Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 21:59:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524307.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_SRR10524307 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524307.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 21:59:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524307.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	518,839
Mapped reads	471,892 / 90.95%
Unmapped reads	46,947 / 9.05%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,841 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	7,922 / 1.53%
Duplication rate	1.2%
Clipped reads	472,576 / 91.08%

2.2. ACGT Content

Number/percentage of A's	6,708,528 / 24.66%
Number/percentage of C's	5,396,295 / 19.84%
Number/percentage of T's	8,444,962 / 31.05%
Number/percentage of G's	6,646,255 / 24.44%
Number/percentage of N's	3,529 / 0.01%
GC Percentage	44.27%

2.3. Coverage

Mean	0.0088

Standard Deviation	0.1154

2.4. Mapping Quality

Mean Mapping Quality	43.59

2.5. Mismatches and indels

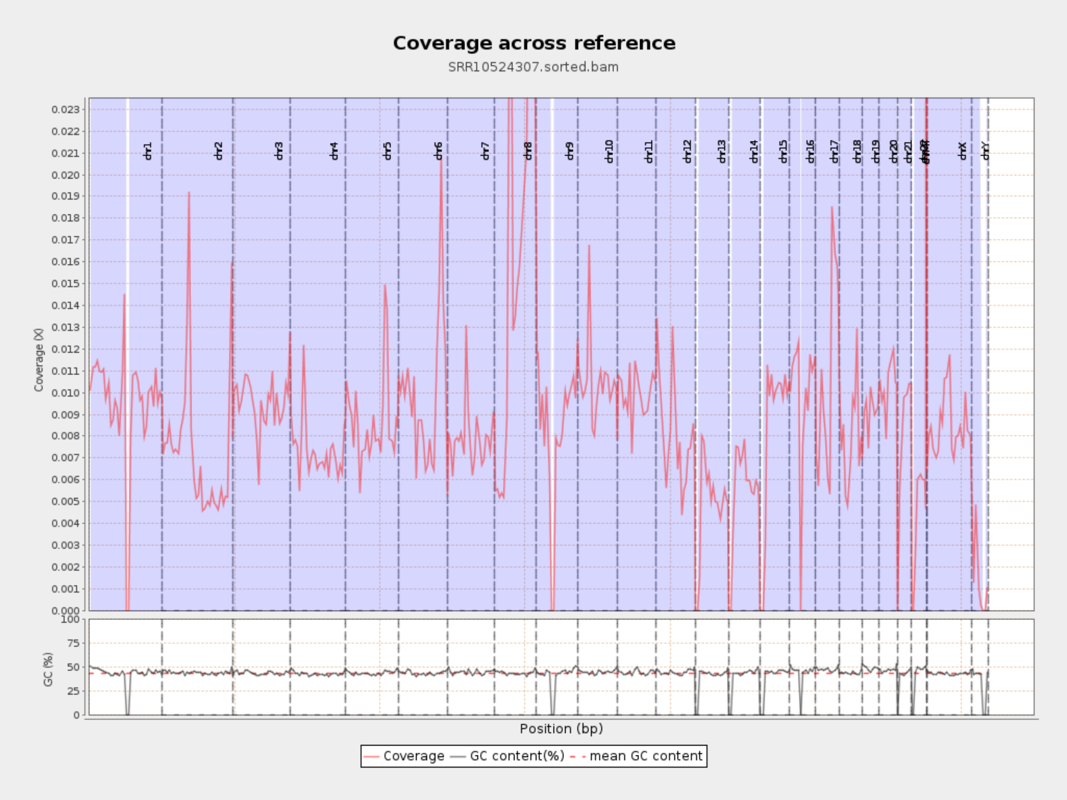
General error rate	0.53%
Mismatches	140,084
Insertions	1,781
Mapped reads with at least one insertion	0.38%
Deletions	4,634
Mapped reads with at least one deletion	0.97%
Homopolymer indels	42.88%

2.6. Chromosome stats

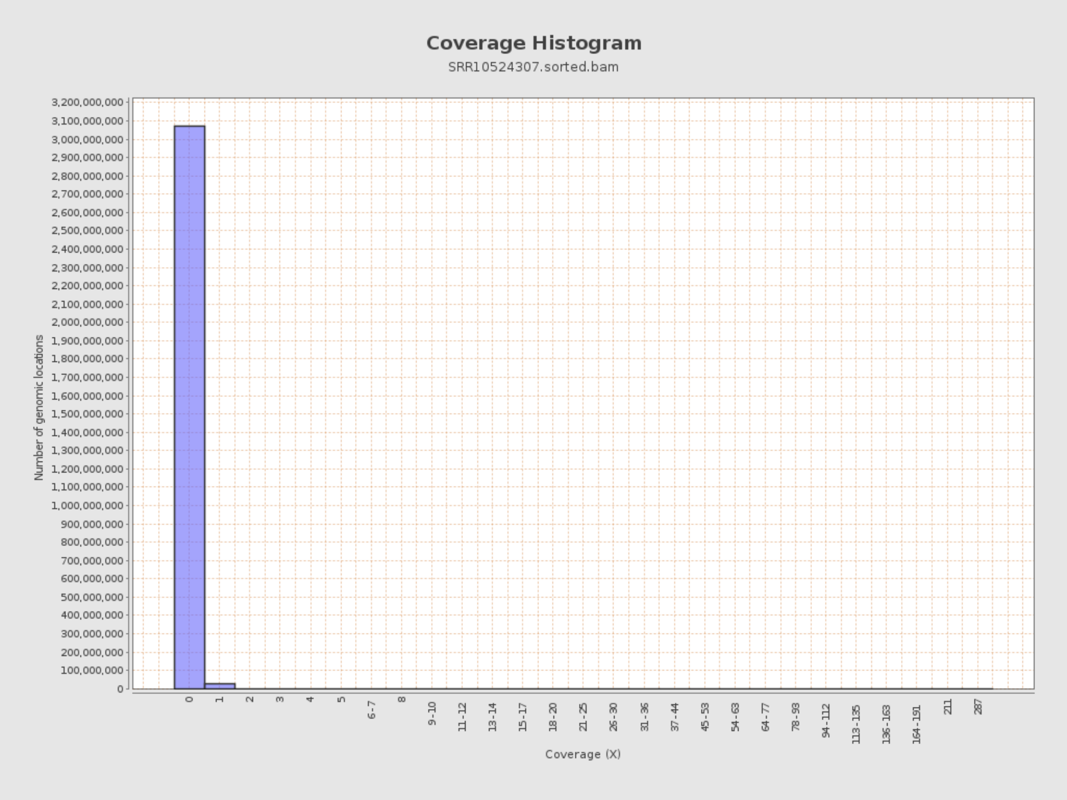
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2362296	0.0095	0.1741
chr2	243199373	1782558	0.0073	0.144
chr3	198022430	1876052	0.0095	0.1006
chr4	191154276	1391354	0.0073	0.0921
chr5	180915260	1572915	0.0087	0.096
chr6	171115067	1703941	0.01	0.1058
chr7	159138663	1259222	0.0079	0.1212

chr8	146364022	2713582	0.0185	0.1537
chr9	141213431	1147315	0.0081	0.1
chr10	135534747	1415673	0.0104	0.1183
chr11	135006516	1338844	0.0099	0.1101
chr12	133851895	1090965	0.0082	0.0935
chr13	115169878	551054	0.0048	0.0711
chr14	107349540	582941	0.0054	0.0768
chr15	102531392	850365	0.0083	0.0941
chr16	90354753	890325	0.0099	0.104
chr17	81195210	855538	0.0105	0.1086
chr18	78077248	631468	0.0081	0.1351
chr19	59128983	539214	0.0091	0.1277
chr20	63025520	652811	0.0104	0.1053
chr21	48129895	386662	0.008	0.0939
chr22	51304566	216924	0.0042	0.0668
chrMT	16571	2544	0.1535	0.3989
chrX	155270560	1308407	0.0084	0.0983
chrY	59373566	83991	0.0014	0.0522

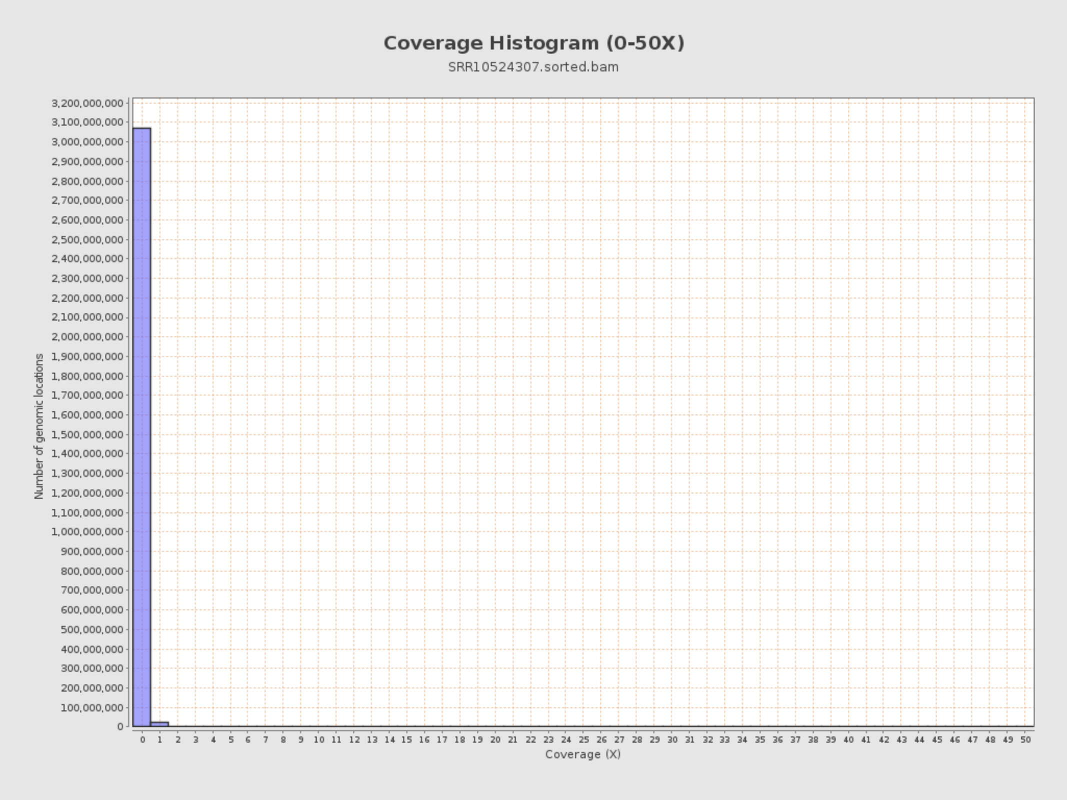
3. Results : Coverage across reference



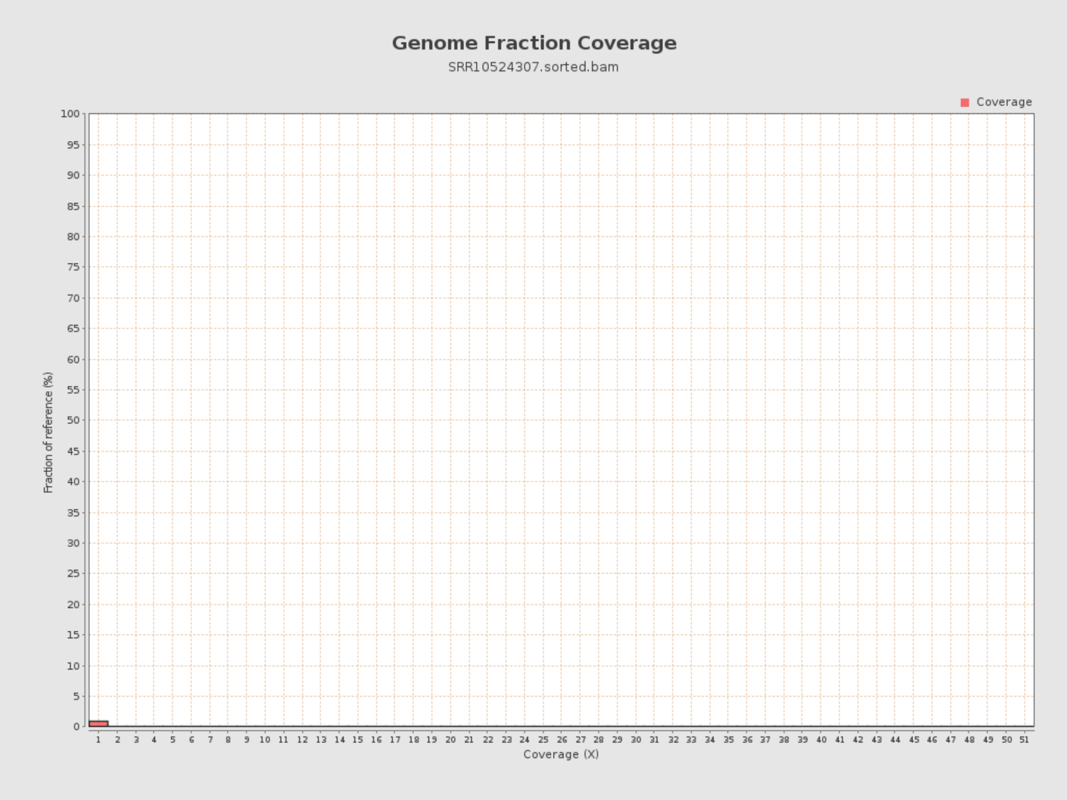
4. Results : Coverage Histogram



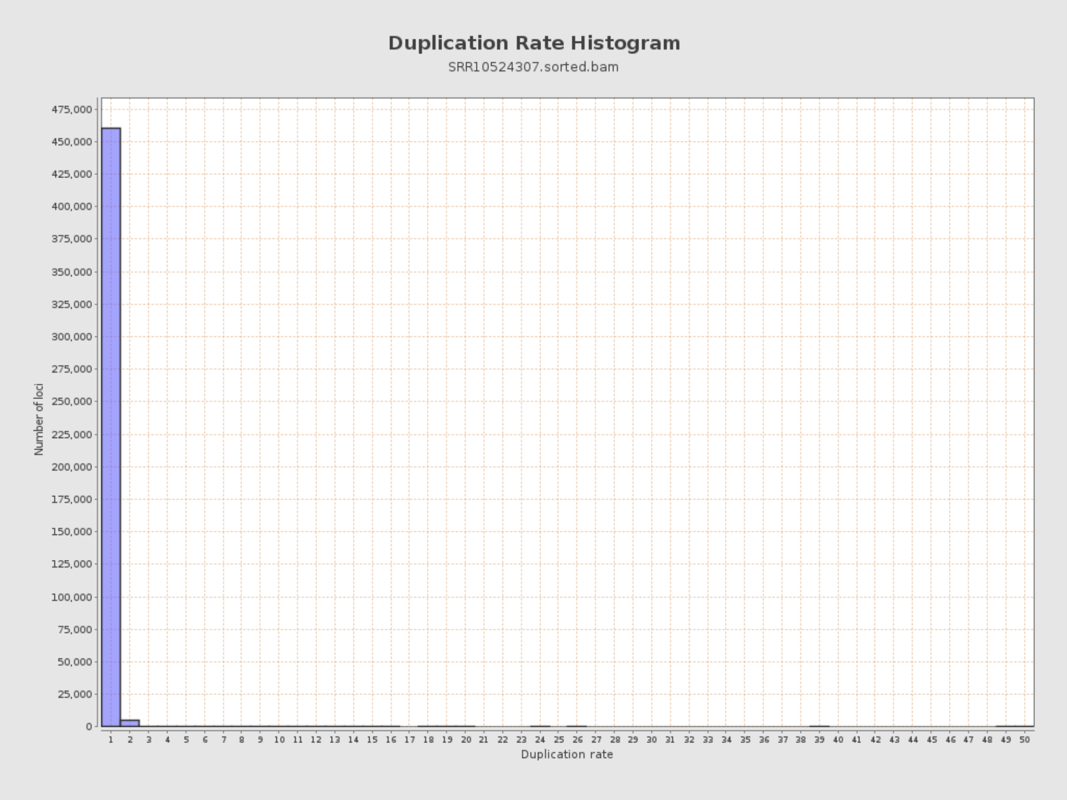
5. Results : Coverage Histogram (0-50X)



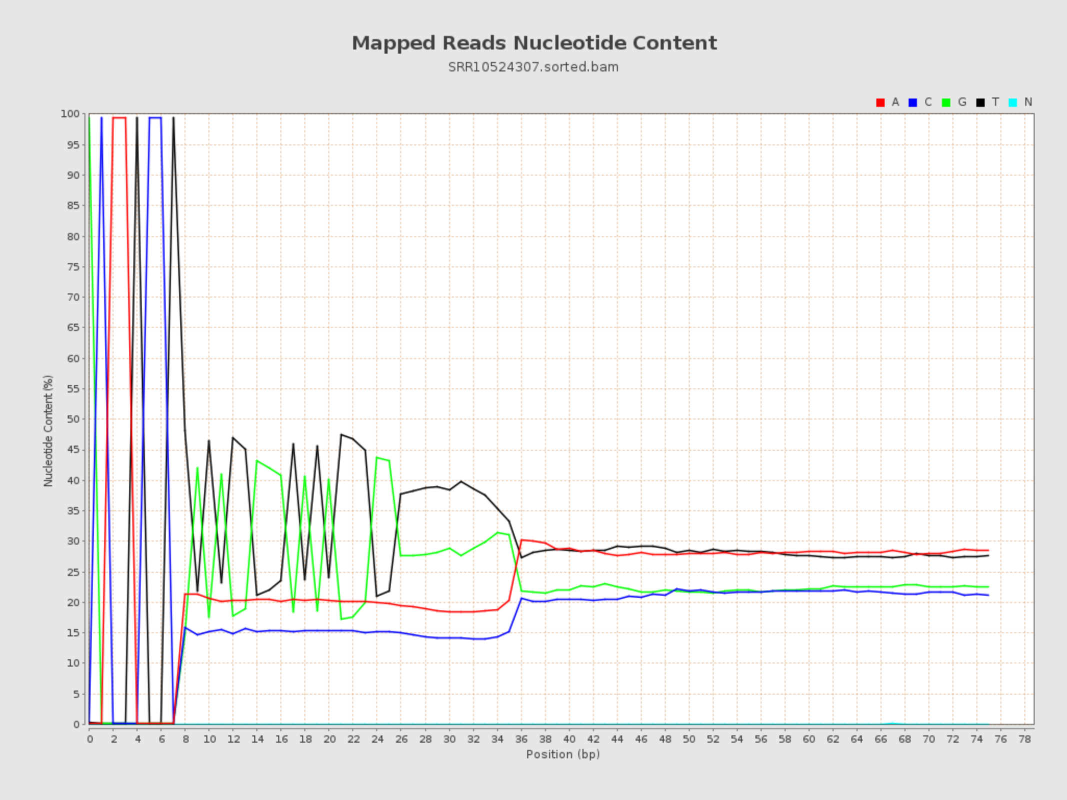
6. Results : Genome Fraction Coverage



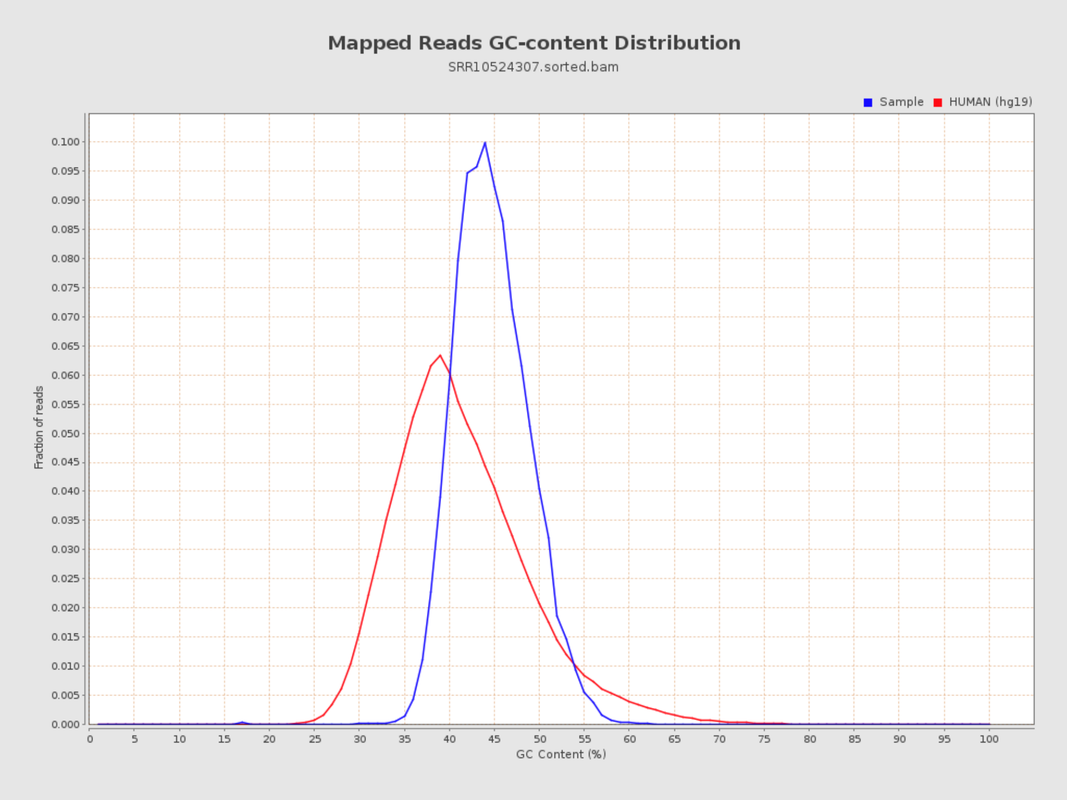
7. Results : Duplication Rate Histogram



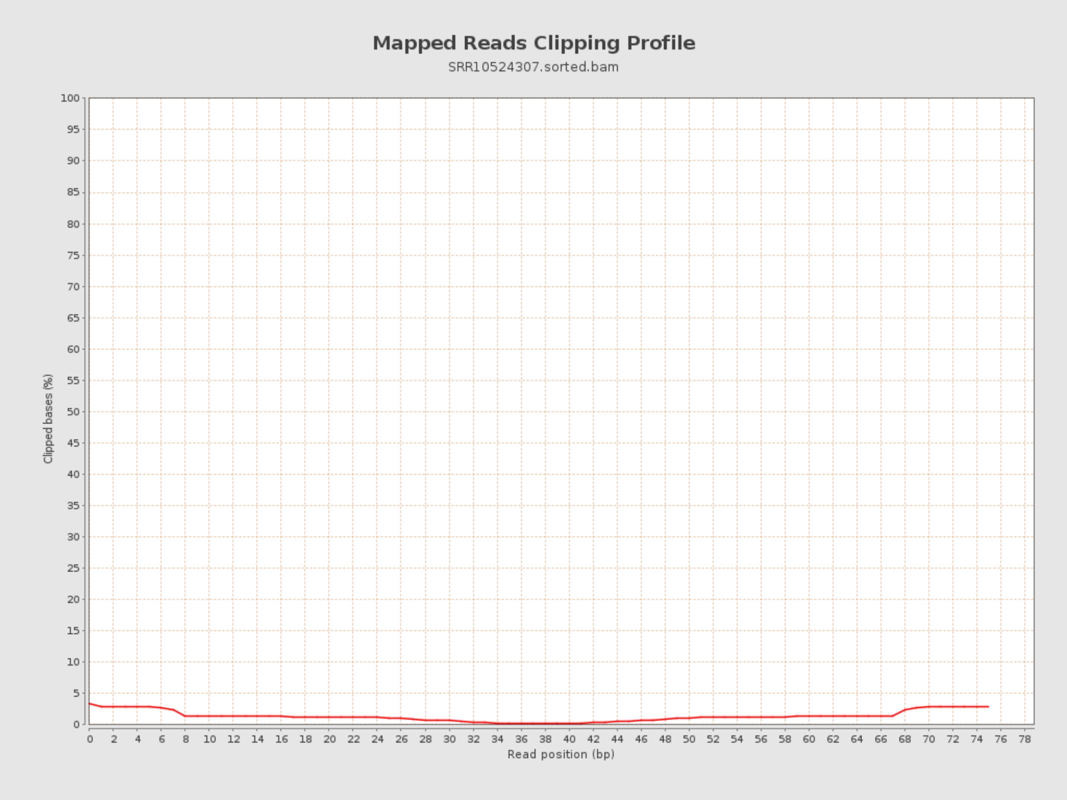
8. Results : Mapped Reads Nucleotide Content



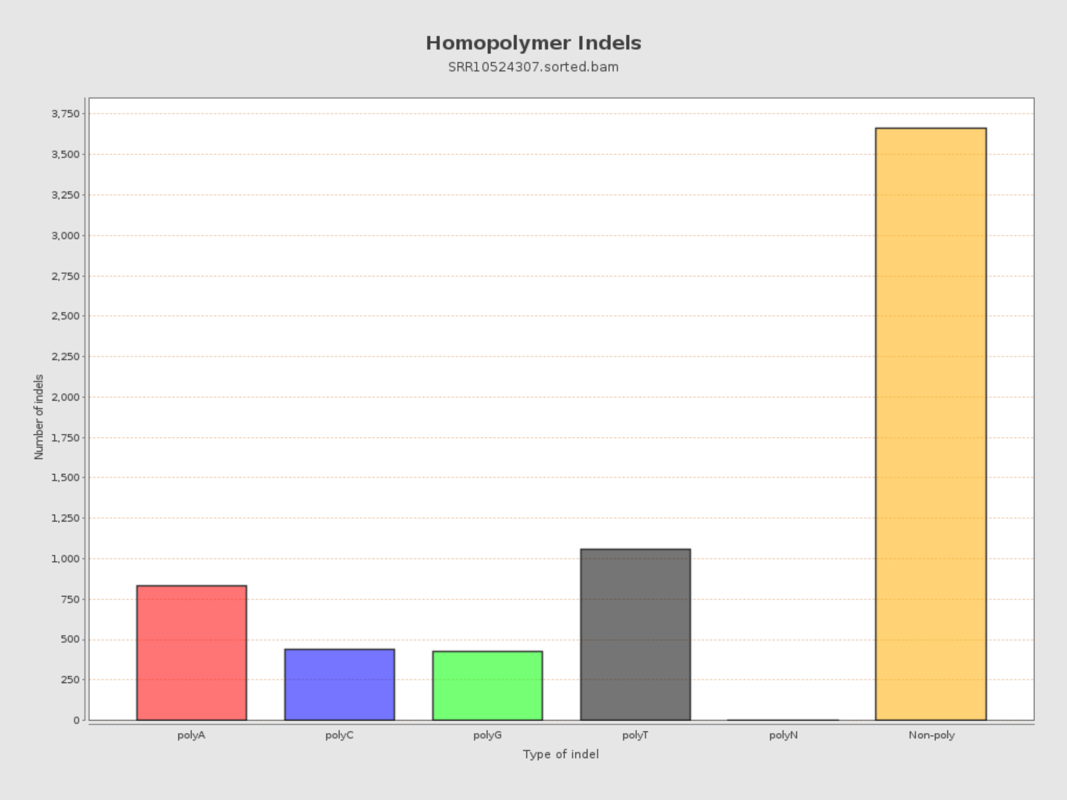
9. Results : Mapped Reads GC-content Distribution



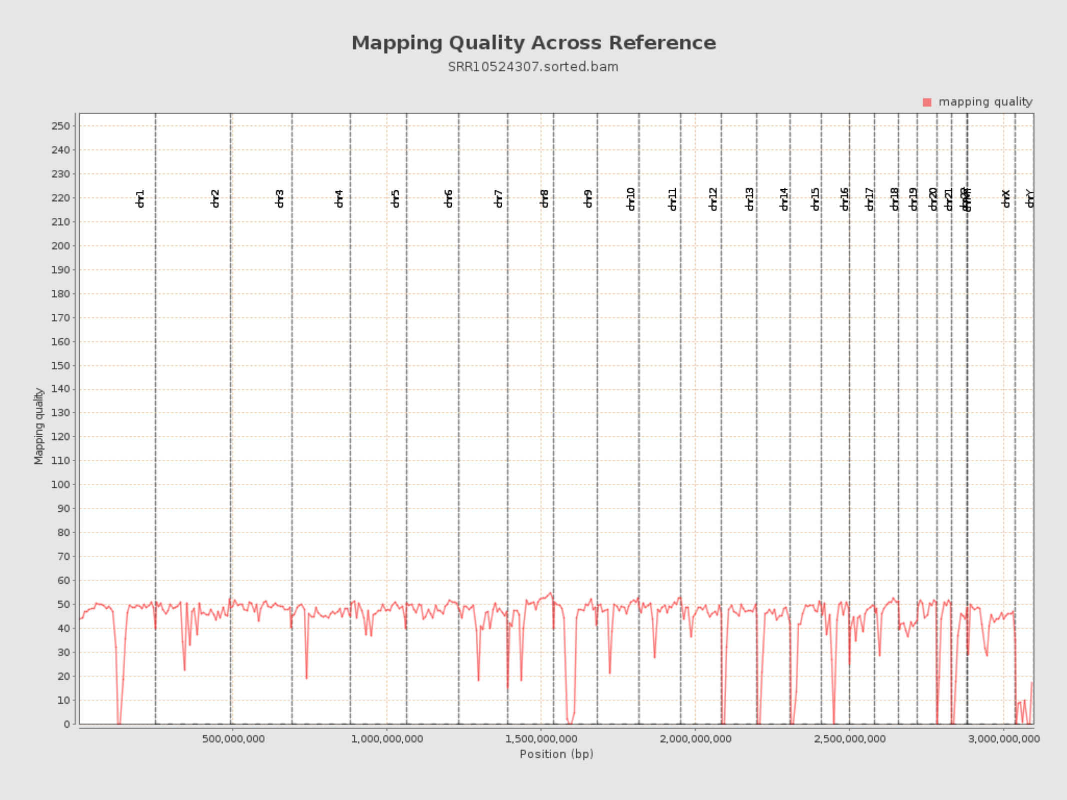
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram