Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 03:20:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524911.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_SRR10524911 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524911.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 03:20:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524911.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	489,148
Mapped reads	437,956 / 89.53%
Unmapped reads	51,192 / 10.47%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,497 / 0.51%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	5,297 / 1.08%
Duplication rate	0.83%
Clipped reads	439,723 / 89.9%

2.2. ACGT Content

Number/percentage of A's	6,329,654 / 25.3%
Number/percentage of C's	4,524,987 / 18.08%
Number/percentage of T's	7,756,785 / 31%
Number/percentage of G's	6,410,054 / 25.62%
Number/percentage of N's	868 / 0%
GC Percentage	43.7%

2.3. Coverage

Mean	0.0081

Standard Deviation	0.1048

2.4. Mapping Quality

Mean Mapping Quality	44.31

2.5. Mismatches and indels

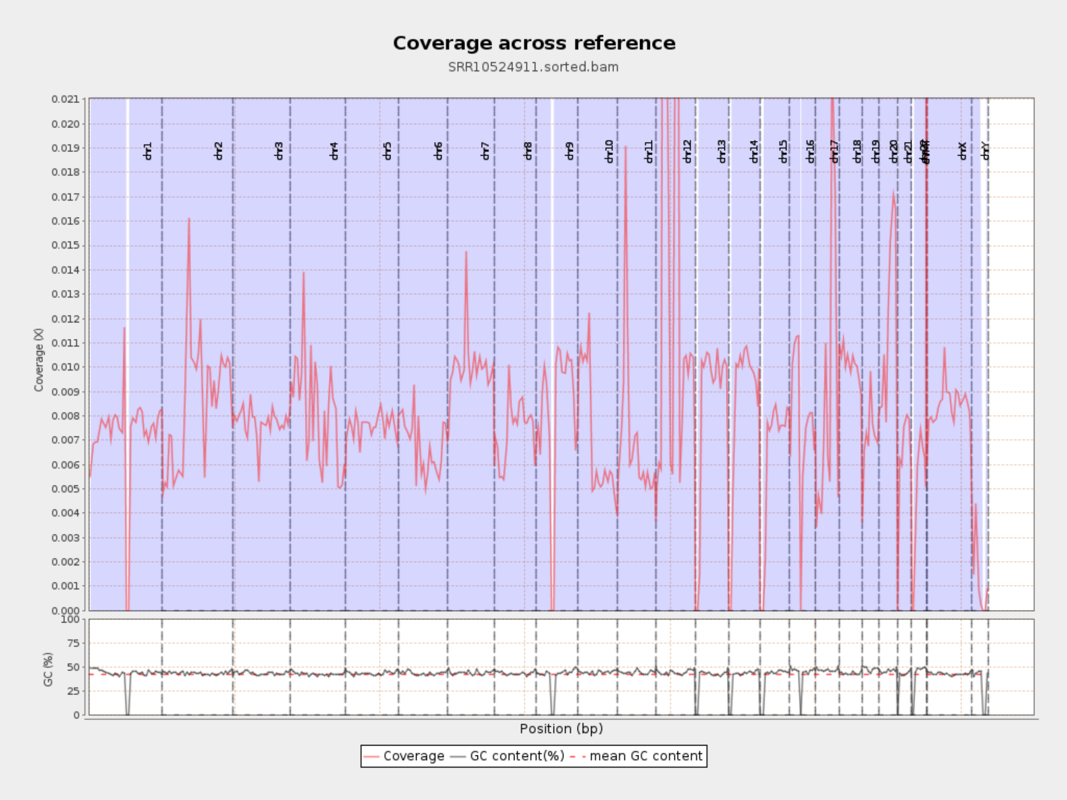
General error rate	0.51%
Mismatches	124,602
Insertions	1,613
Mapped reads with at least one insertion	0.37%
Deletions	4,460
Mapped reads with at least one deletion	1.01%
Homopolymer indels	42.12%

2.6. Chromosome stats

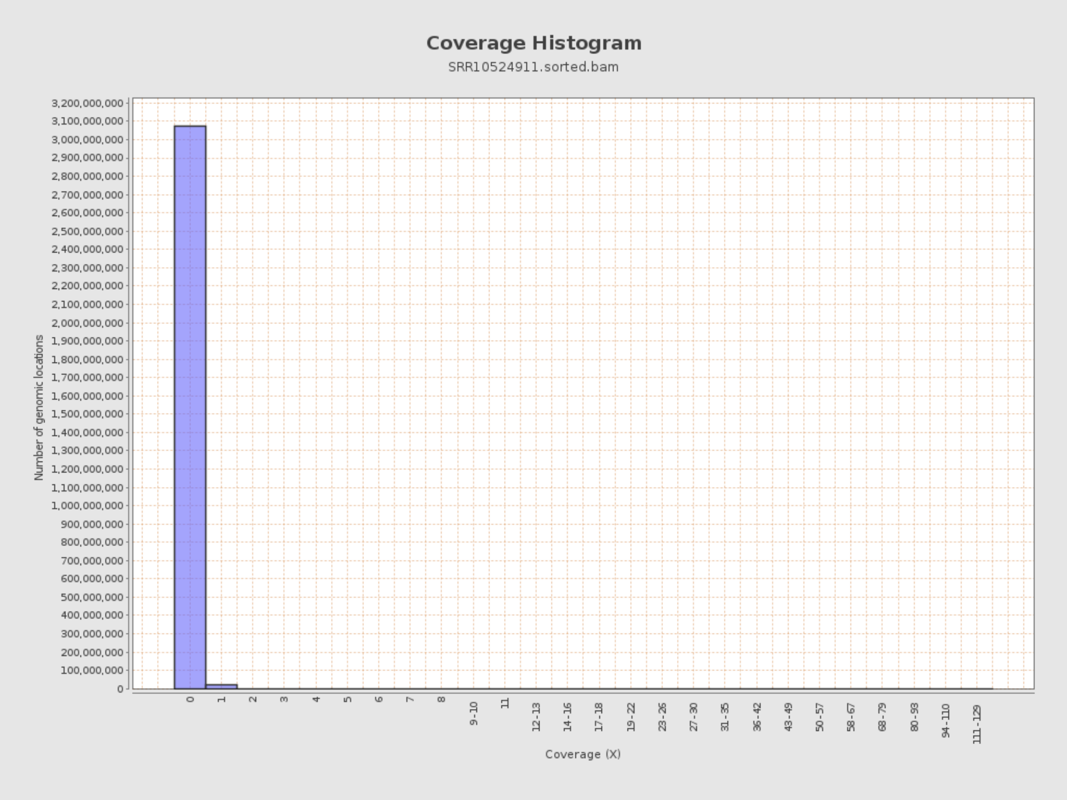
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1792551	0.0072	0.1314
chr2	243199373	2106295	0.0087	0.1136
chr3	198022430	1529591	0.0077	0.0894
chr4	191154276	1560154	0.0082	0.0959
chr5	180915260	1375989	0.0076	0.0892
chr6	171115067	1164534	0.0068	0.0873
chr7	159138663	1607312	0.0101	0.13

chr8	146364022	1089827	0.0074	0.0965
chr9	141213431	1155926	0.0082	0.106
chr10	135534747	959372	0.0071	0.1003
chr11	135006516	960582	0.0071	0.0965
chr12	133851895	1894923	0.0142	0.126
chr13	115169878	955610	0.0083	0.0931
chr14	107349540	898428	0.0084	0.0967
chr15	102531392	643455	0.0063	0.0815
chr16	90354753	710568	0.0079	0.0928
chr17	81195210	712852	0.0088	0.0966
chr18	78077248	794396	0.0102	0.1614
chr19	59128983	431123	0.0073	0.1141
chr20	63025520	757731	0.012	0.1139
chr21	48129895	305403	0.0063	0.084
chr22	51304566	237755	0.0046	0.0693
chrMT	16571	1212	0.0731	0.2634
chrX	155270560	1308358	0.0084	0.0985
chrY	59373566	75872	0.0013	0.0439

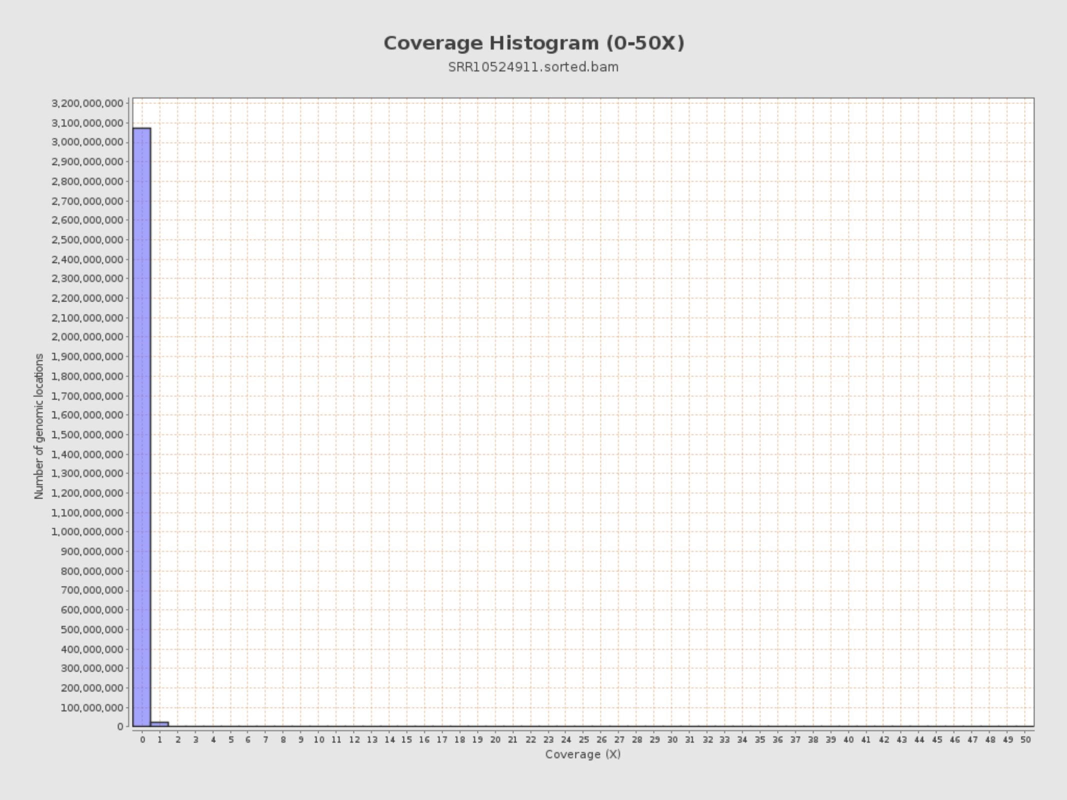
3. Results : Coverage across reference



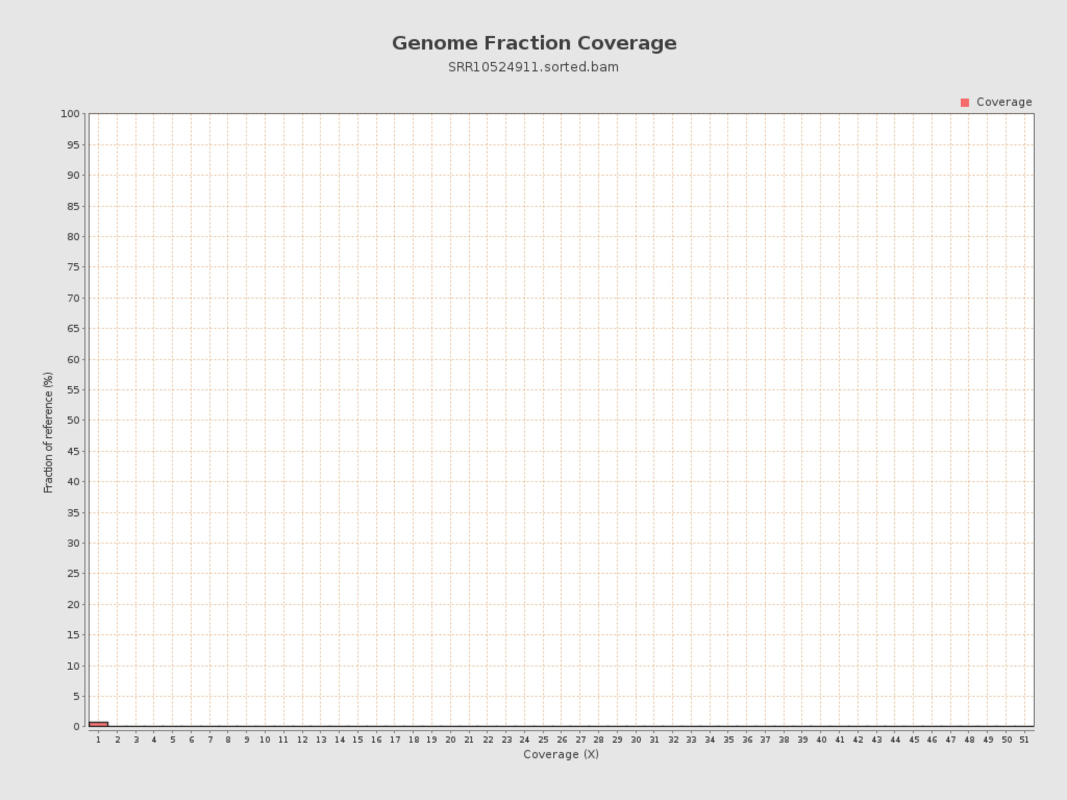
4. Results : Coverage Histogram



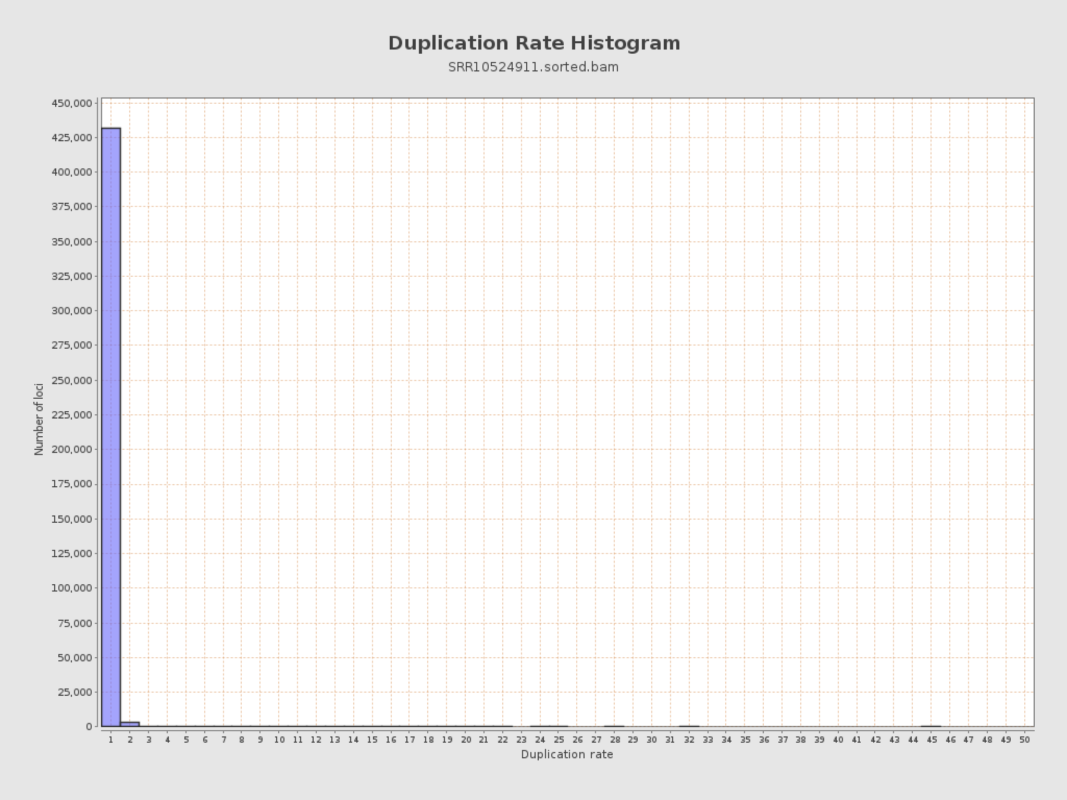
5. Results : Coverage Histogram (0-50X)



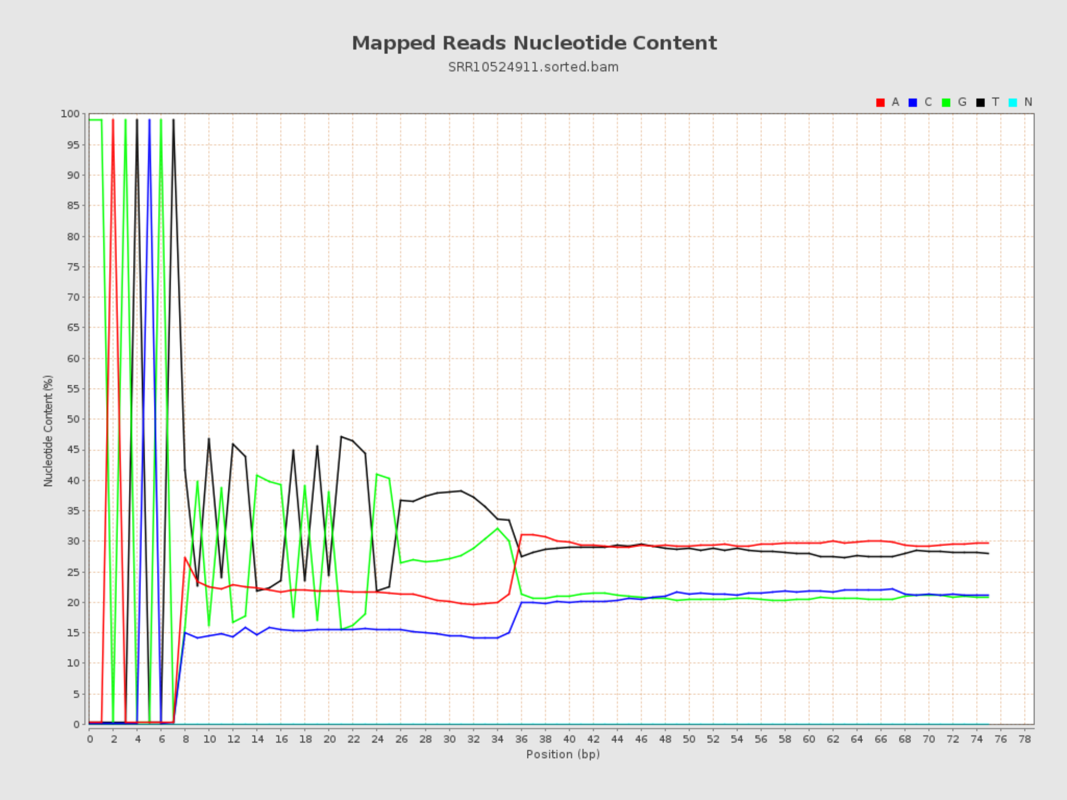
6. Results : Genome Fraction Coverage



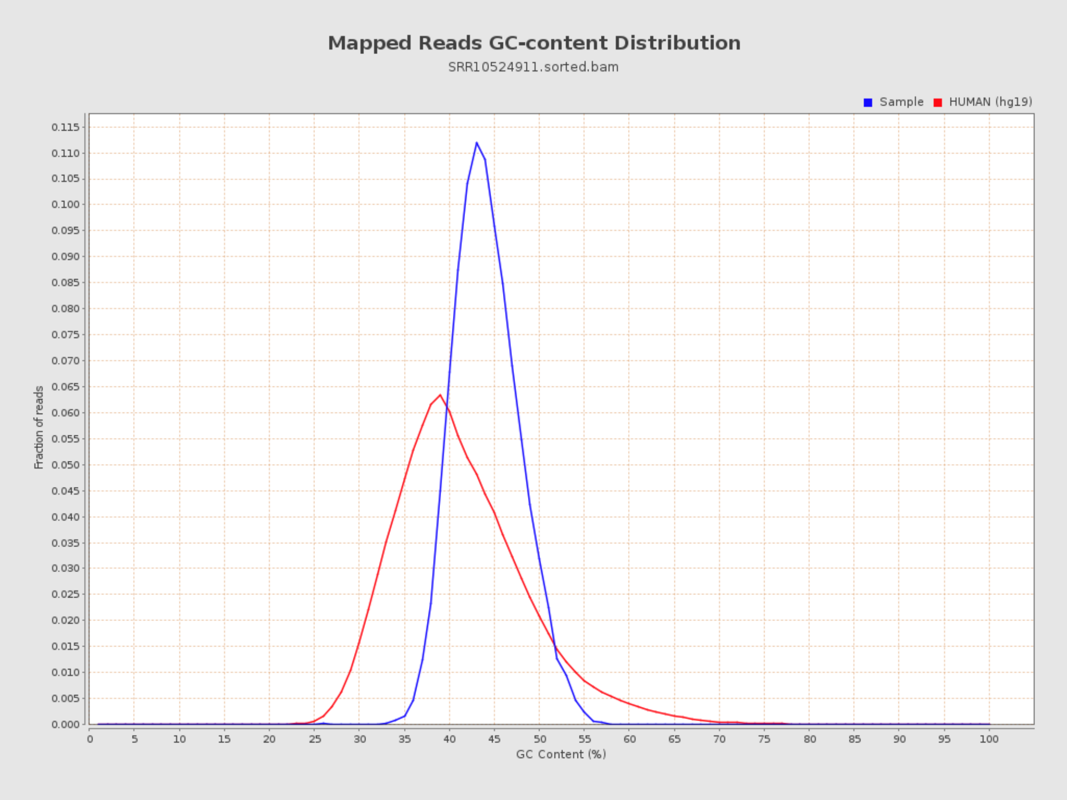
7. Results : Duplication Rate Histogram



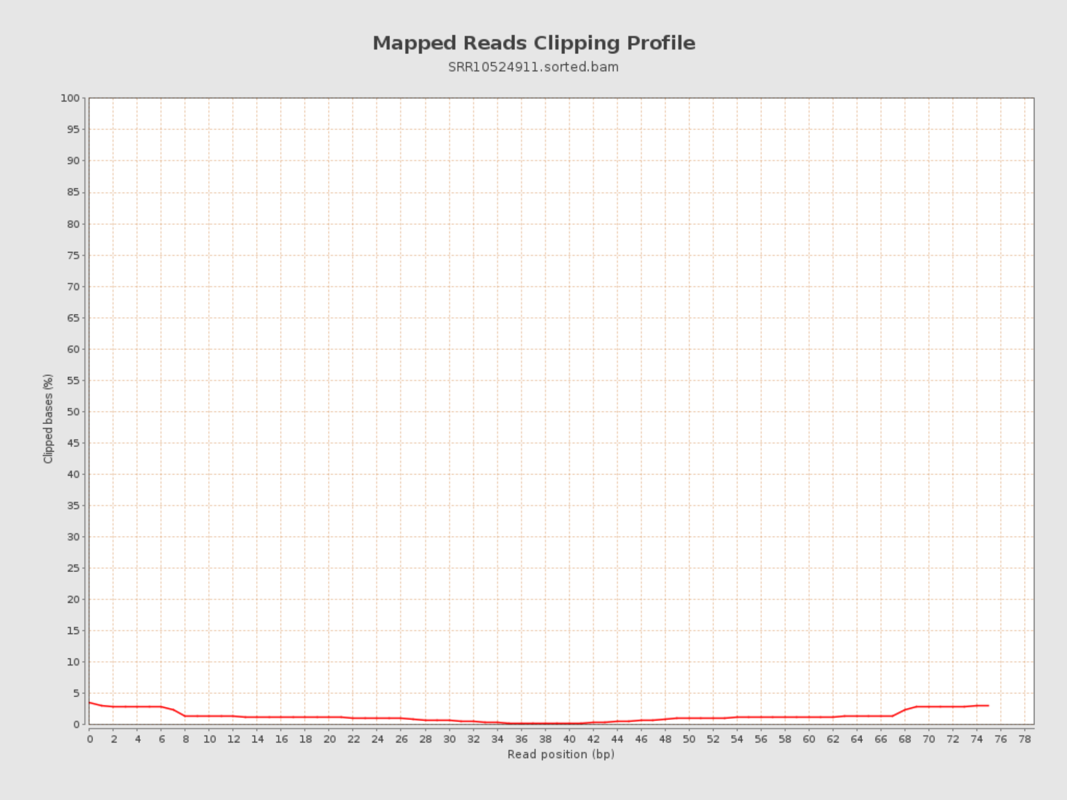
8. Results : Mapped Reads Nucleotide Content



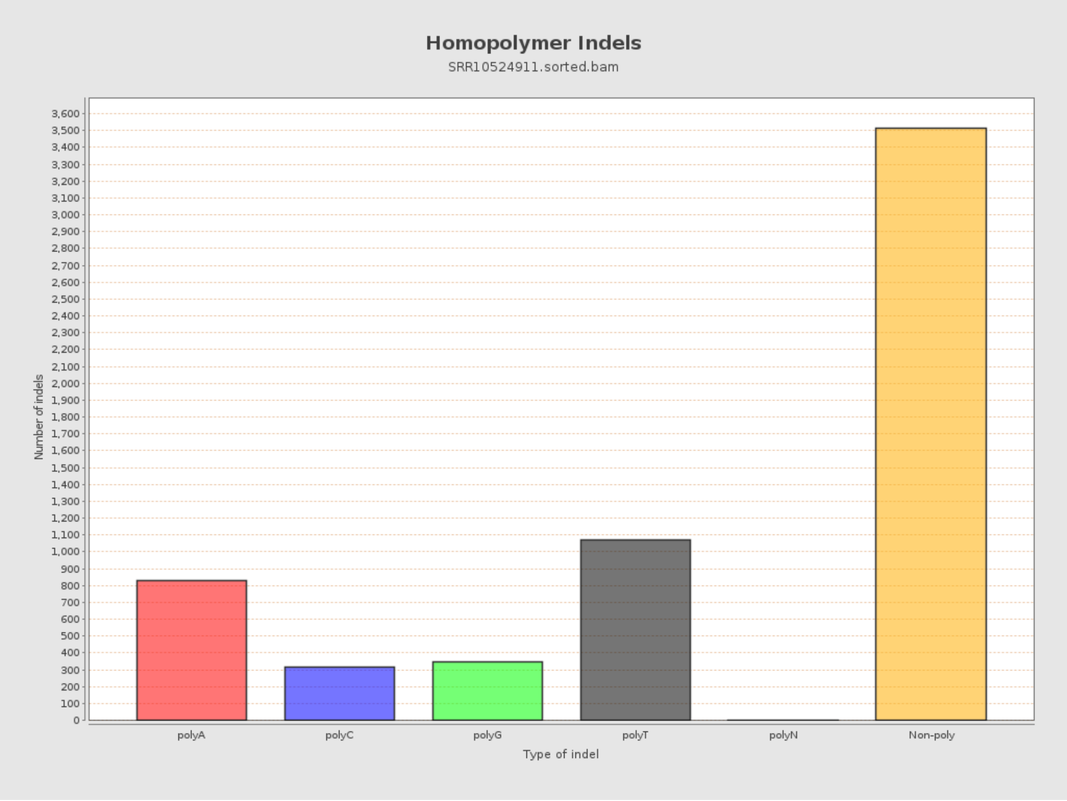
9. Results : Mapped Reads GC-content Distribution



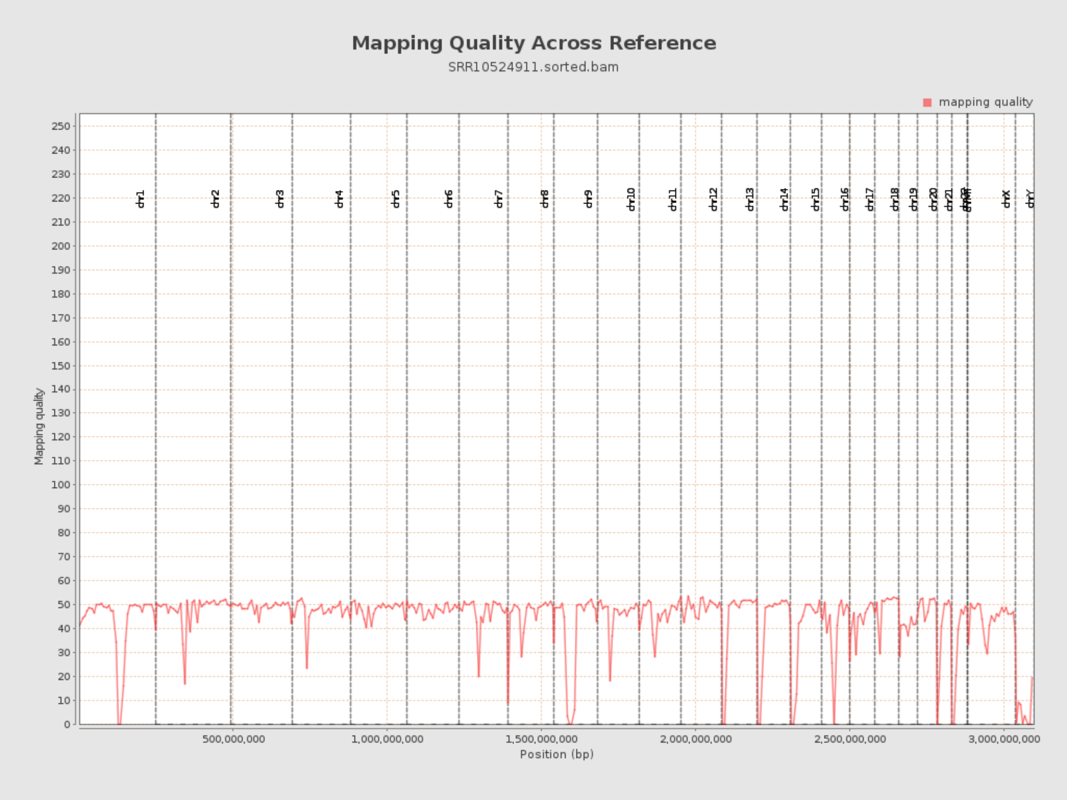
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram