Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 03:24:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524422.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_SRR10524422 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524422.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 03:24:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524422.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	537,800
Mapped reads	494,007 / 91.86%
Unmapped reads	43,793 / 8.14%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,729 / 0.32%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	10,658 / 1.98%
Duplication rate	1.66%
Clipped reads	495,245 / 92.09%

2.2. ACGT Content

Number/percentage of A's	7,176,577 / 24.98%
Number/percentage of C's	5,040,921 / 17.55%
Number/percentage of T's	9,093,028 / 31.65%
Number/percentage of G's	7,419,542 / 25.82%
Number/percentage of N's	631 / 0%
GC Percentage	43.37%

2.3. Coverage

Mean	0.0093

Standard Deviation	0.1195

2.4. Mapping Quality

Mean Mapping Quality	45.65

2.5. Mismatches and indels

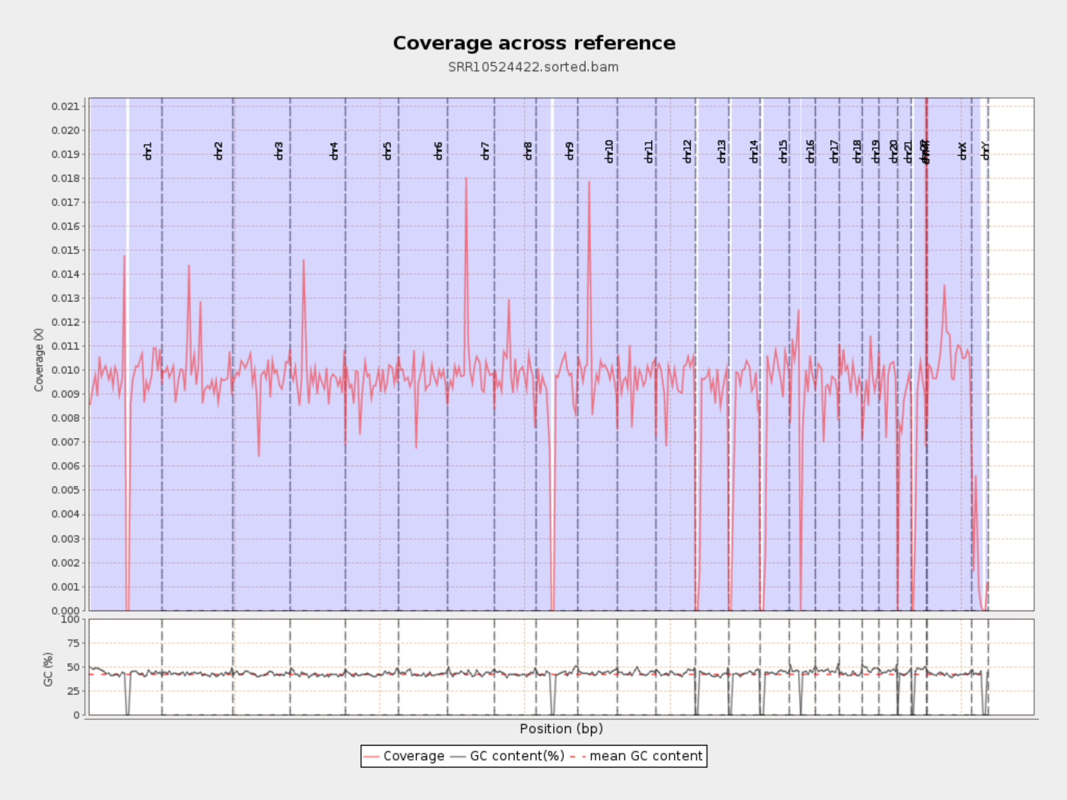
General error rate	0.51%
Mismatches	144,245
Insertions	1,761
Mapped reads with at least one insertion	0.36%
Deletions	5,875
Mapped reads with at least one deletion	1.18%
Homopolymer indels	46.06%

2.6. Chromosome stats

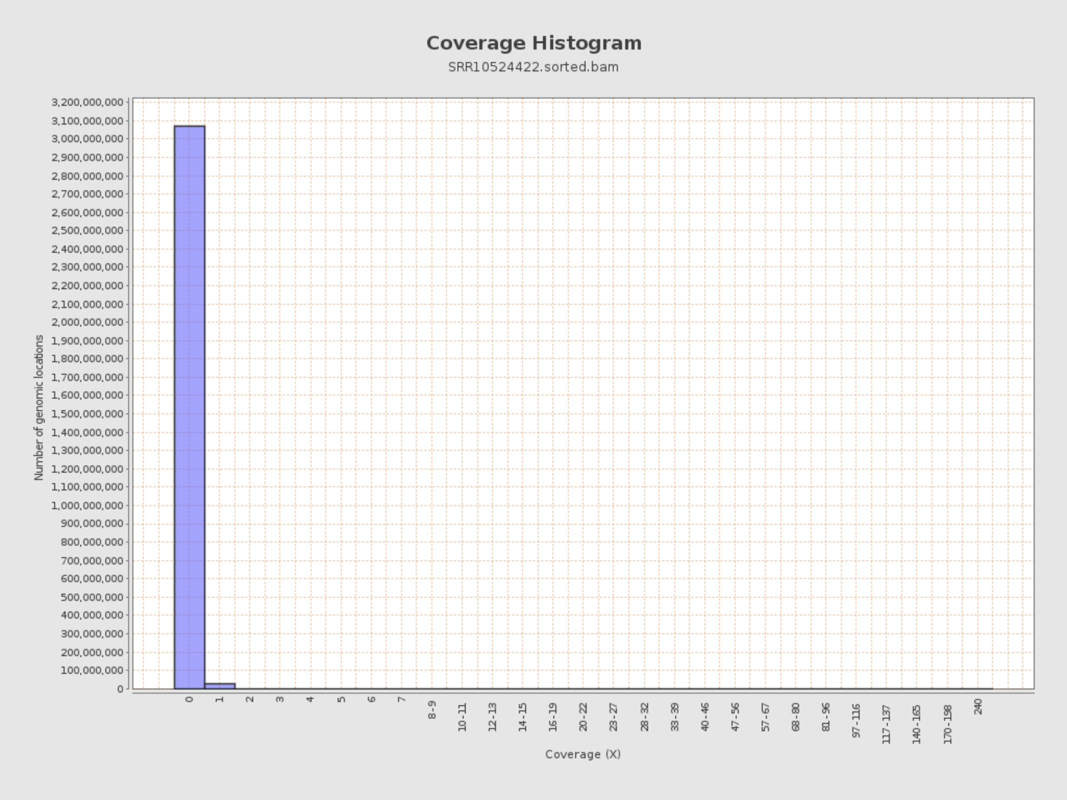
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2330244	0.0093	0.1667
chr2	243199373	2412847	0.0099	0.1457
chr3	198022430	1932611	0.0098	0.1022
chr4	191154276	1865158	0.0098	0.1057
chr5	180915260	1719025	0.0095	0.1008
chr6	171115067	1650921	0.0096	0.1056
chr7	159138663	1636177	0.0103	0.1623

chr8	146364022	1449996	0.0099	0.1304
chr9	141213431	1189581	0.0084	0.1045
chr10	135534747	1388998	0.0102	0.1231
chr11	135006516	1307045	0.0097	0.1096
chr12	133851895	1293526	0.0097	0.1023
chr13	115169878	906809	0.0079	0.0915
chr14	107349540	864705	0.0081	0.094
chr15	102531392	825449	0.0081	0.0935
chr16	90354753	832088	0.0092	0.1022
chr17	81195210	751080	0.0093	0.1009
chr18	78077248	770735	0.0099	0.147
chr19	59128983	561425	0.0095	0.1322
chr20	63025520	593558	0.0094	0.1018
chr21	48129895	378219	0.0079	0.0954
chr22	51304566	335590	0.0065	0.0836
chrMT	16571	8116	0.4898	0.7881
chrX	155270560	1641166	0.0106	0.1099
chrY	59373566	95146	0.0016	0.0563

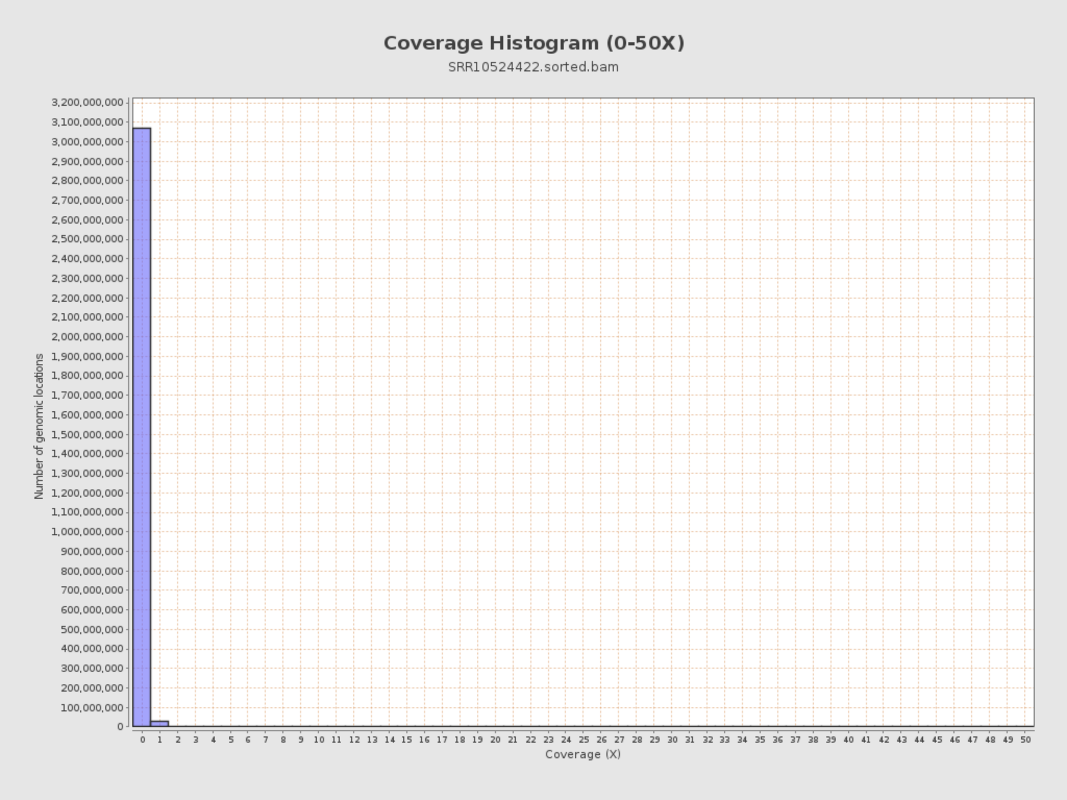
3. Results : Coverage across reference



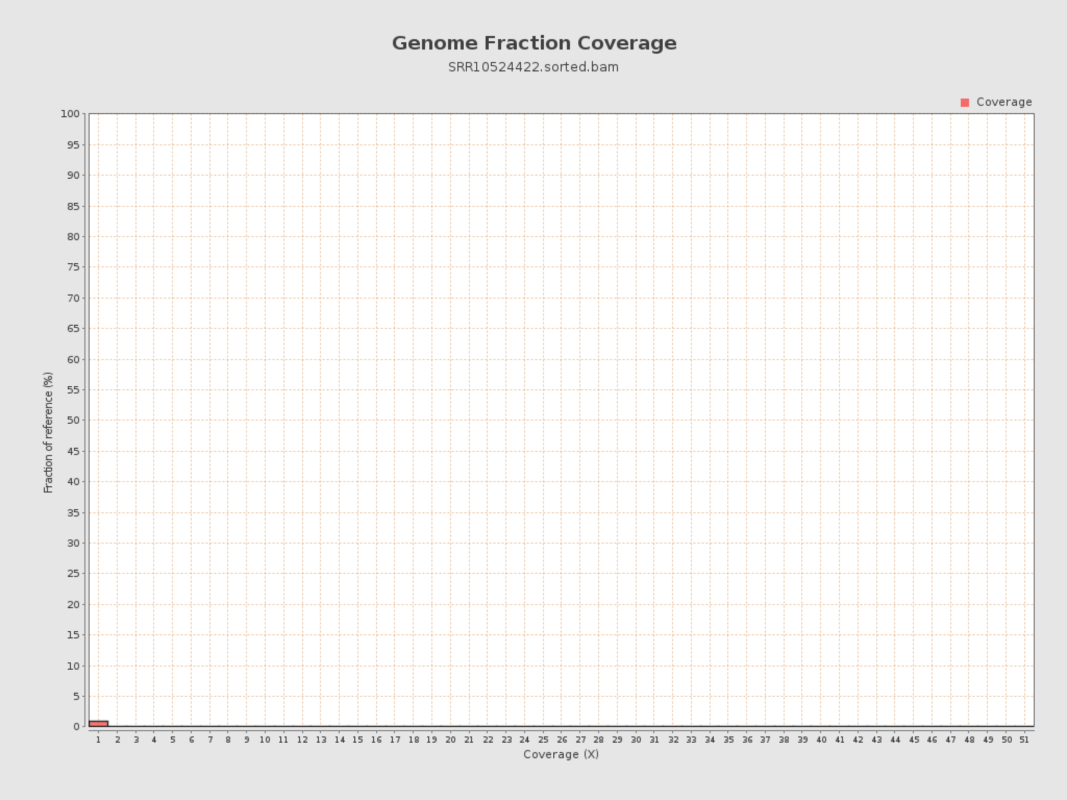
4. Results : Coverage Histogram



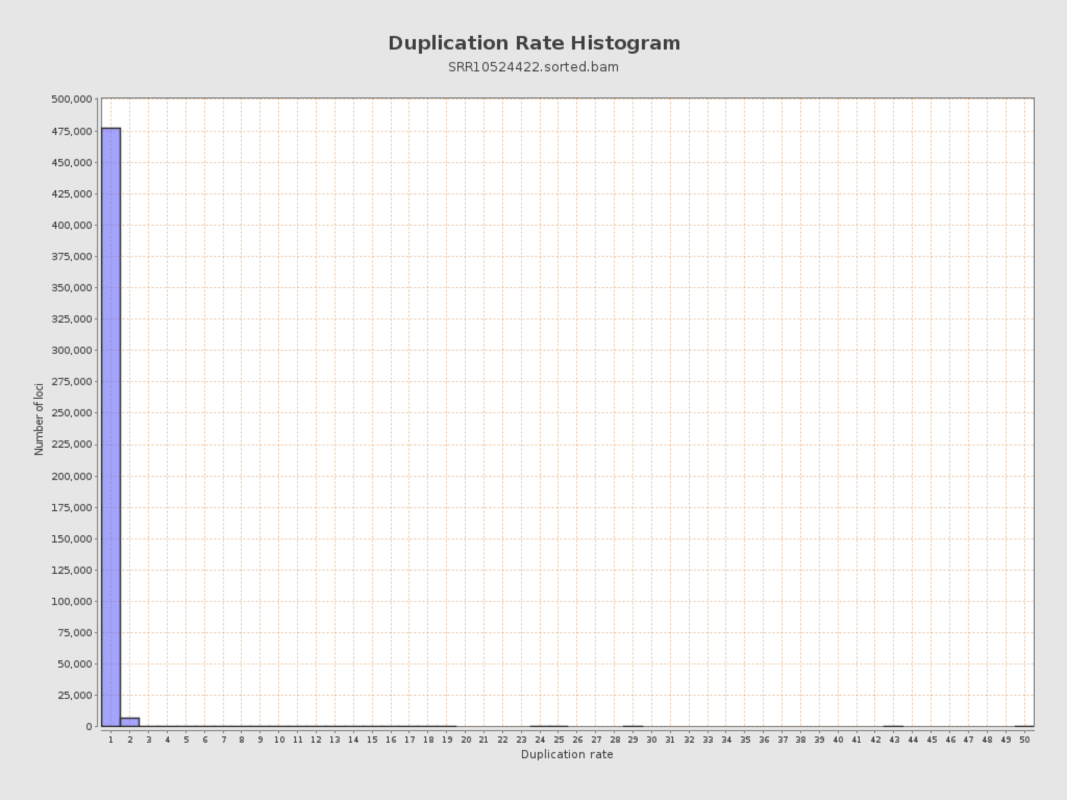
5. Results : Coverage Histogram (0-50X)



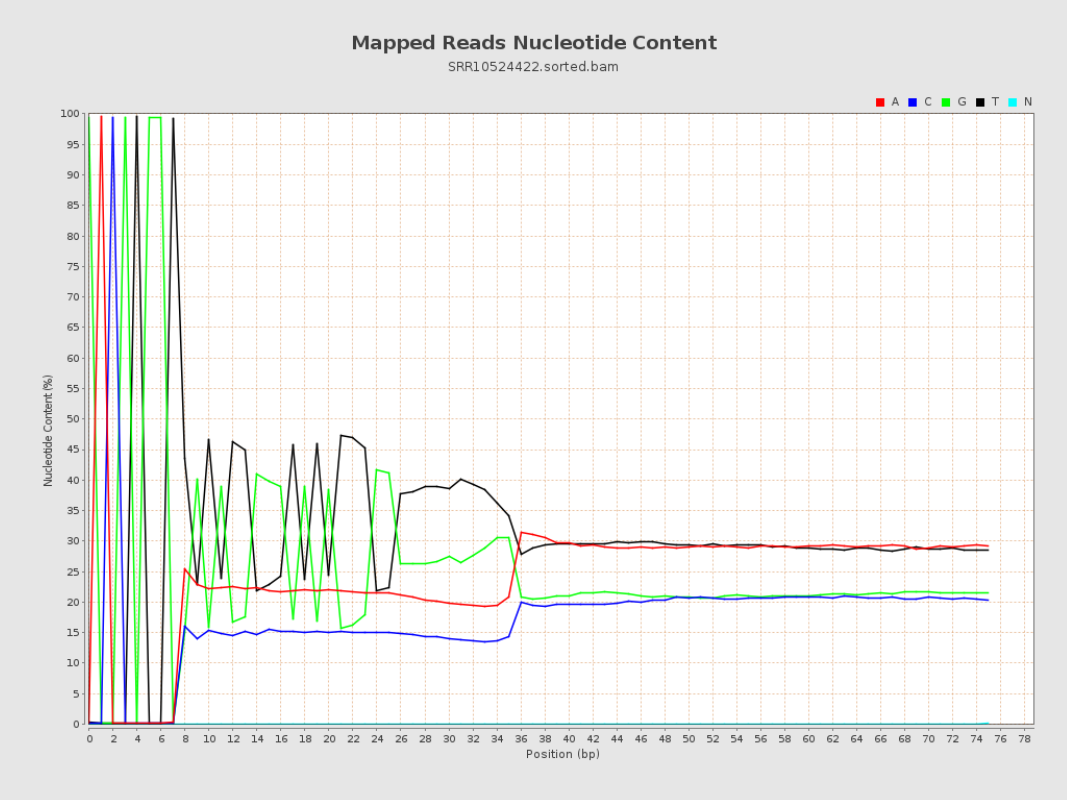
6. Results : Genome Fraction Coverage



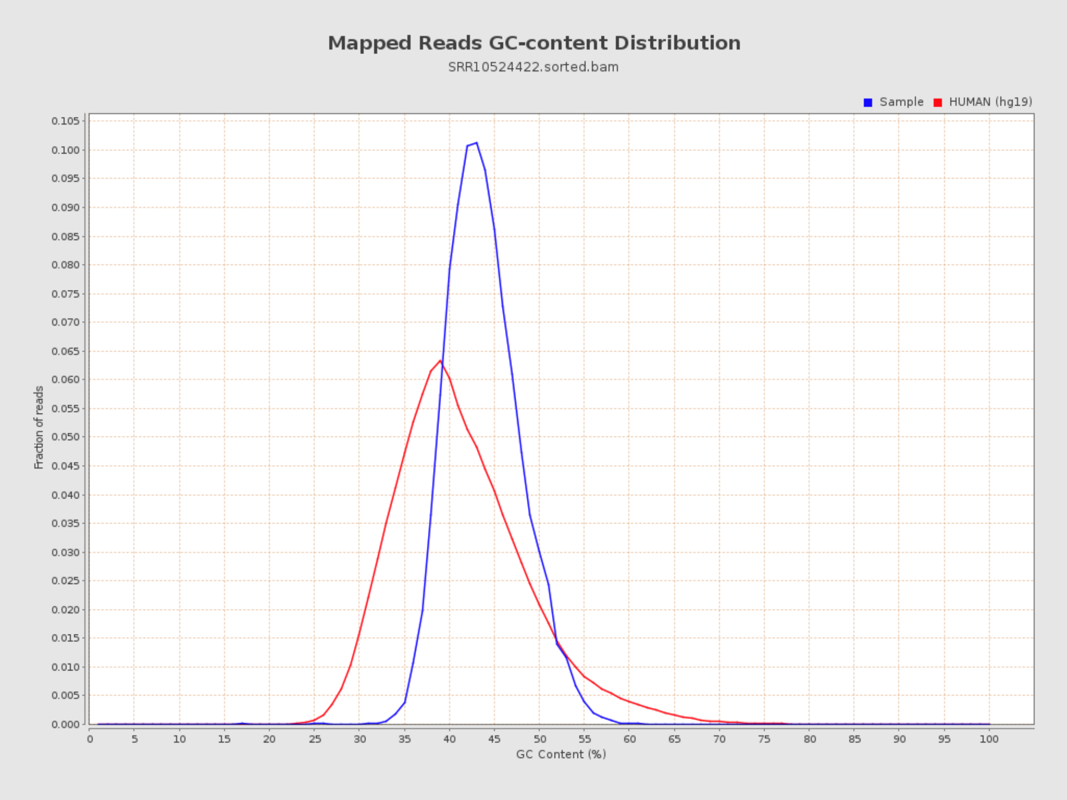
7. Results : Duplication Rate Histogram



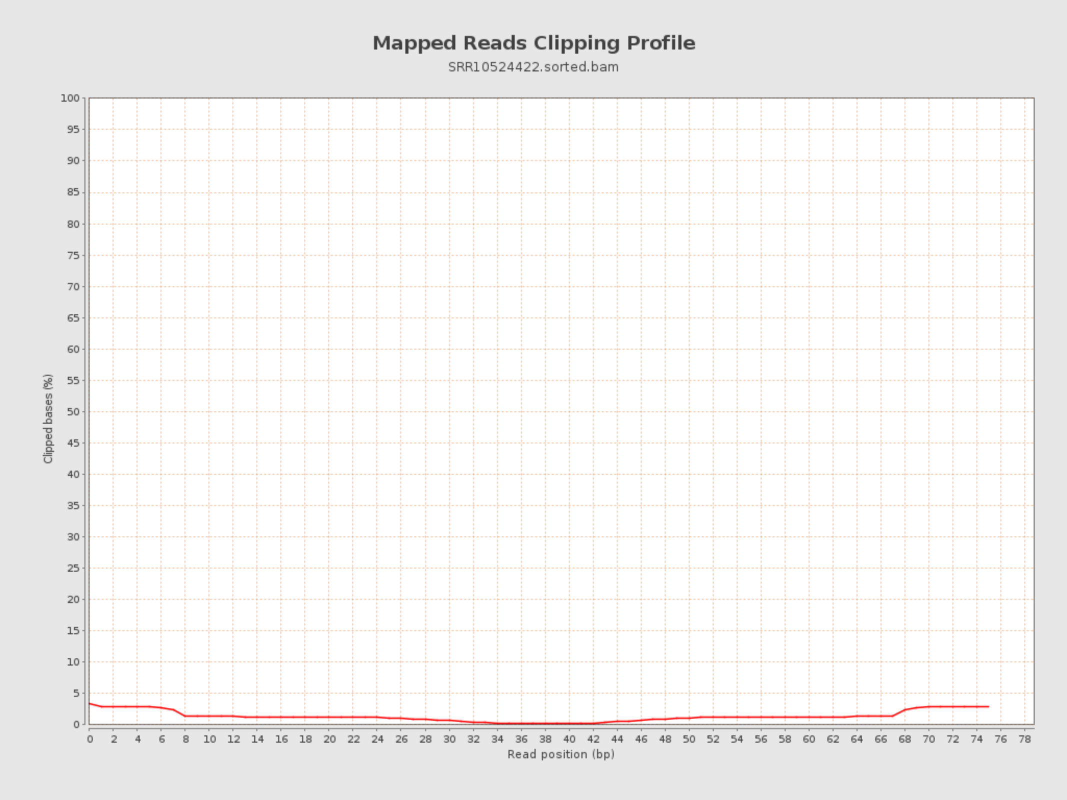
8. Results : Mapped Reads Nucleotide Content



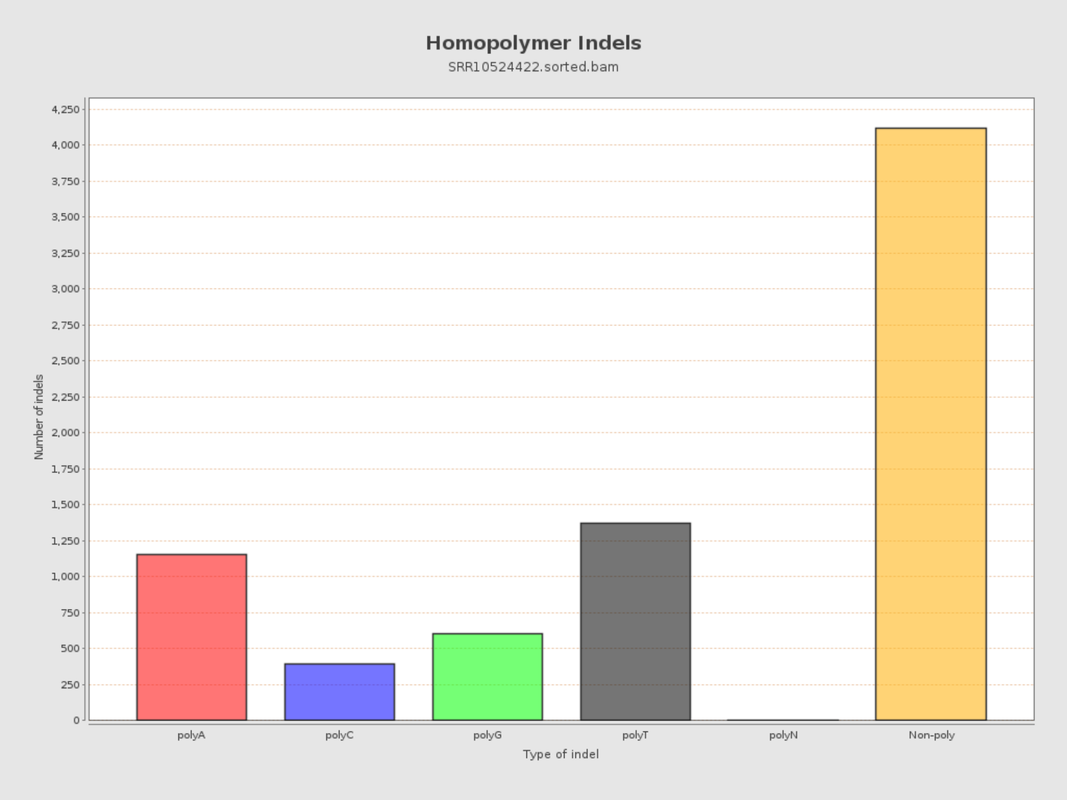
9. Results : Mapped Reads GC-content Distribution



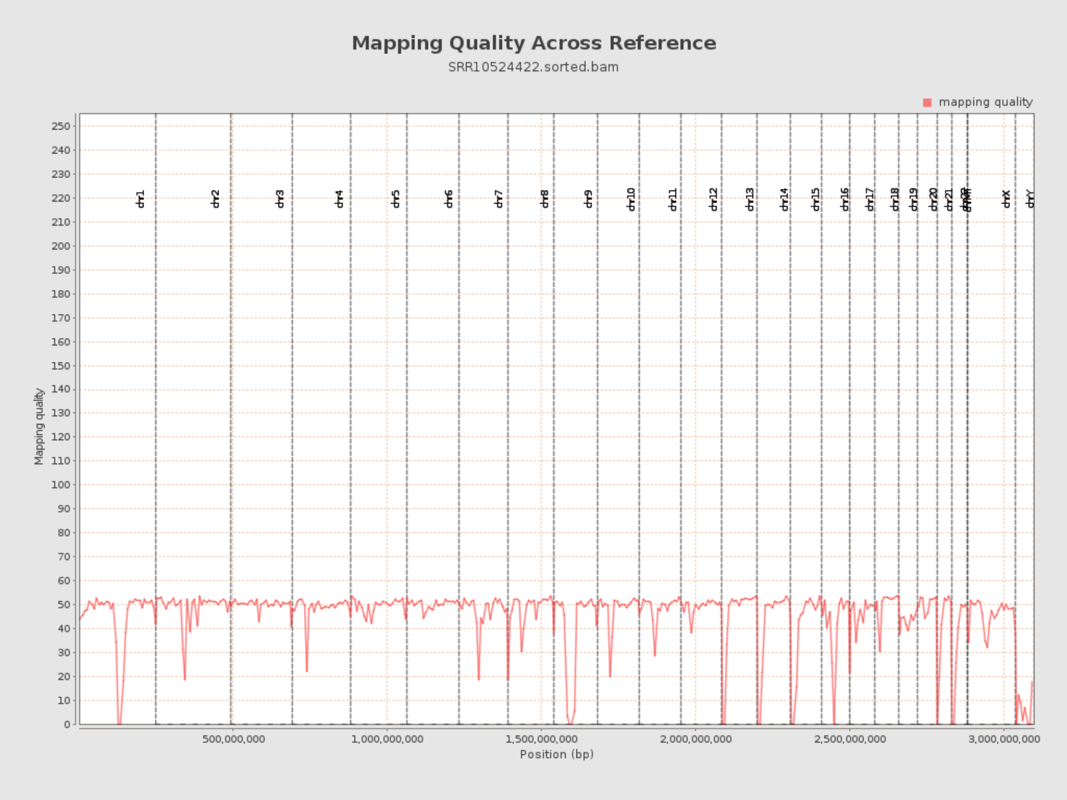
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram