Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 21:44:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524300.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_SRR10524300 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524300.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 21:44:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524300.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	760,720
Mapped reads	686,853 / 90.29%
Unmapped reads	73,867 / 9.71%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,592 / 0.34%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	17,662 / 2.32%
Duplication rate	1.94%
Clipped reads	688,743 / 90.54%

2.2. ACGT Content

Number/percentage of A's	10,418,145 / 26%
Number/percentage of C's	7,681,061 / 19.17%
Number/percentage of T's	12,682,816 / 31.65%
Number/percentage of G's	9,284,714 / 23.17%
Number/percentage of N's	818 / 0%
GC Percentage	42.34%

2.3. Coverage

Mean	0.0129

Standard Deviation	0.1533

2.4. Mapping Quality

Mean Mapping Quality	45.75

2.5. Mismatches and indels

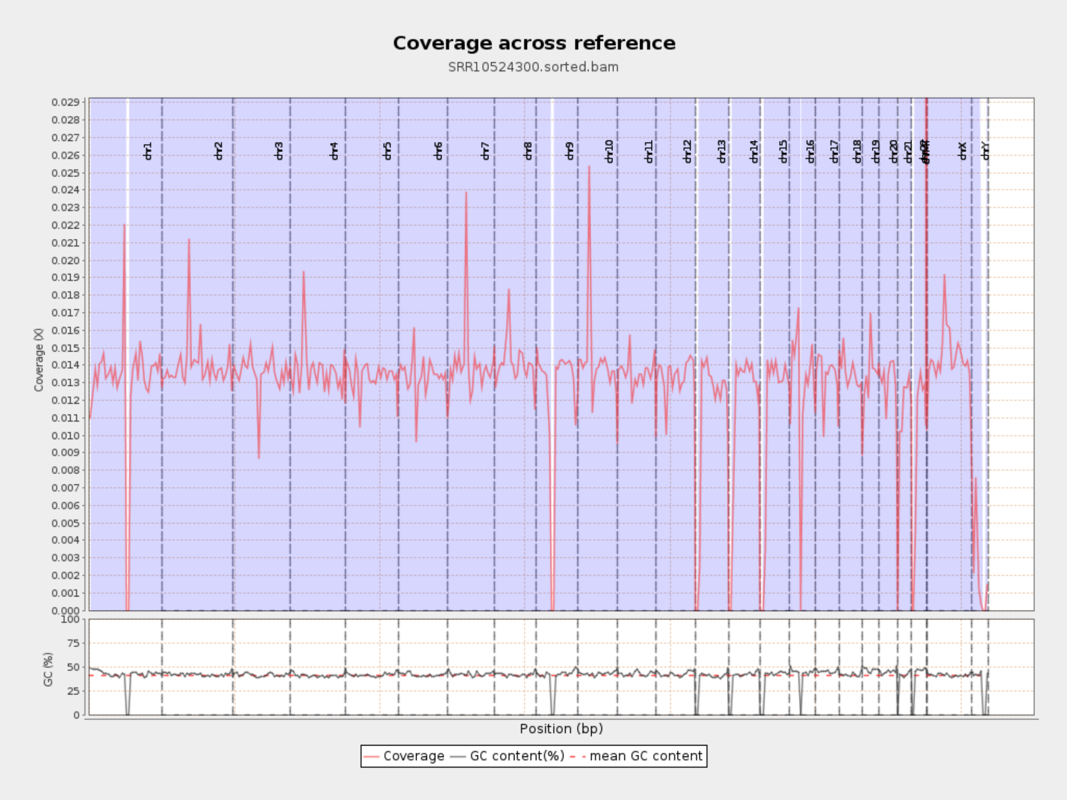
General error rate	0.52%
Mismatches	203,071
Insertions	2,565
Mapped reads with at least one insertion	0.37%
Deletions	8,461
Mapped reads with at least one deletion	1.22%
Homopolymer indels	43.83%

2.6. Chromosome stats

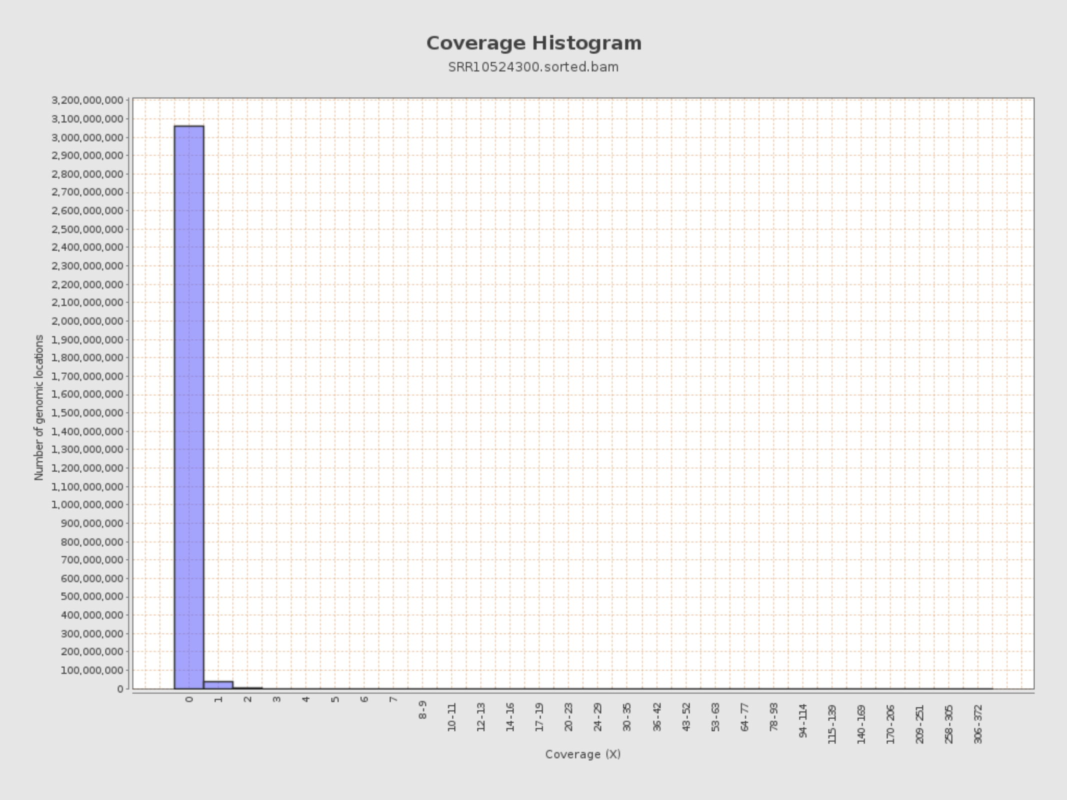
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3230739	0.013	0.2452
chr2	243199373	3412492	0.014	0.1983
chr3	198022430	2683363	0.0136	0.1222
chr4	191154276	2619676	0.0137	0.1263
chr5	180915260	2413518	0.0133	0.1205
chr6	171115067	2288894	0.0134	0.1275
chr7	159138663	2247772	0.0141	0.1939

chr8	146364022	2064994	0.0141	0.1683
chr9	141213431	1693039	0.012	0.1311
chr10	135534747	1946517	0.0144	0.152
chr11	135006516	1826089	0.0135	0.135
chr12	133851895	1790415	0.0134	0.1211
chr13	115169878	1261455	0.011	0.1102
chr14	107349540	1210113	0.0113	0.1132
chr15	102531392	1119567	0.0109	0.1091
chr16	90354753	1156256	0.0128	0.1238
chr17	81195210	1079162	0.0133	0.1228
chr18	78077248	1064041	0.0136	0.2032
chr19	59128983	796851	0.0135	0.1769
chr20	63025520	823926	0.0131	0.1201
chr21	48129895	517975	0.0108	0.1127
chr22	51304566	451887	0.0088	0.0978
chrMT	16571	11034	0.6659	0.9436
chrX	155270560	2243873	0.0145	0.1306
chrY	59373566	127789	0.0022	0.0736

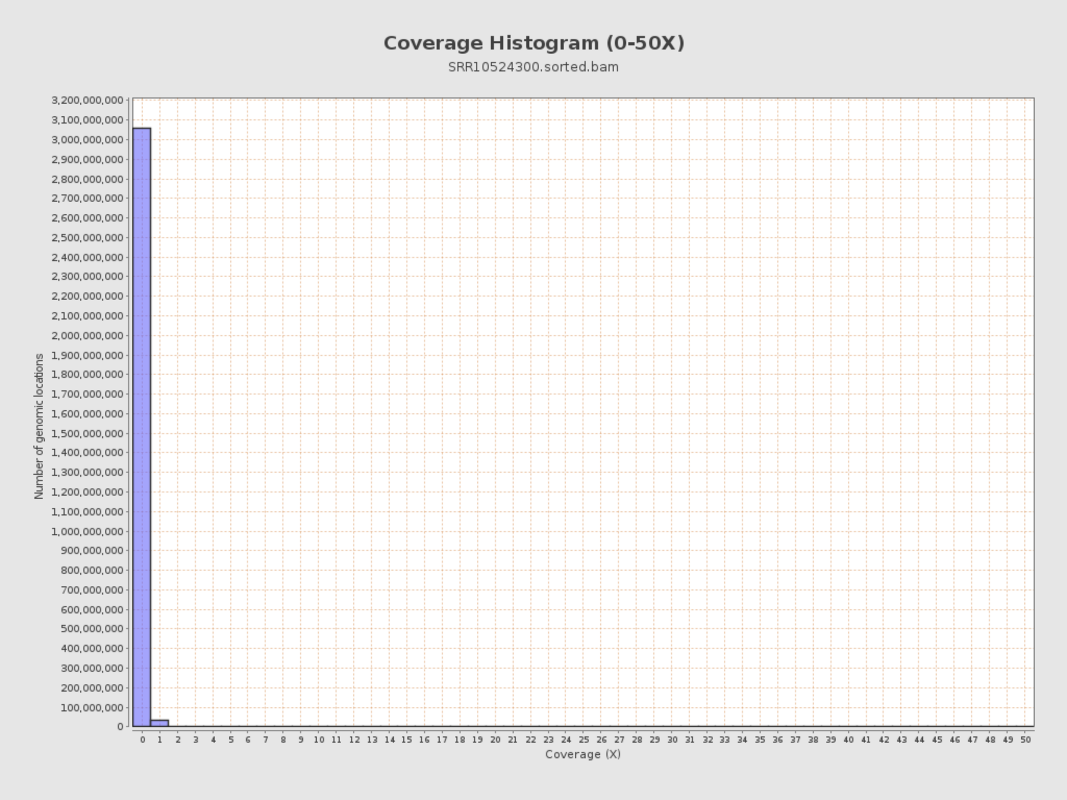
3. Results : Coverage across reference



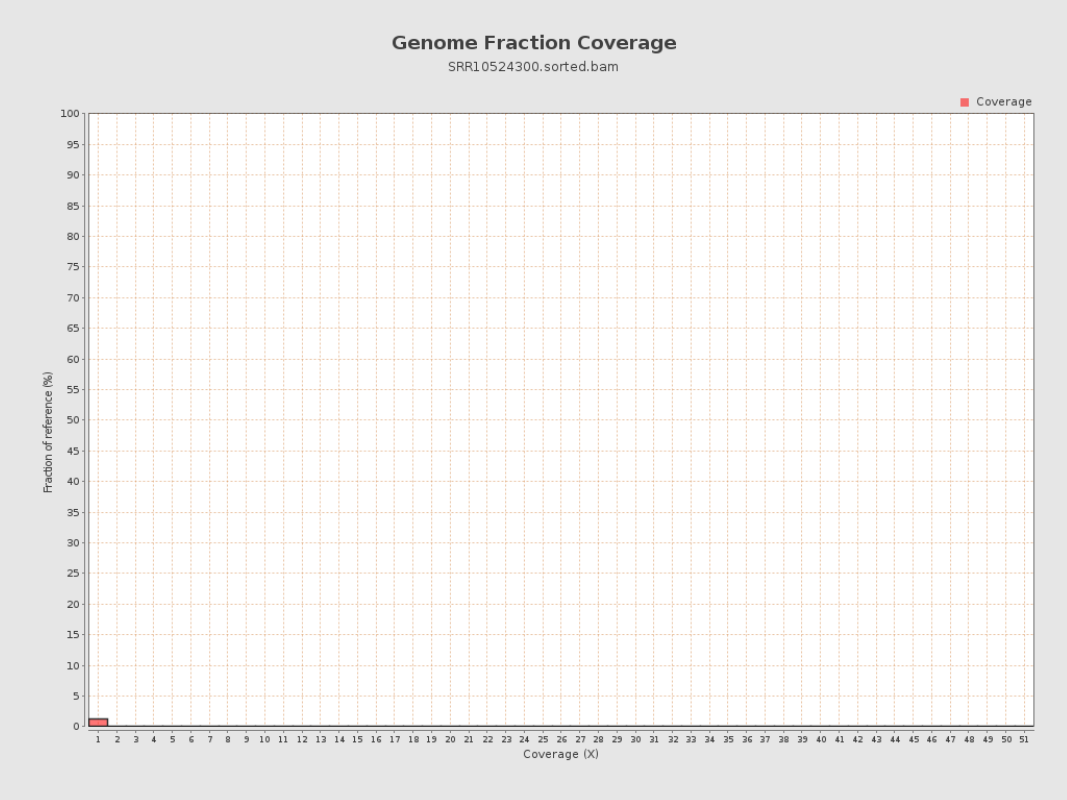
4. Results : Coverage Histogram



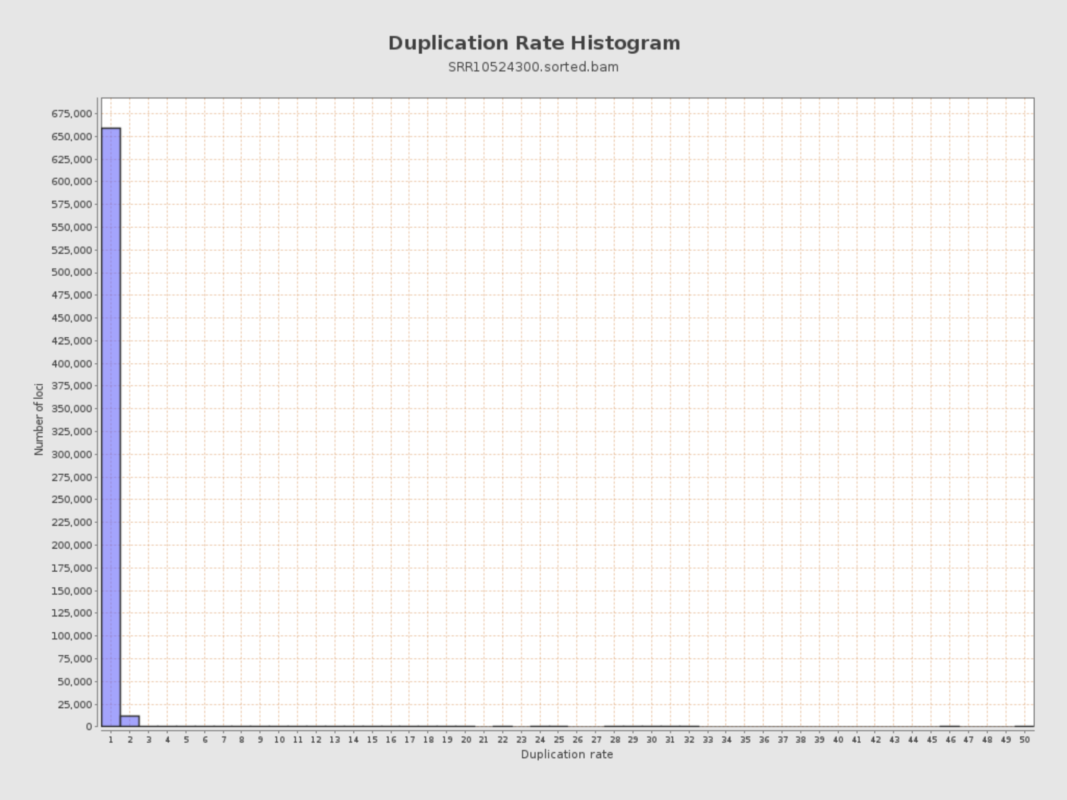
5. Results : Coverage Histogram (0-50X)



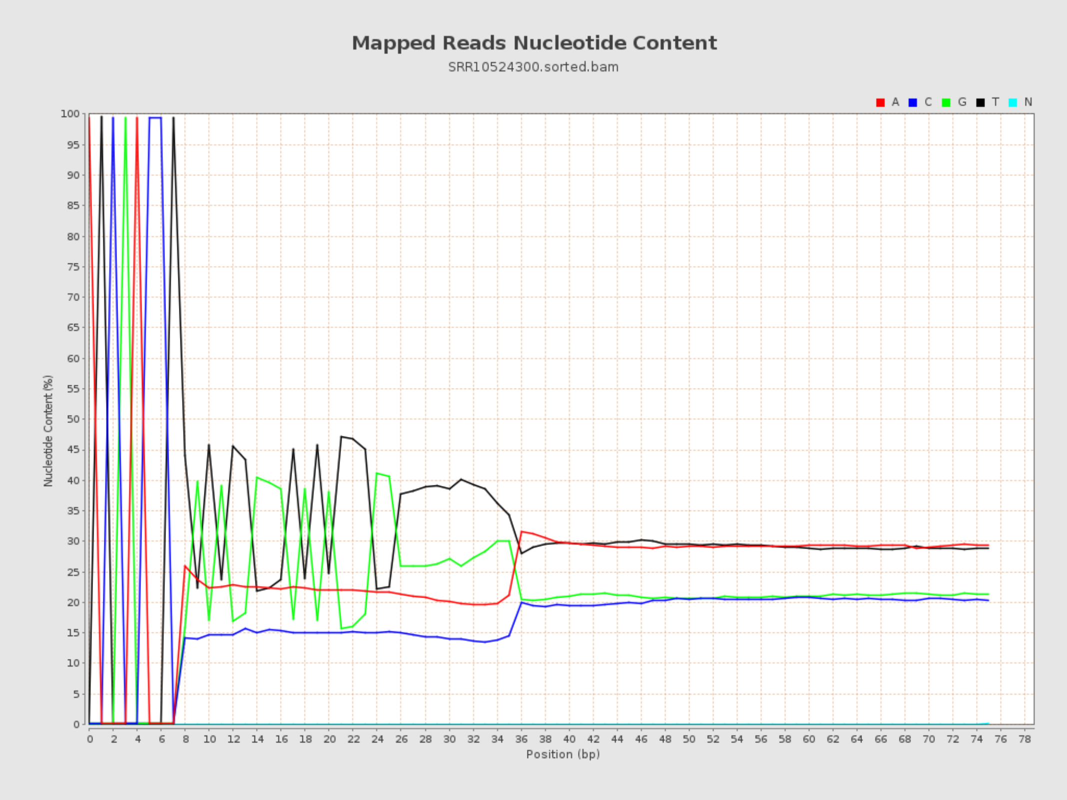
6. Results : Genome Fraction Coverage



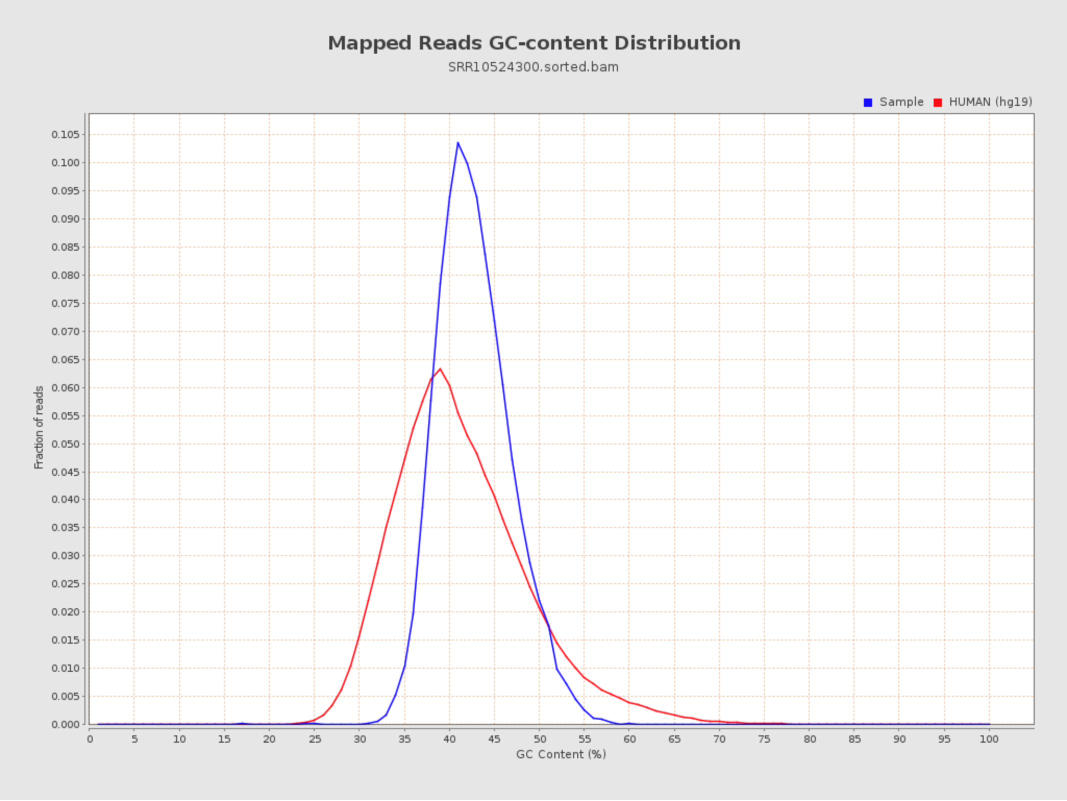
7. Results : Duplication Rate Histogram



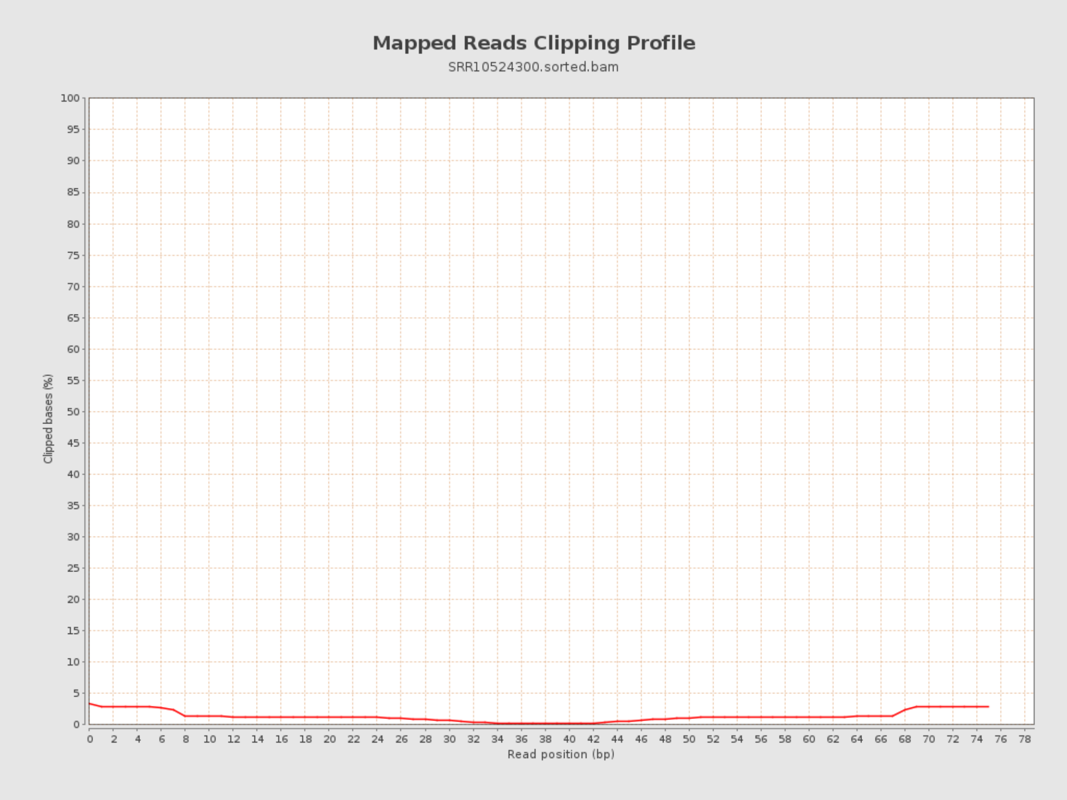
8. Results : Mapped Reads Nucleotide Content



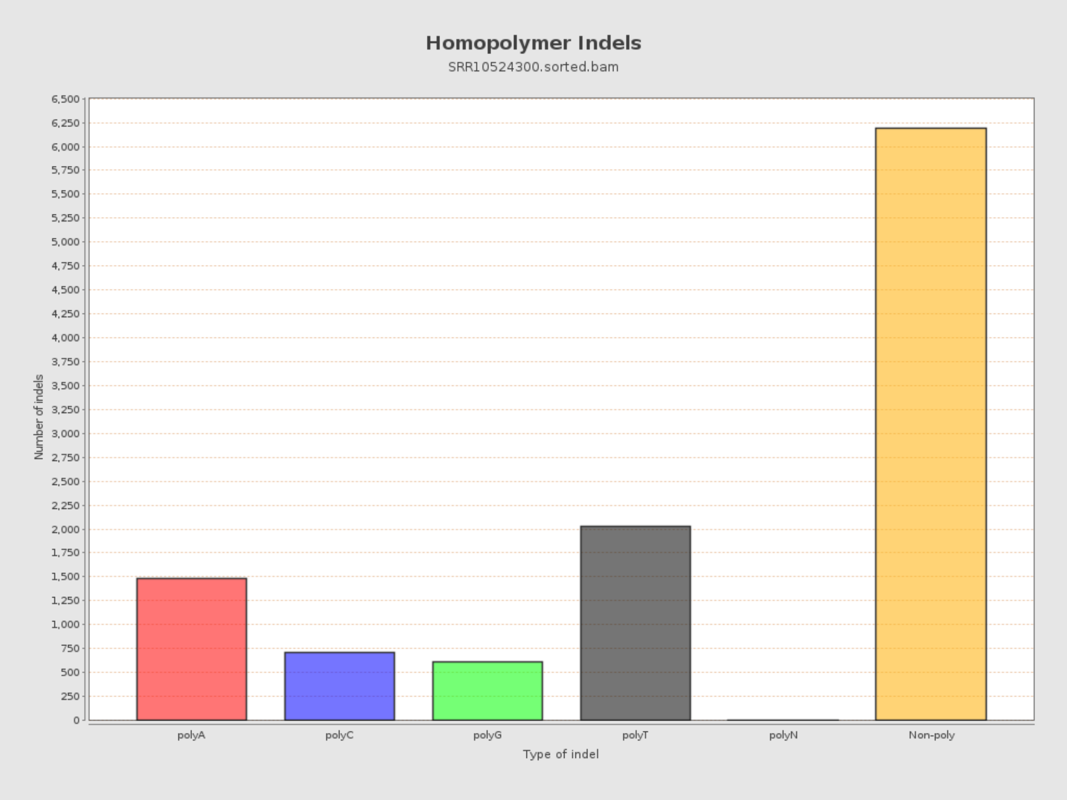
9. Results : Mapped Reads GC-content Distribution



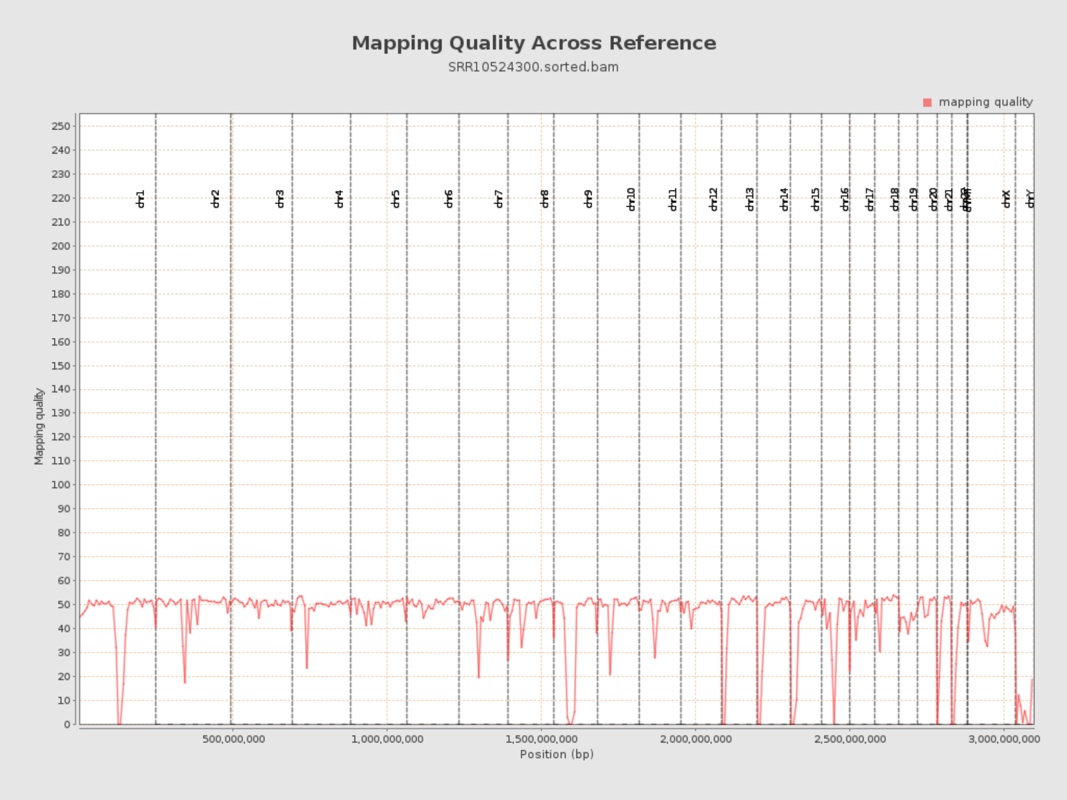
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram