Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 09:39:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524534.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_SRR10524534 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524534.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 09:39:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524534.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,710,685
Mapped reads	1,568,161 / 91.67%
Unmapped reads	142,524 / 8.33%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,099 / 0.36%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	74,804 / 4.37%
Duplication rate	3.65%
Clipped reads	1,568,727 / 91.7%

2.2. ACGT Content

Number/percentage of A's	23,232,587 / 25.4%
Number/percentage of C's	17,993,591 / 19.68%
Number/percentage of T's	28,508,263 / 31.17%
Number/percentage of G's	21,718,201 / 23.75%
Number/percentage of N's	1,271 / 0%
GC Percentage	43.42%

2.3. Coverage

Mean	0.0296

Standard Deviation	0.2765

2.4. Mapping Quality

Mean Mapping Quality	45.1

2.5. Mismatches and indels

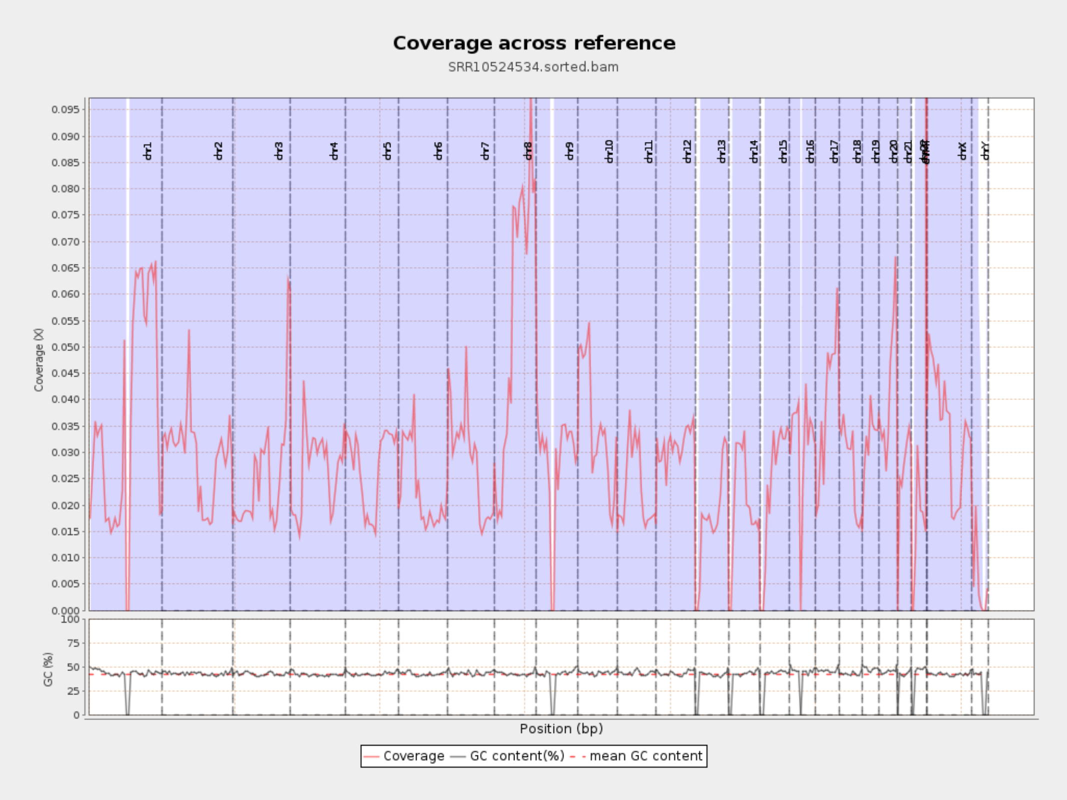
General error rate	0.53%
Mismatches	468,415
Insertions	7,297
Mapped reads with at least one insertion	0.46%
Deletions	17,420
Mapped reads with at least one deletion	1.1%
Homopolymer indels	41.57%

2.6. Chromosome stats

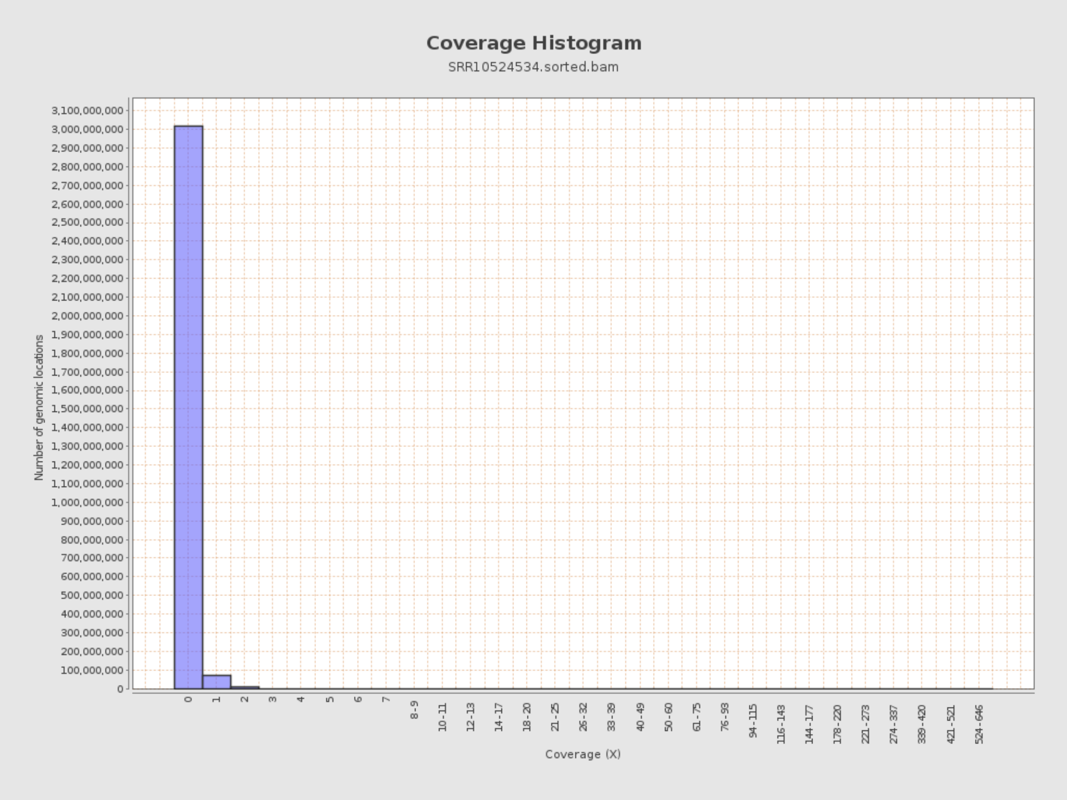
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9087871	0.0365	0.4967
chr2	243199373	7183776	0.0295	0.3238
chr3	198022430	4975501	0.0251	0.176
chr4	191154276	5085557	0.0266	0.2164
chr5	180915260	4959352	0.0274	0.1852
chr6	171115067	3920917	0.0229	0.2082
chr7	159138663	4539633	0.0285	0.3434

chr8	146364022	8331251	0.0569	0.3157
chr9	141213431	3919111	0.0278	0.234
chr10	135534747	4802161	0.0354	0.2807
chr11	135006516	3146494	0.0233	0.2583
chr12	133851895	4213339	0.0315	0.198
chr13	115169878	2026738	0.0176	0.1481
chr14	107349540	2169483	0.0202	0.1616
chr15	102531392	2464029	0.024	0.1759
chr16	90354753	2885148	0.0319	0.2117
chr17	81195210	3254433	0.0401	0.2343
chr18	78077248	2147821	0.0275	0.4168
chr19	59128983	1930547	0.0326	0.363
chr20	63025520	2666444	0.0423	0.2314
chr21	48129895	1262355	0.0262	0.2055
chr22	51304566	767349	0.015	0.1353
chrMT	16571	24592	1.484	1.5187
chrX	155270560	5398092	0.0348	0.2271
chrY	59373566	320709	0.0054	0.1799

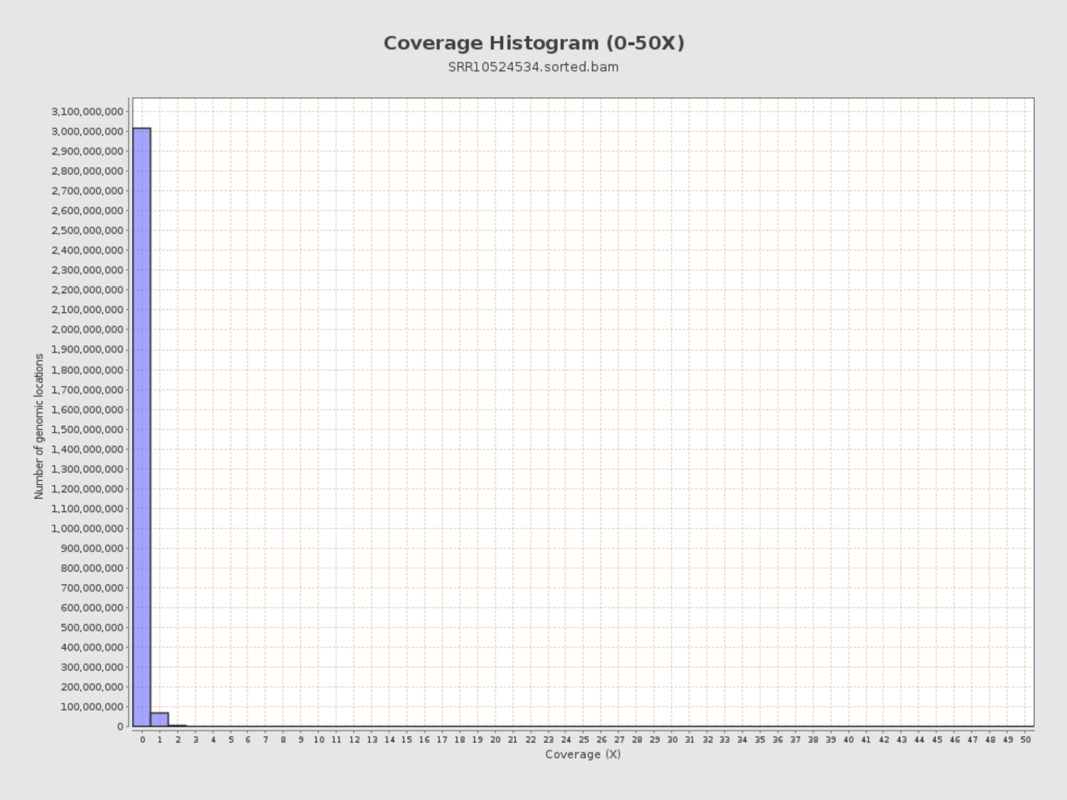
3. Results : Coverage across reference



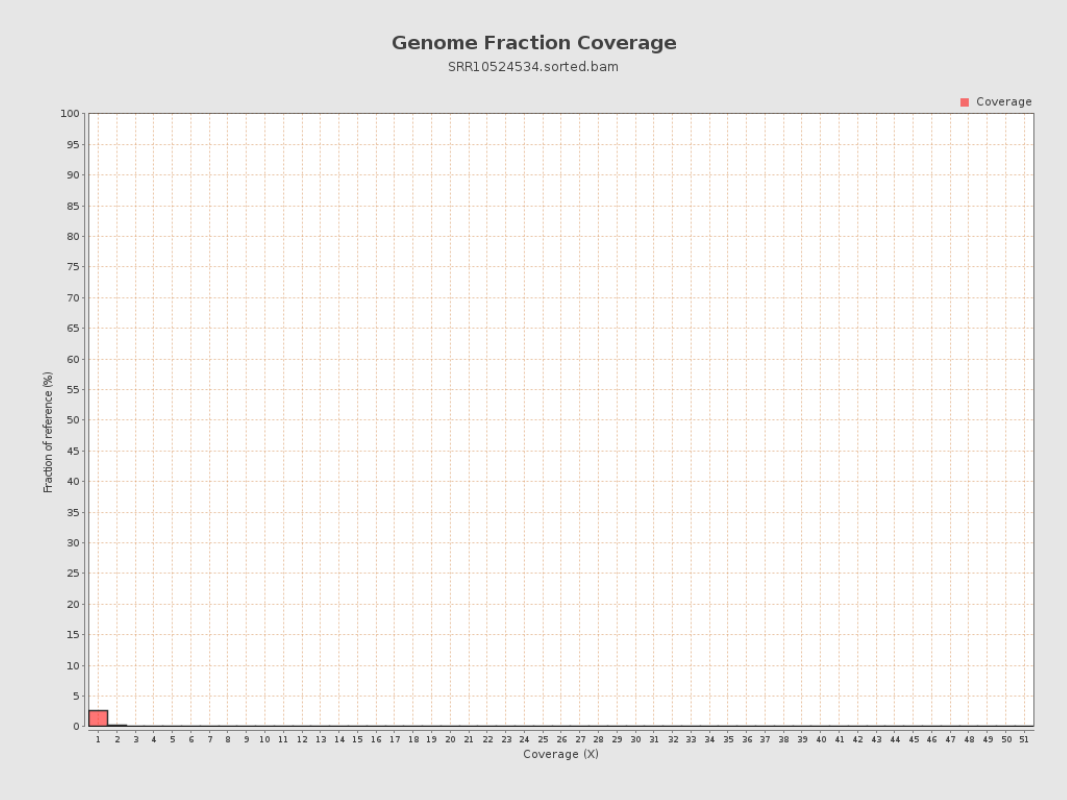
4. Results : Coverage Histogram



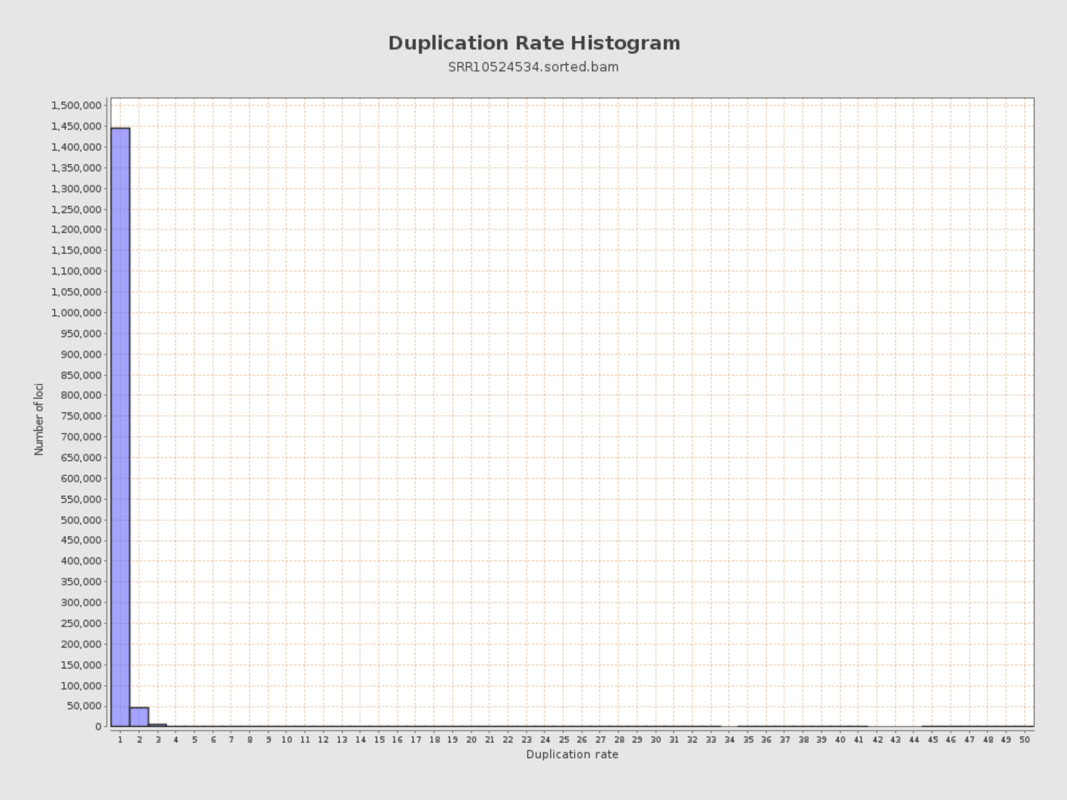
5. Results : Coverage Histogram (0-50X)



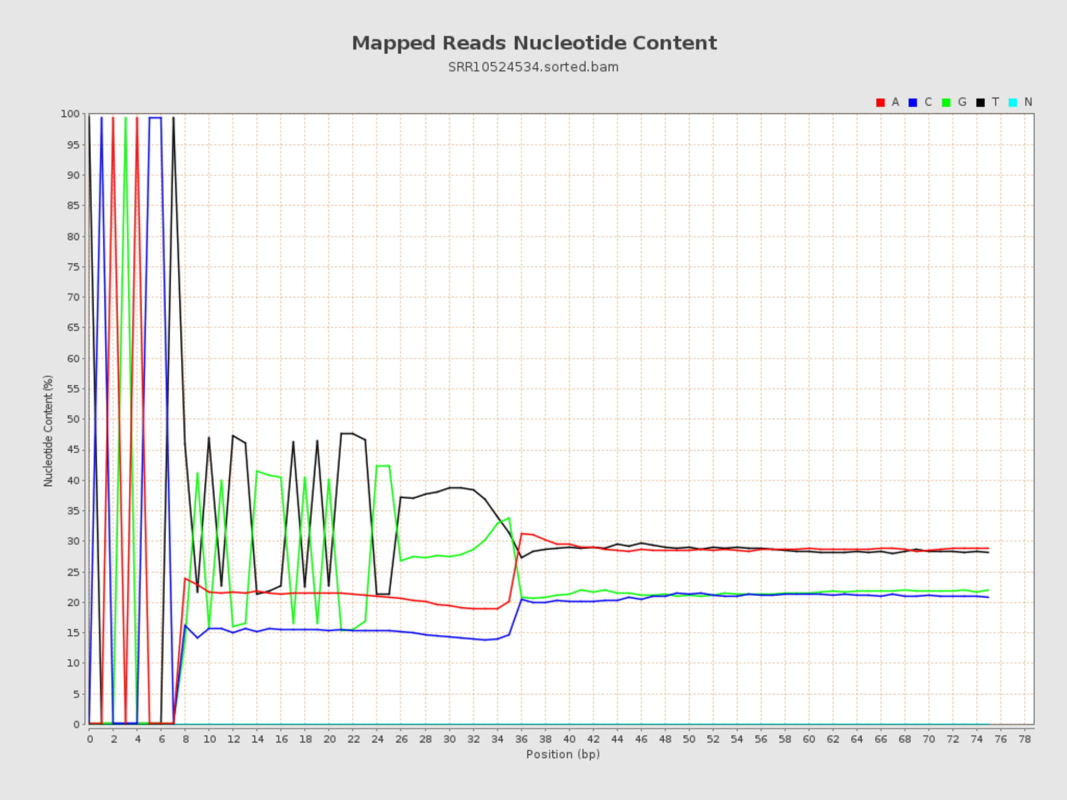
6. Results : Genome Fraction Coverage



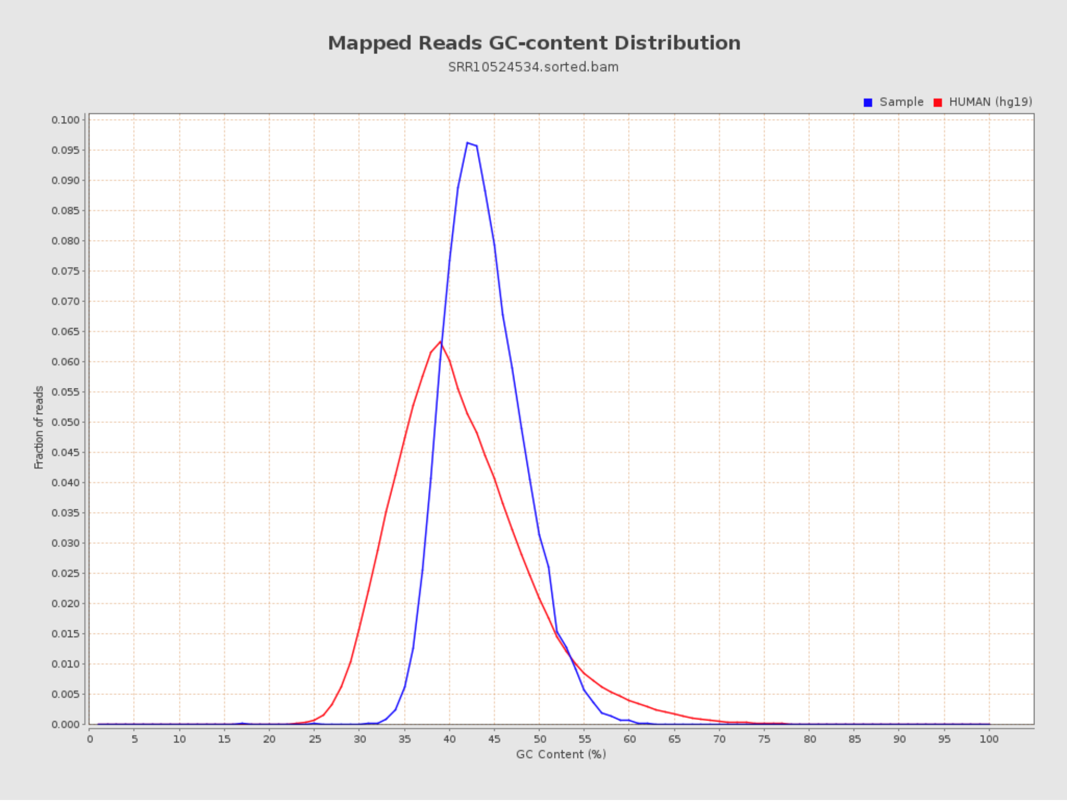
7. Results : Duplication Rate Histogram



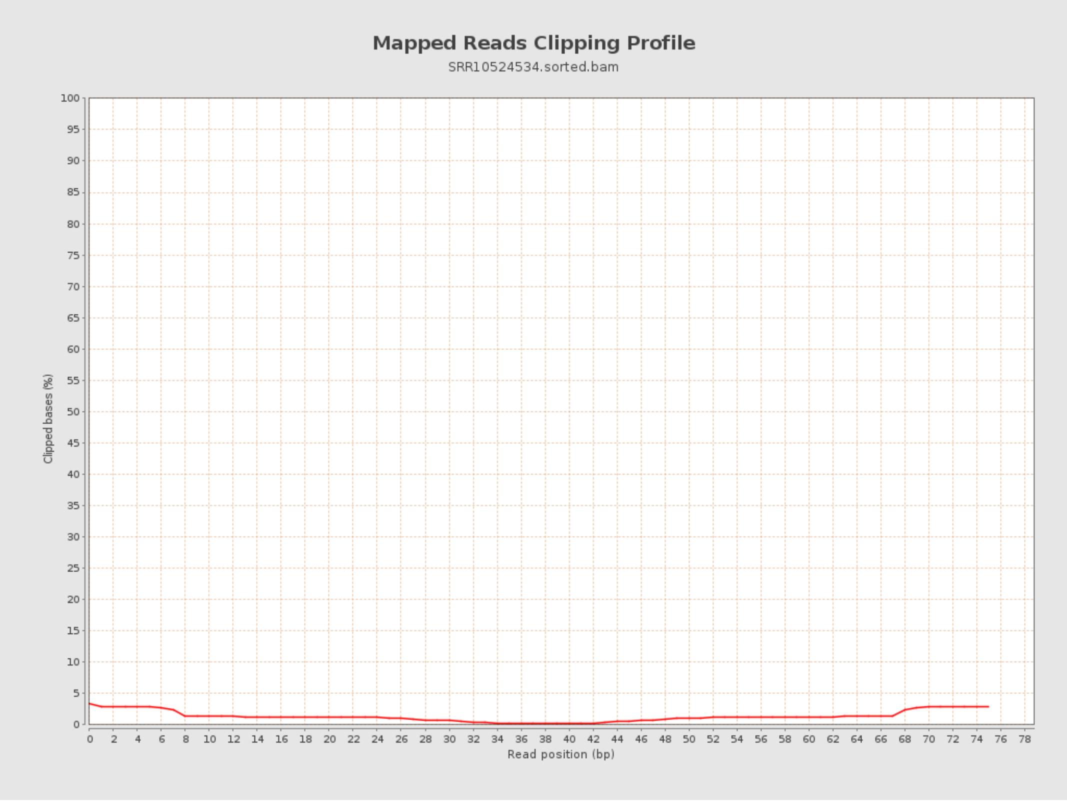
8. Results : Mapped Reads Nucleotide Content



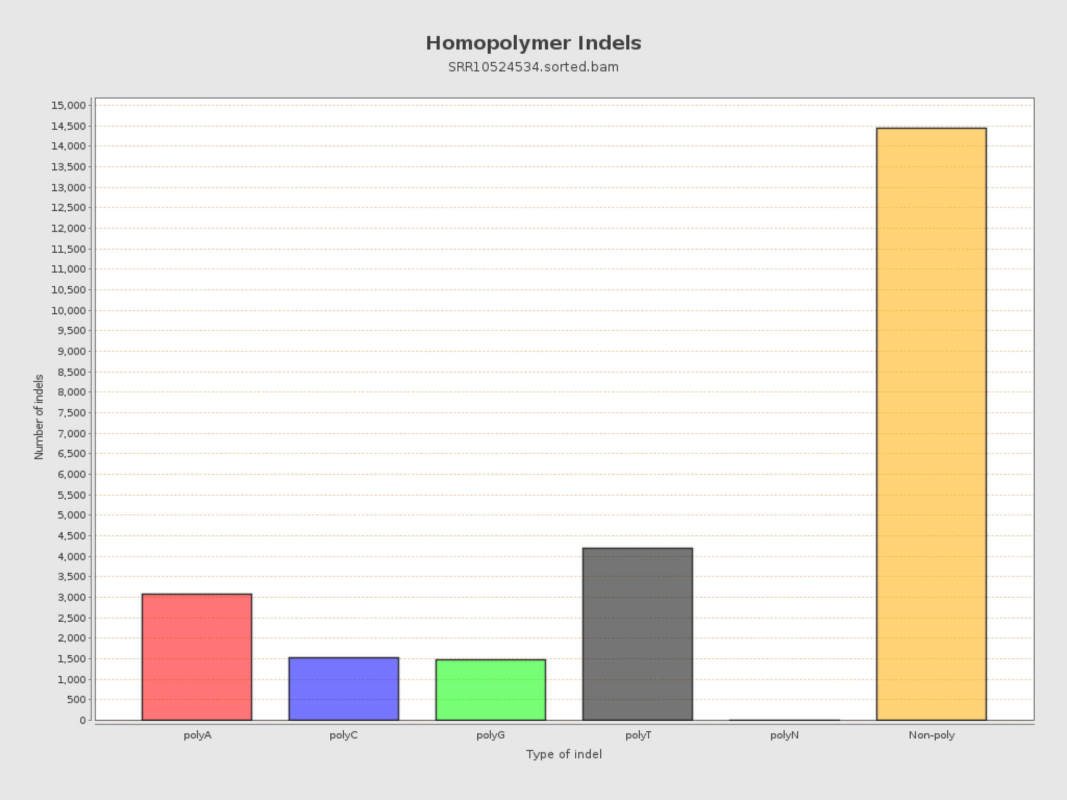
9. Results : Mapped Reads GC-content Distribution



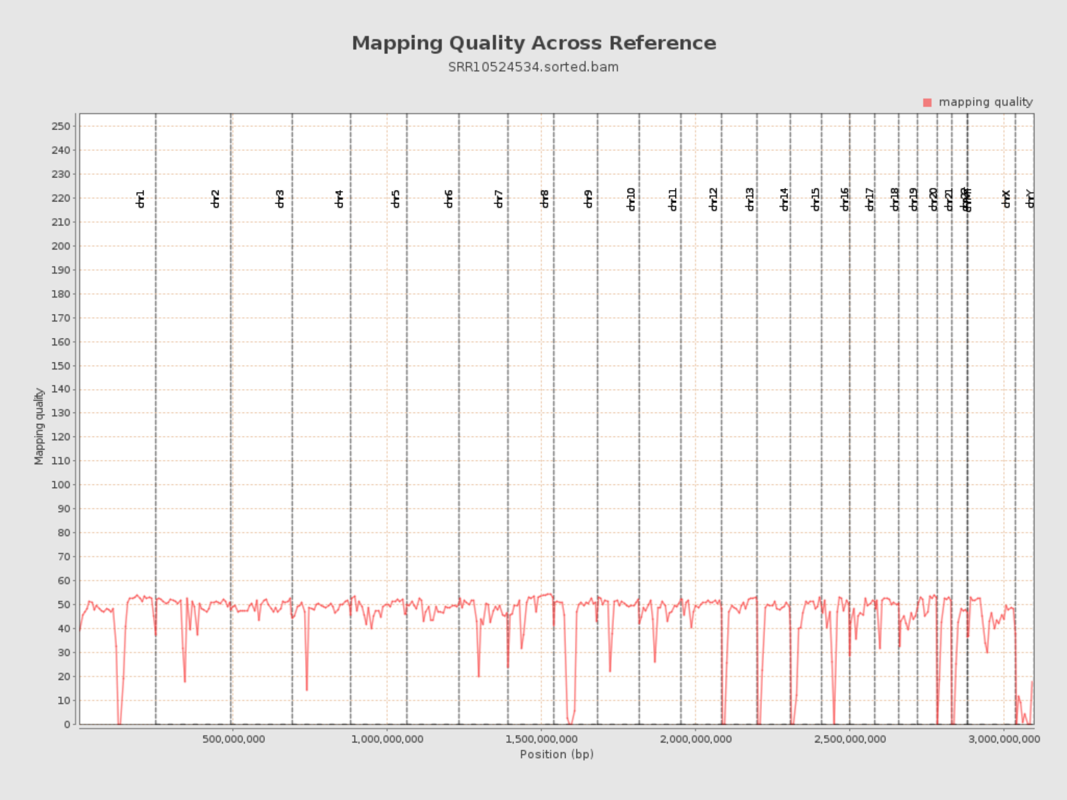
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram