Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 18:23:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524736.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_SRR10524736 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524736.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 18:23:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524736.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	886,683
Mapped reads	763,901 / 86.15%
Unmapped reads	122,782 / 13.85%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,480 / 1.07%
Read min/max/mean length	30 / 76 / 76.36
Duplicated reads (estimated)	16,987 / 1.92%
Duplication rate	1.21%
Clipped reads	770,754 / 86.93%

2.2. ACGT Content

Number/percentage of A's	11,312,143 / 25.94%
Number/percentage of C's	8,109,484 / 18.6%
Number/percentage of T's	13,253,118 / 30.39%
Number/percentage of G's	10,926,974 / 25.06%
Number/percentage of N's	6,081 / 0.01%
GC Percentage	43.65%

2.3. Coverage

Mean	0.0141

Standard Deviation	0.1765

2.4. Mapping Quality

Mean Mapping Quality	39.84

2.5. Mismatches and indels

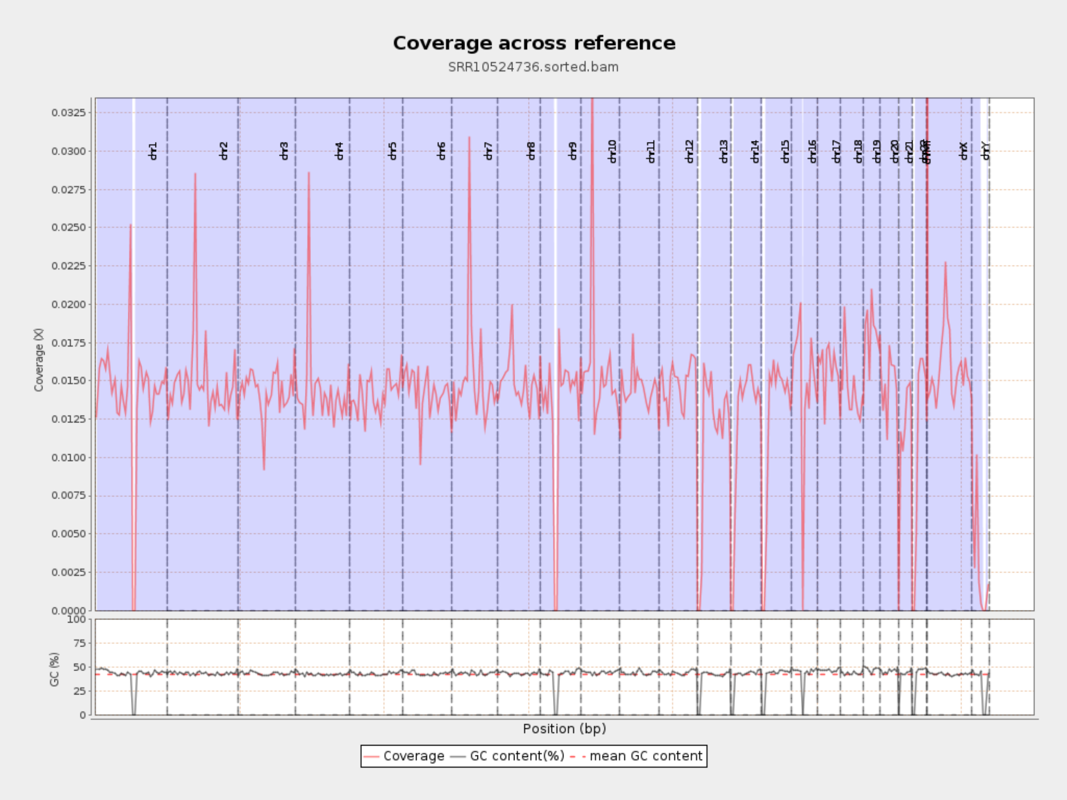
General error rate	0.52%
Mismatches	220,137
Insertions	4,170
Mapped reads with at least one insertion	0.54%
Deletions	7,238
Mapped reads with at least one deletion	0.94%
Homopolymer indels	37.68%

2.6. Chromosome stats

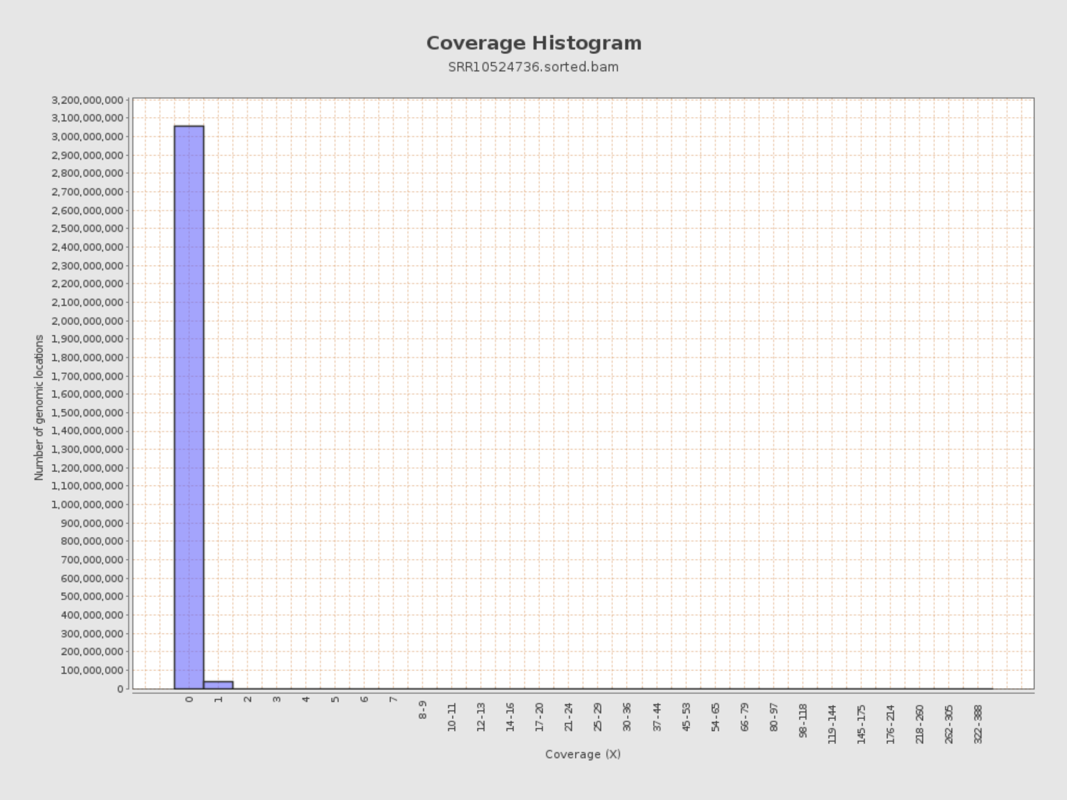
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3507986	0.0141	0.2887
chr2	243199373	3625370	0.0149	0.232
chr3	198022430	2821813	0.0142	0.1257
chr4	191154276	2763099	0.0145	0.1401
chr5	180915260	2567182	0.0142	0.1242
chr6	171115067	2431130	0.0142	0.1313
chr7	159138663	2429946	0.0153	0.242

chr8	146364022	2177635	0.0149	0.1691
chr9	141213431	1852559	0.0131	0.1576
chr10	135534747	2154982	0.0159	0.2034
chr11	135006516	1967128	0.0146	0.1545
chr12	133851895	1987233	0.0148	0.1285
chr13	115169878	1296976	0.0113	0.1109
chr14	107349540	1308094	0.0122	0.1203
chr15	102531392	1246236	0.0122	0.1169
chr16	90354753	1318213	0.0146	0.1354
chr17	81195210	1279624	0.0158	0.1365
chr18	78077248	1125656	0.0144	0.2572
chr19	59128983	1070833	0.0181	0.223
chr20	63025520	916206	0.0145	0.1291
chr21	48129895	555914	0.0116	0.1223
chr22	51304566	556889	0.0109	0.1086
chrMT	16571	23221	1.4013	1.4121
chrX	155270560	2469108	0.0159	0.1456
chrY	59373566	166834	0.0028	0.0867

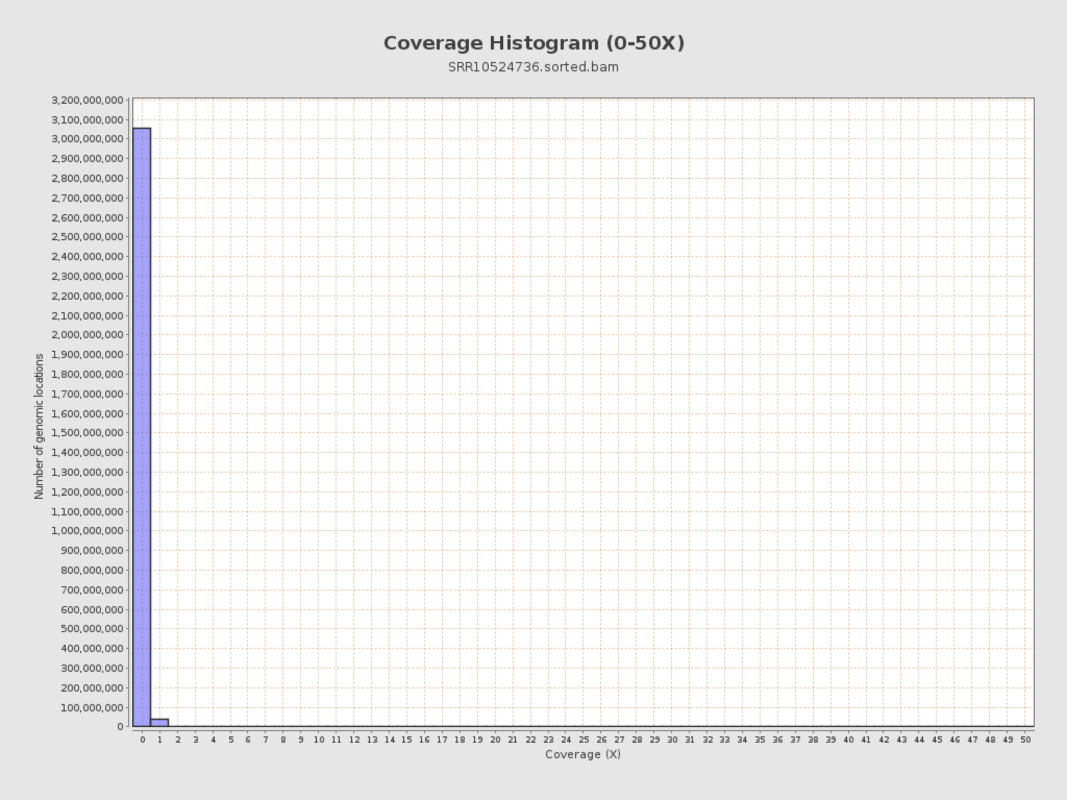
3. Results : Coverage across reference



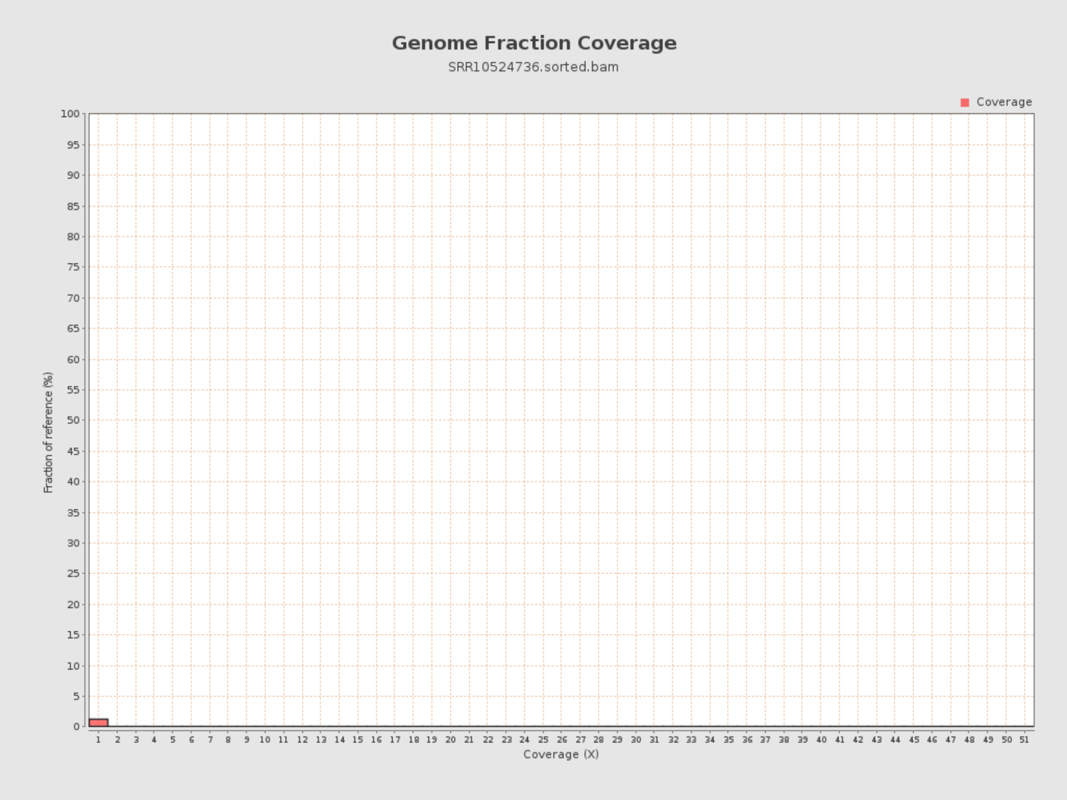
4. Results : Coverage Histogram



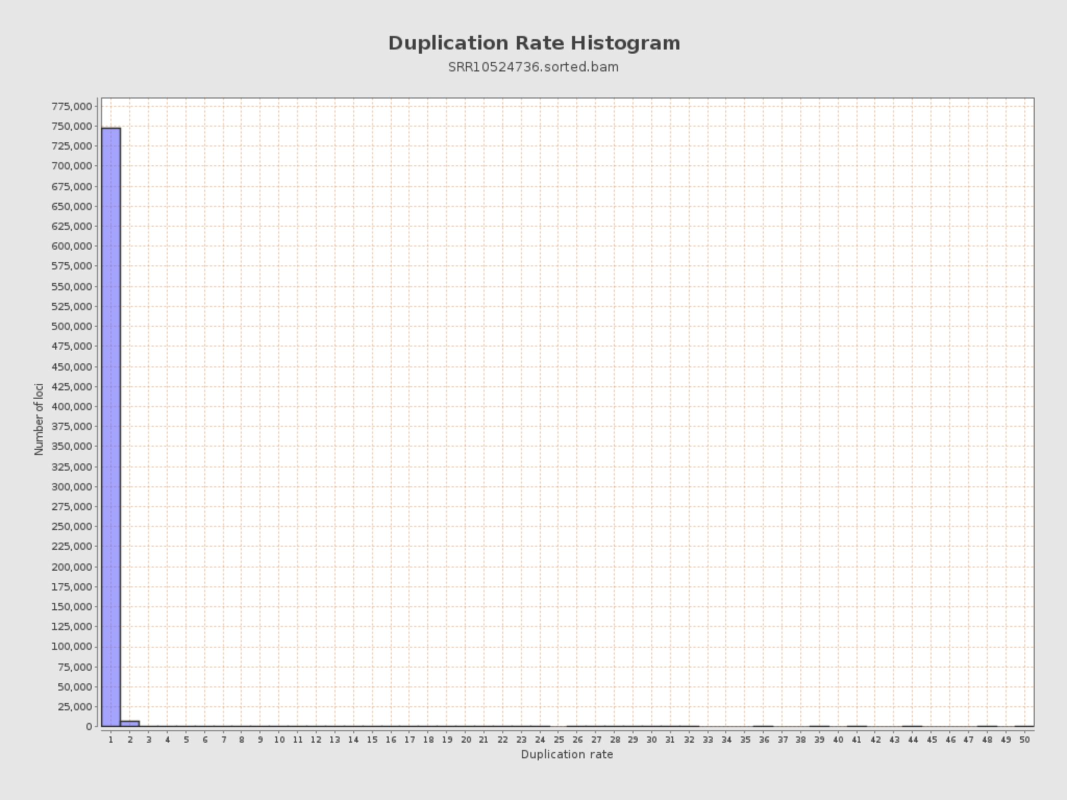
5. Results : Coverage Histogram (0-50X)



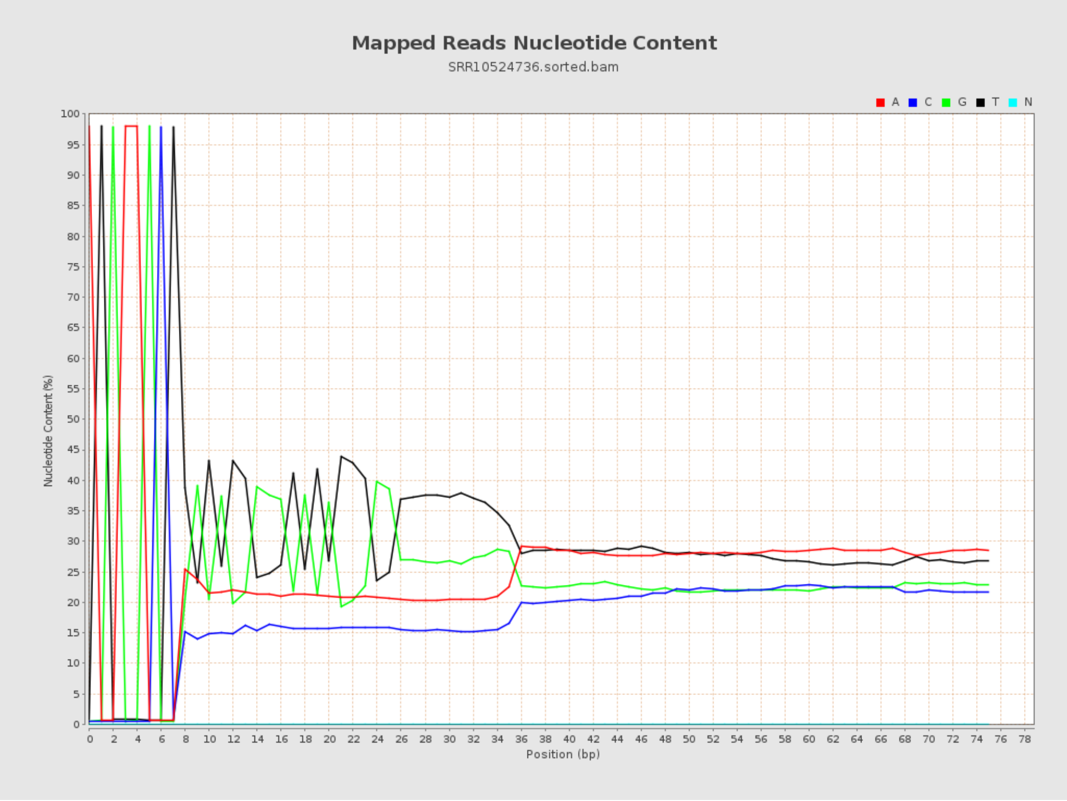
6. Results : Genome Fraction Coverage



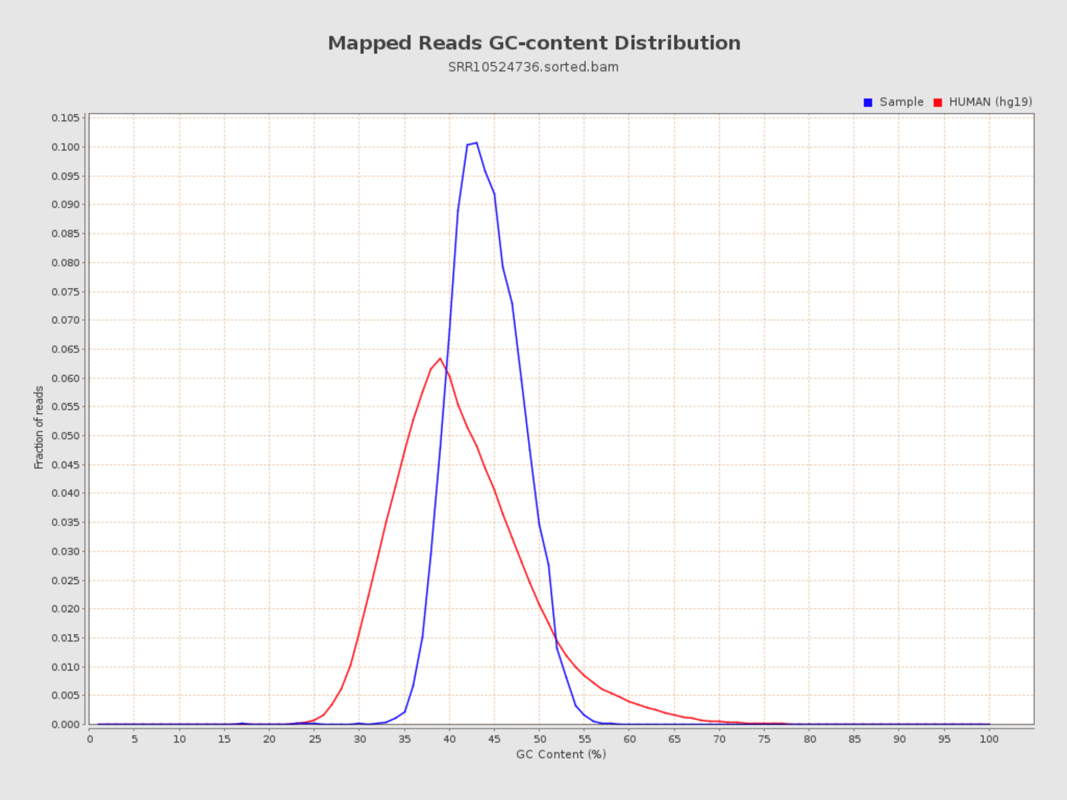
7. Results : Duplication Rate Histogram



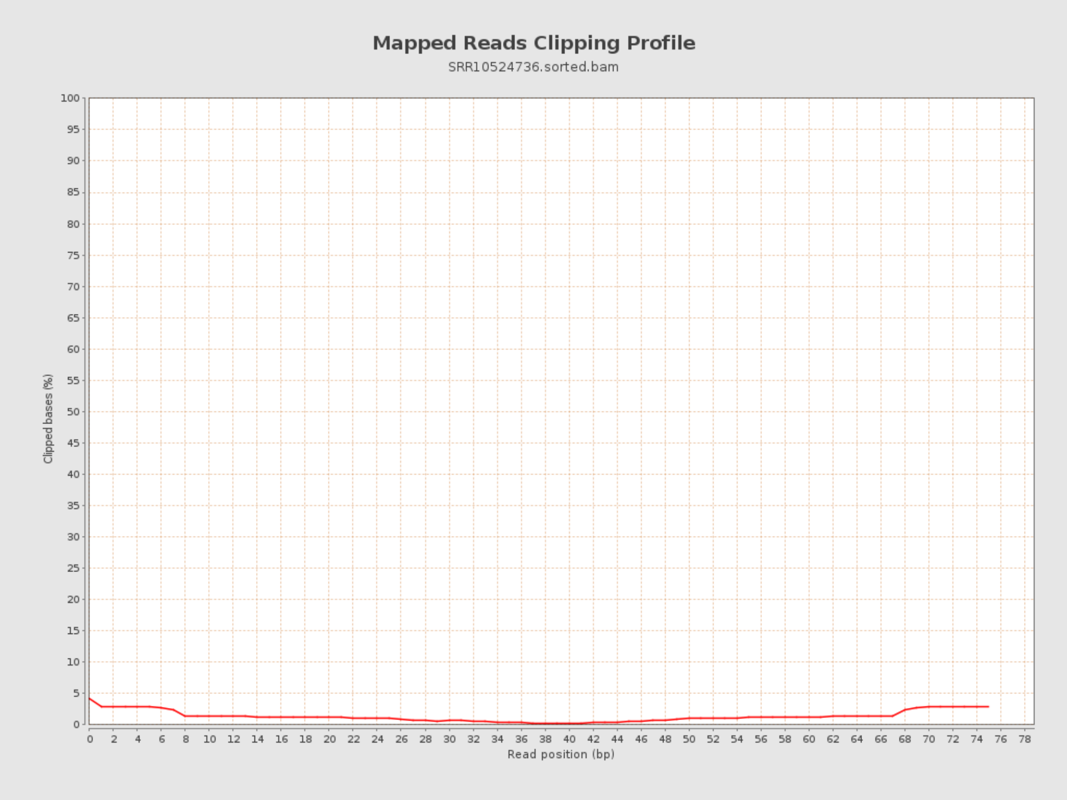
8. Results : Mapped Reads Nucleotide Content



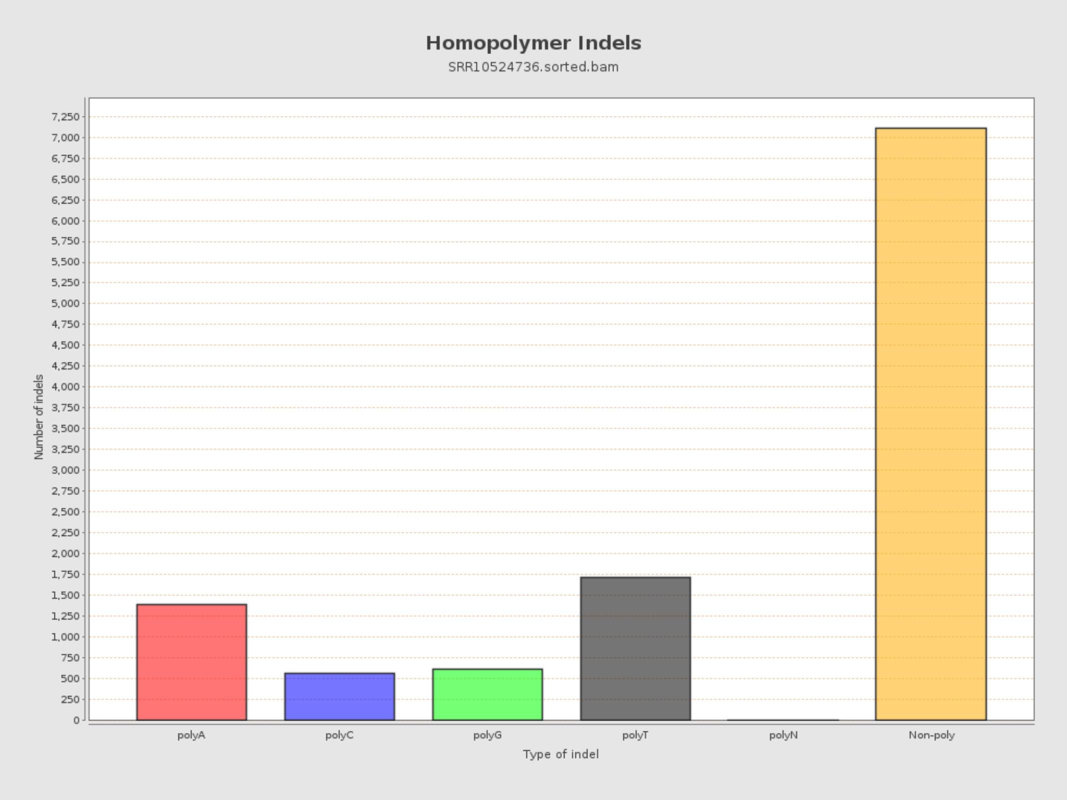
9. Results : Mapped Reads GC-content Distribution



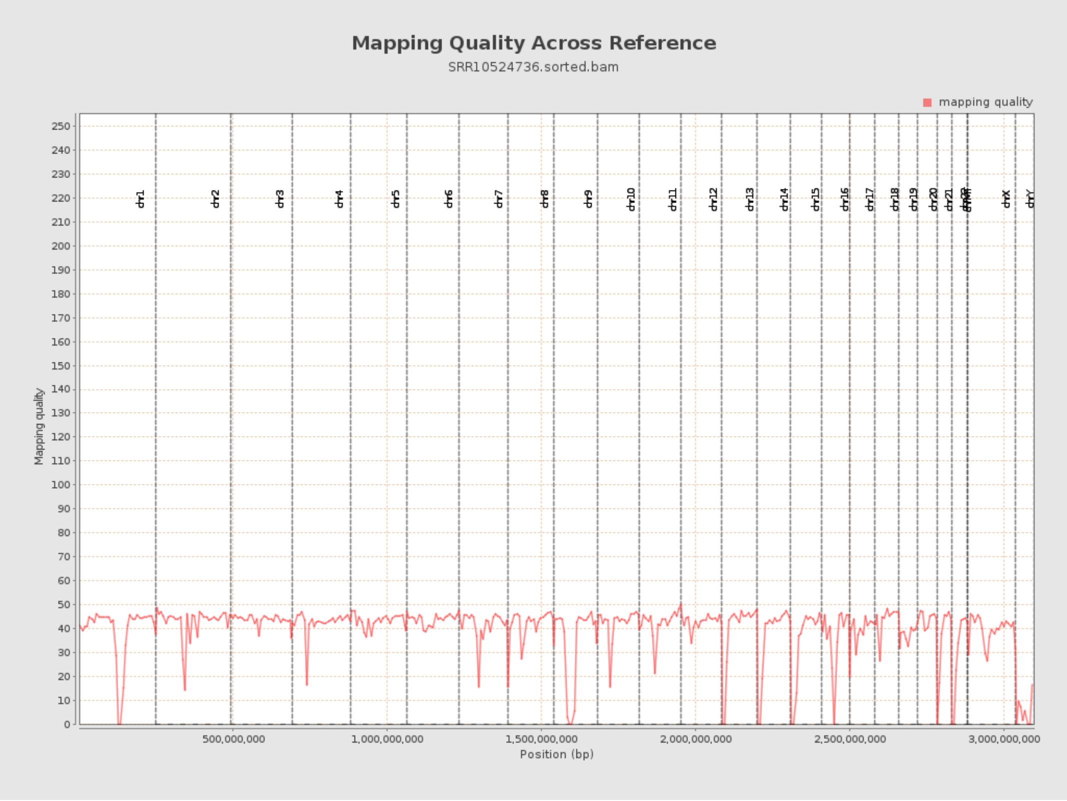
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram