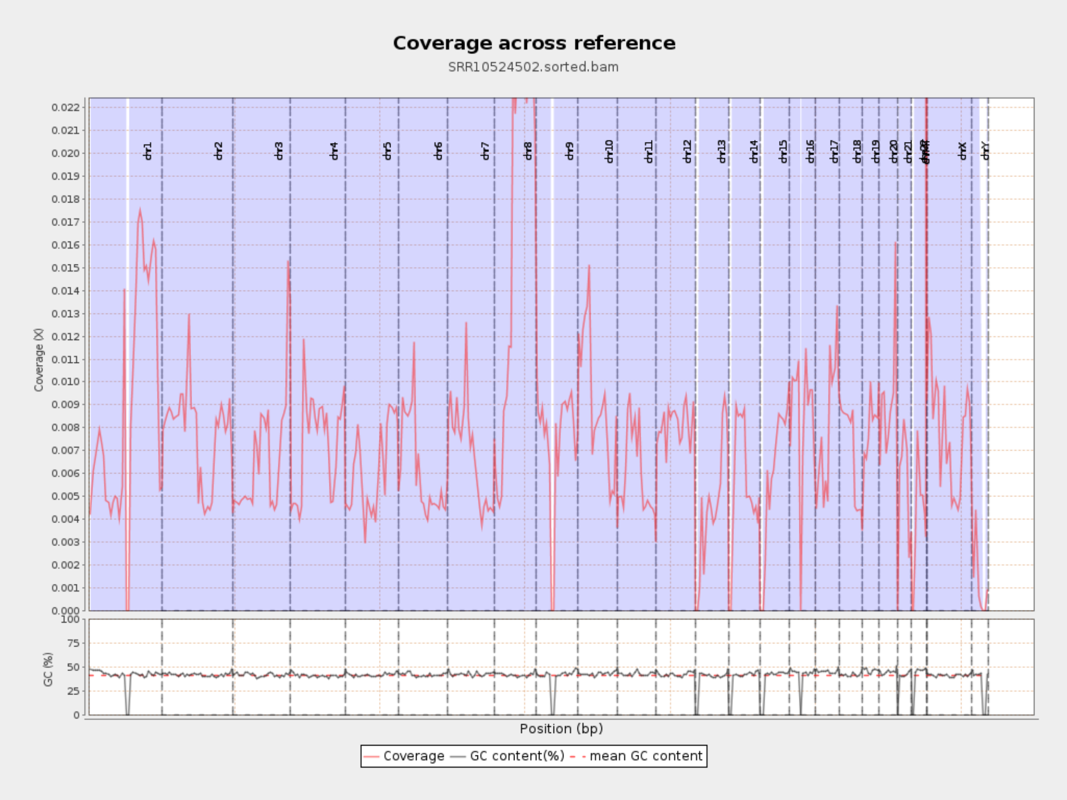
General error rate	0.49%
Mismatches	111,056
Insertions	1,424
Mapped reads with at least one insertion	0.35%
Deletions	4,489
Mapped reads with at least one deletion	1.11%
Homopolymer indels	43.94%

2.6. Chromosome stats

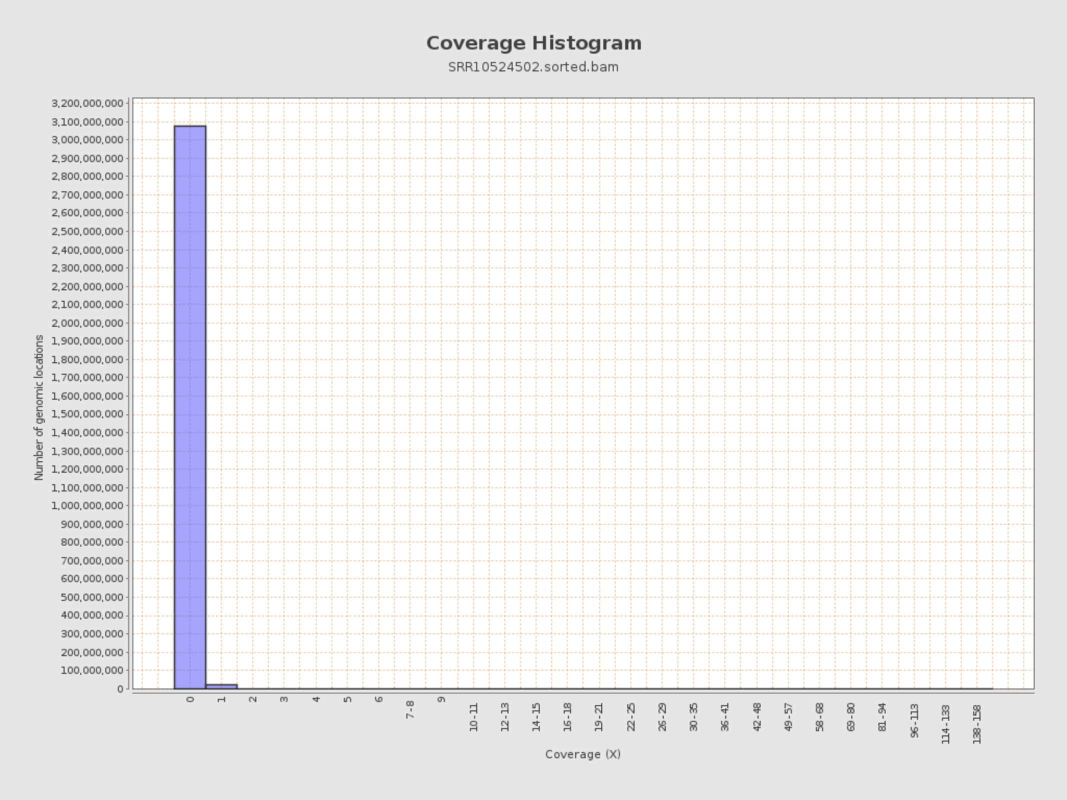
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2248952	0.009	0.1544
chr2	243199373	1906148	0.0078	0.1102
chr3	198022430	1310278	0.0066	0.0842
chr4	191154276	1402477	0.0073	0.0921
chr5	180915260	1123903	0.0062	0.0815
chr6	171115067	1051413	0.0061	0.0888
chr7	159138663	1108145	0.007	0.1163

chr8	146364022	2434904	0.0166	0.1407
chr9	141213431	1028864	0.0073	0.0971
chr10	135534747	1243969	0.0092	0.1118
chr11	135006516	813536	0.006	0.0941
chr12	133851895	1090547	0.0081	0.0933
chr13	115169878	525364	0.0046	0.0701
chr14	107349540	581888	0.0054	0.0773
chr15	102531392	603141	0.0059	0.0807
chr16	90354753	767023	0.0085	0.0979
chr17	81195210	648012	0.008	0.0944
chr18	78077248	556998	0.0071	0.1307
chr19	59128983	467425	0.0079	0.1205
chr20	63025520	588317	0.0093	0.1003
chr21	48129895	255000	0.0053	0.0773
chr22	51304566	200864	0.0039	0.0648
chrMT	16571	10960	0.6614	0.9948
chrX	155270560	1225127	0.0079	0.096
chrY	59373566	72629	0.0012	0.0453

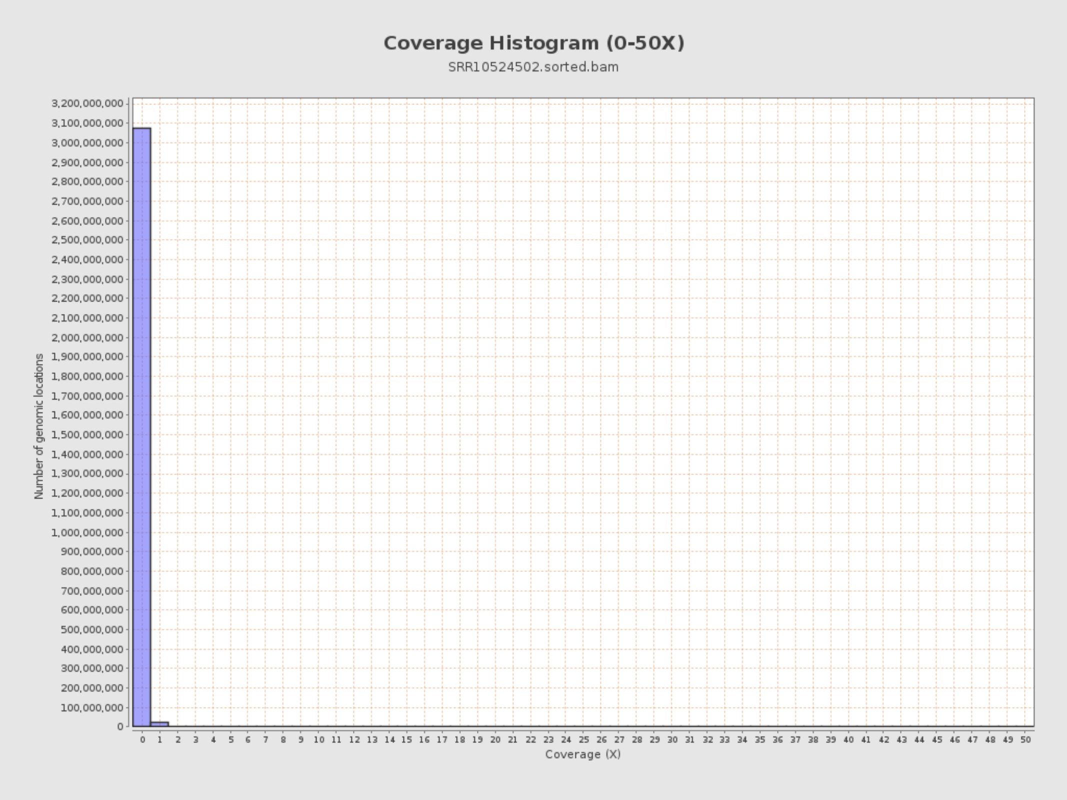
3. Results : Coverage across reference



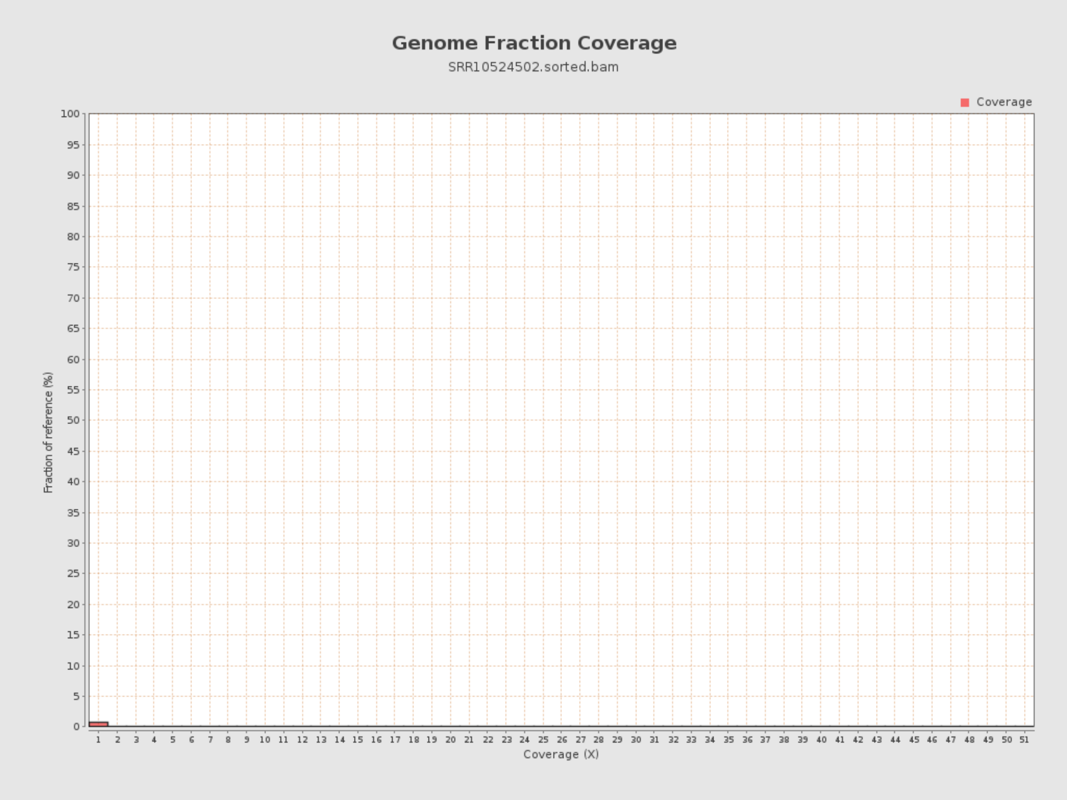
4. Results : Coverage Histogram



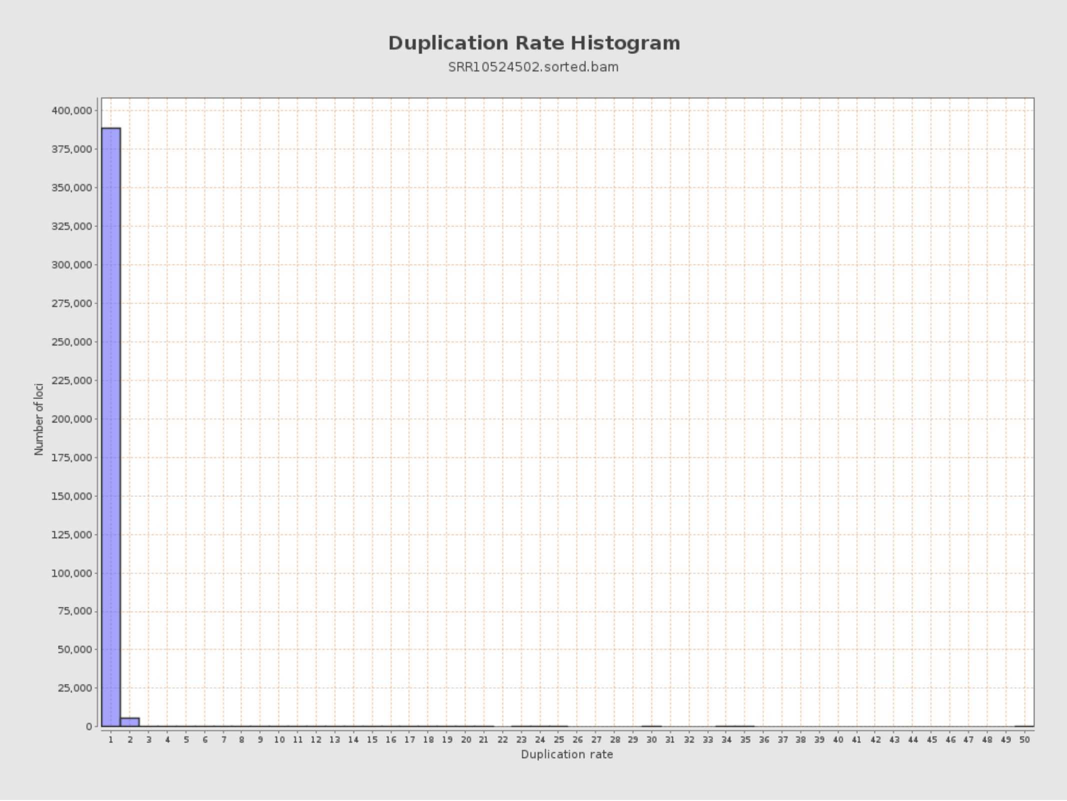
5. Results : Coverage Histogram (0-50X)



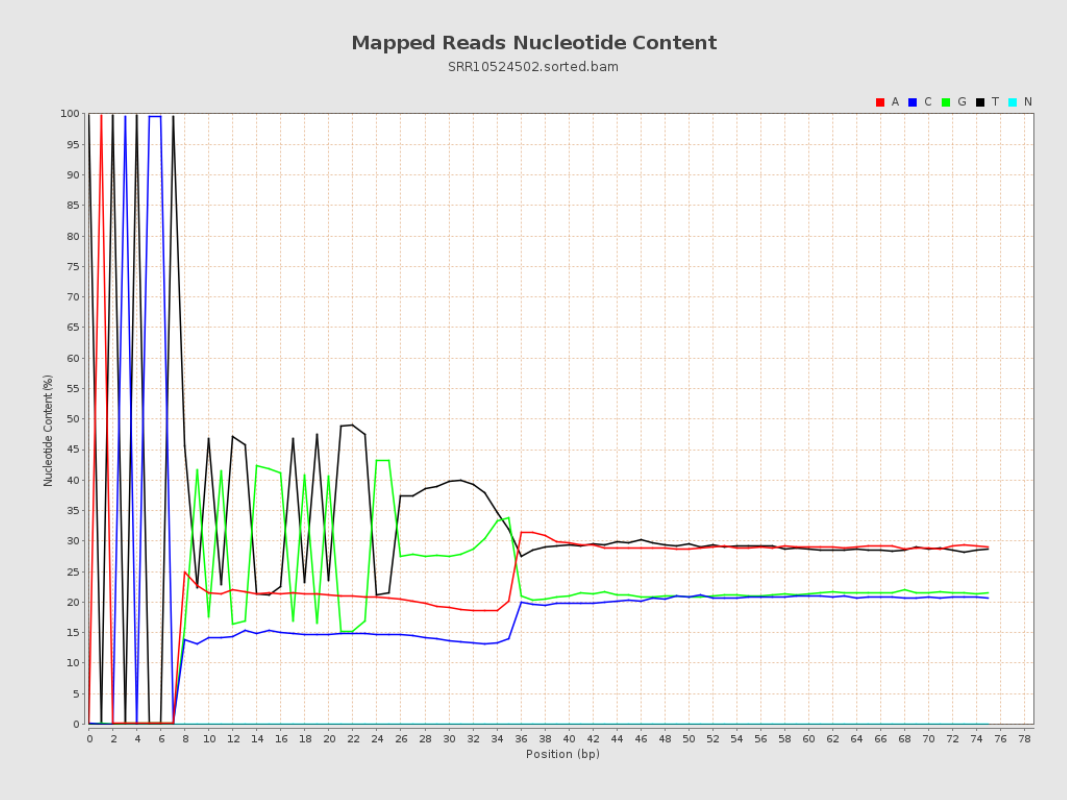
6. Results : Genome Fraction Coverage



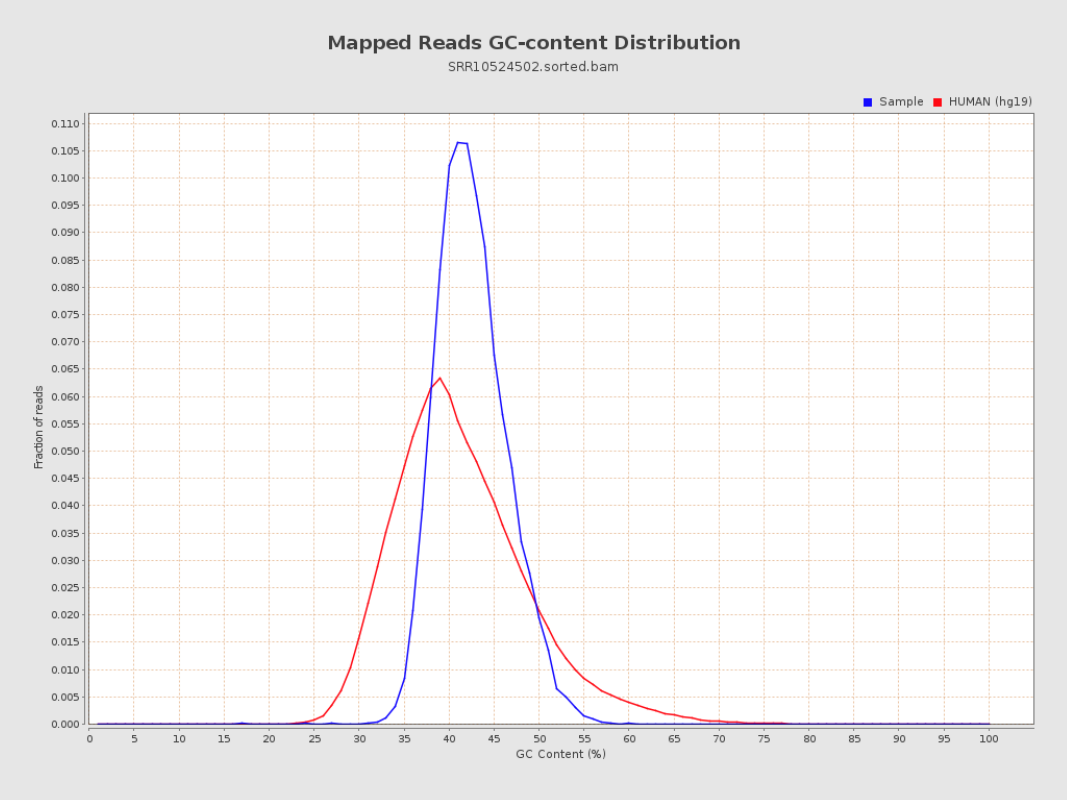
7. Results : Duplication Rate Histogram



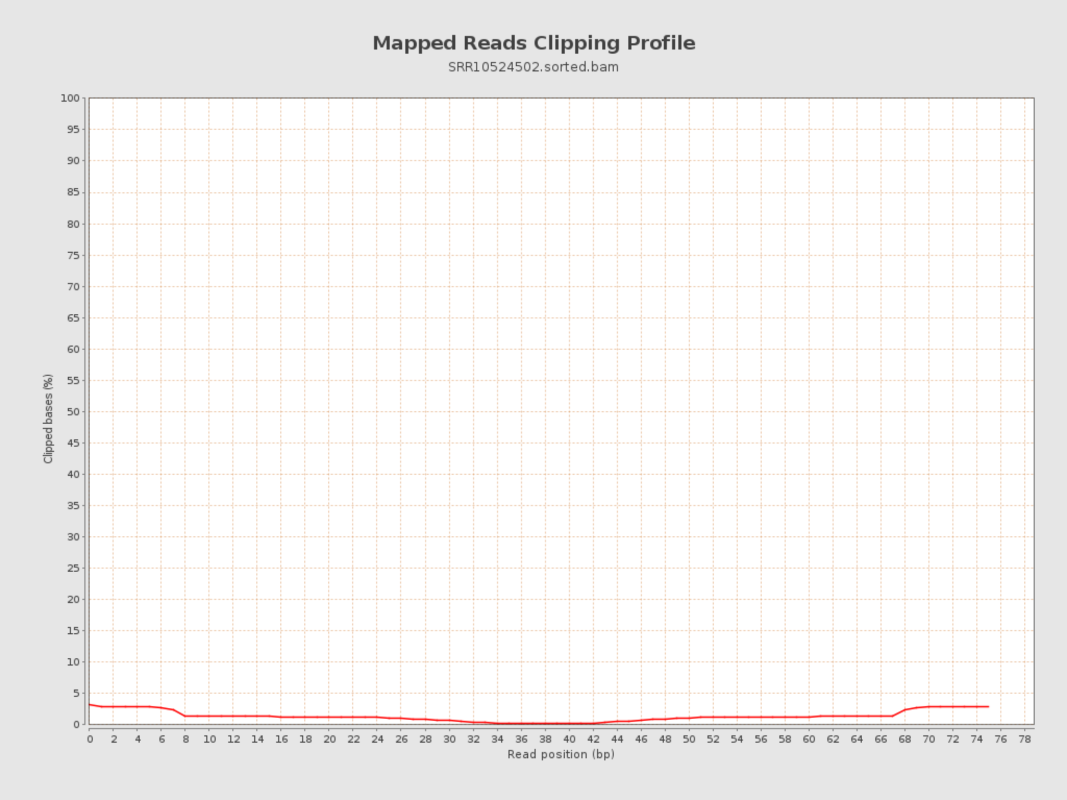
8. Results : Mapped Reads Nucleotide Content



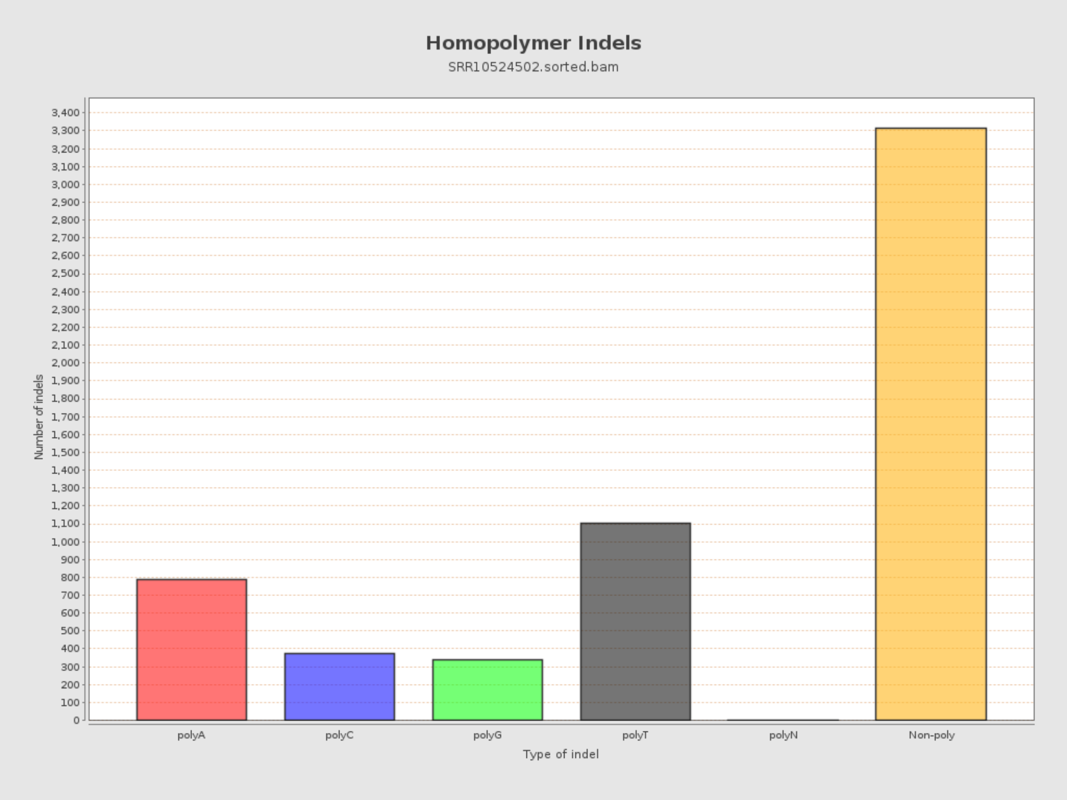
9. Results : Mapped Reads GC-content Distribution



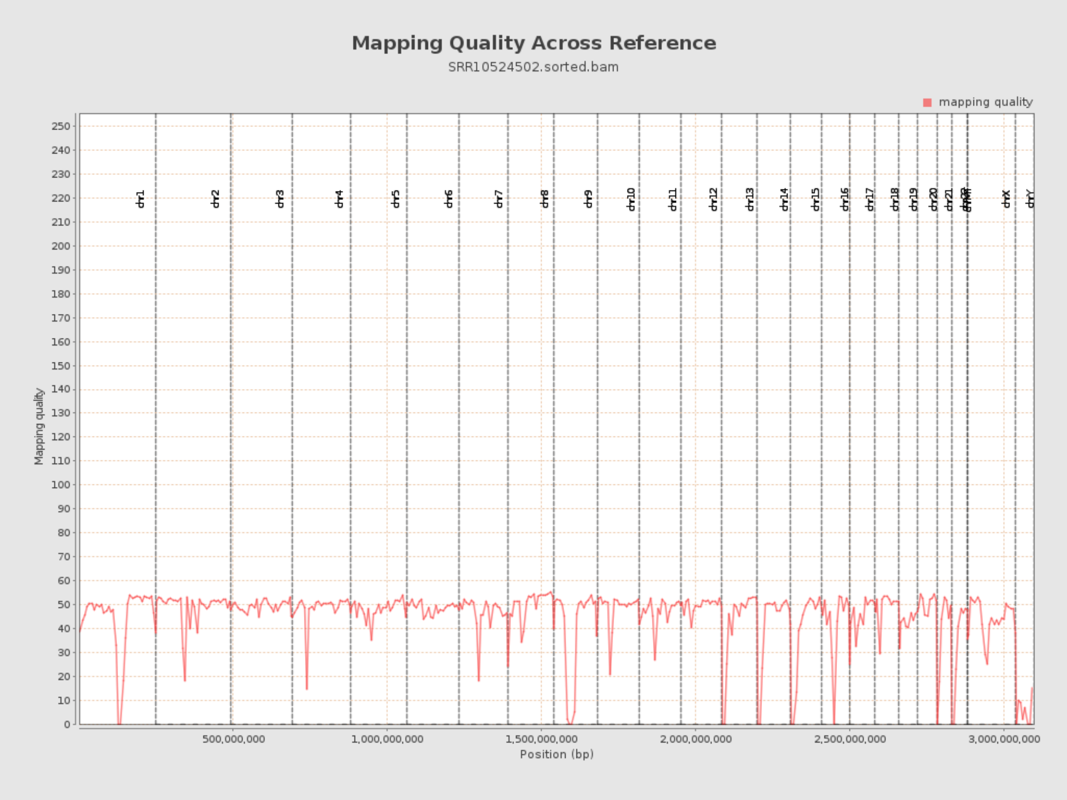
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram