Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 04:08:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524434.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_SRR10524434 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524434.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 04:08:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524434.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	516,740
Mapped reads	474,171 / 91.76%
Unmapped reads	42,569 / 8.24%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,105 / 0.41%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	10,400 / 2.01%
Duplication rate	1.7%
Clipped reads	474,918 / 91.91%

2.2. ACGT Content

Number/percentage of A's	6,725,676 / 24.23%
Number/percentage of C's	5,113,790 / 18.42%
Number/percentage of T's	9,040,856 / 32.57%
Number/percentage of G's	6,878,016 / 24.78%
Number/percentage of N's	2,966 / 0.01%
GC Percentage	43.2%

2.3. Coverage

Mean	0.009

Standard Deviation	0.1198

2.4. Mapping Quality

Mean Mapping Quality	44.62

2.5. Mismatches and indels

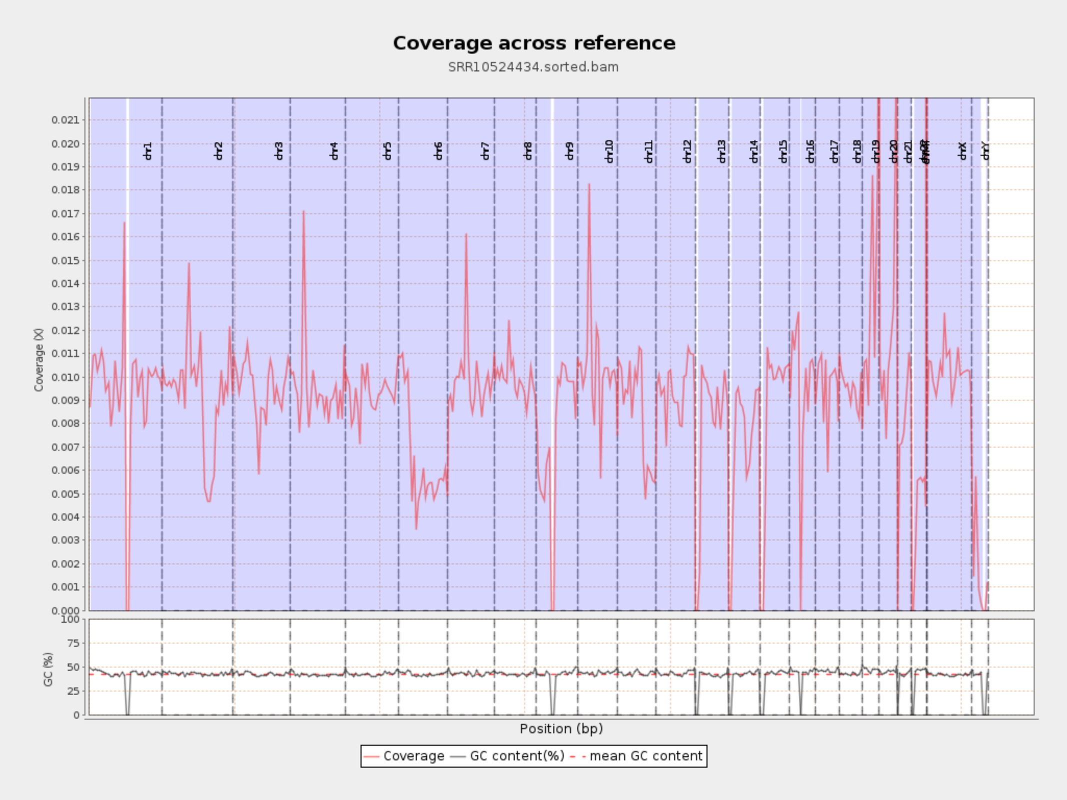
General error rate	0.52%
Mismatches	139,718
Insertions	2,215
Mapped reads with at least one insertion	0.47%
Deletions	4,901
Mapped reads with at least one deletion	1.03%
Homopolymer indels	41.64%

2.6. Chromosome stats

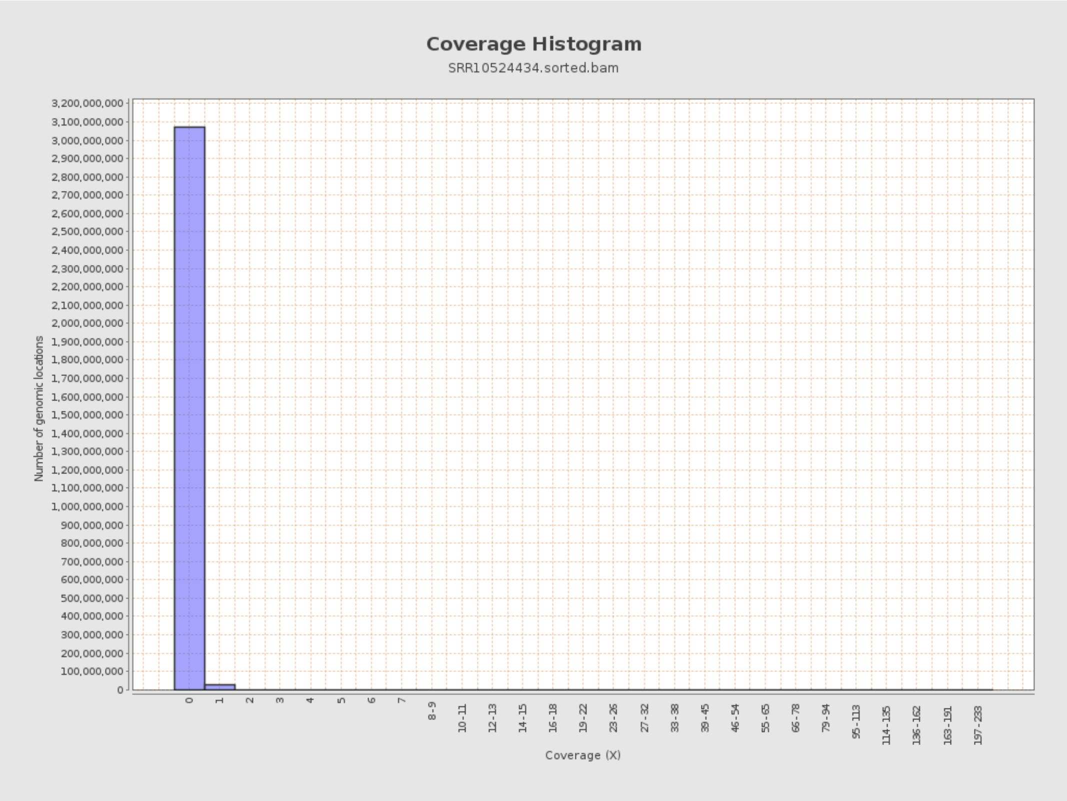
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2341038	0.0094	0.1965
chr2	243199373	2264437	0.0093	0.1423
chr3	198022430	1891166	0.0096	0.1016
chr4	191154276	1812355	0.0095	0.1093
chr5	180915260	1675225	0.0093	0.0997
chr6	171115067	1115070	0.0065	0.0857
chr7	159138663	1575603	0.0099	0.1428

chr8	146364022	1453390	0.0099	0.1104
chr9	141213431	1026906	0.0073	0.0945
chr10	135534747	1410806	0.0104	0.1278
chr11	135006516	1142408	0.0085	0.1029
chr12	133851895	1275762	0.0095	0.1022
chr13	115169878	885367	0.0077	0.0911
chr14	107349540	751853	0.007	0.0881
chr15	102531392	865379	0.0084	0.0958
chr16	90354753	868492	0.0096	0.1034
chr17	81195210	773024	0.0095	0.1031
chr18	78077248	742547	0.0095	0.1301
chr19	59128983	816787	0.0138	0.1584
chr20	63025520	774027	0.0123	0.1165
chr21	48129895	376750	0.0078	0.097
chr22	51304566	202014	0.0039	0.0655
chrMT	16571	43604	2.6313	2.3314
chrX	155270560	1589555	0.0102	0.1077
chrY	59373566	95784	0.0016	0.0626

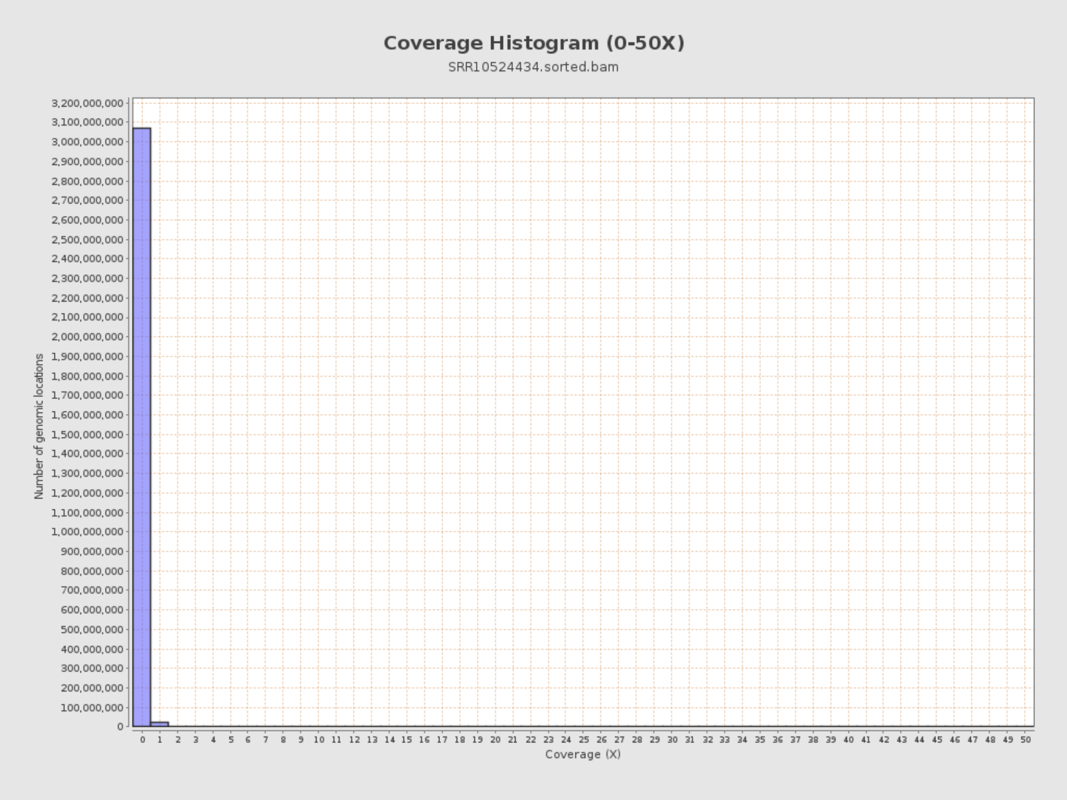
3. Results : Coverage across reference



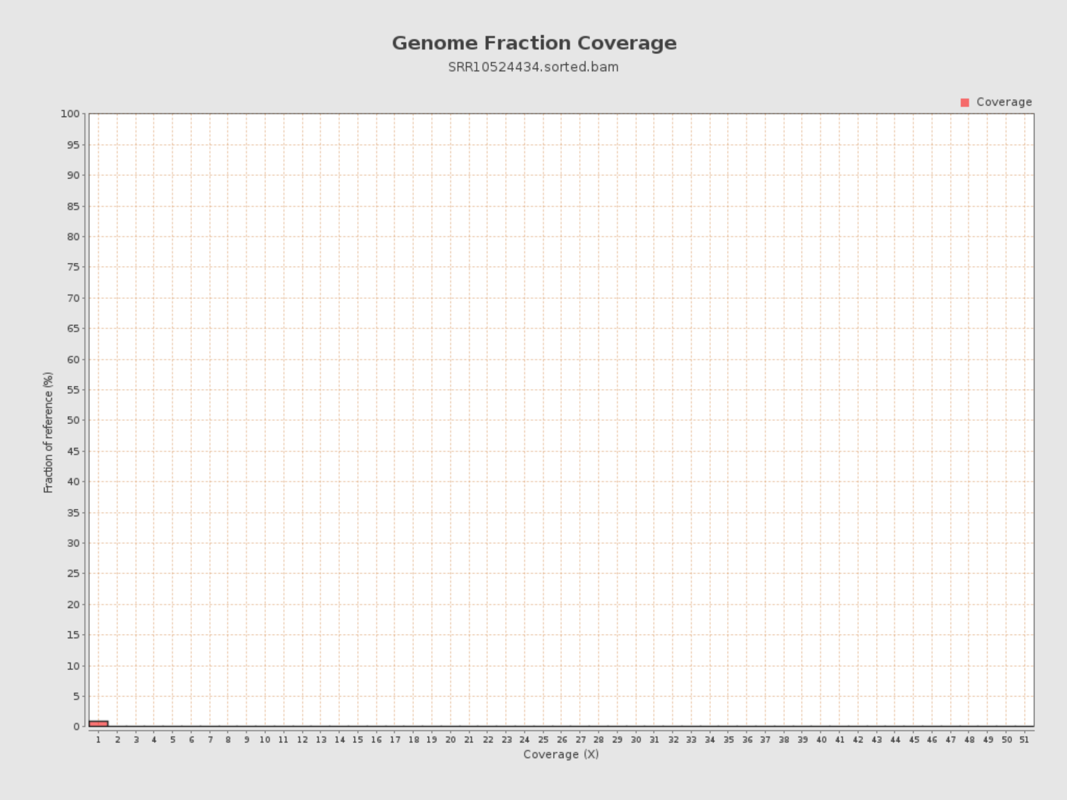
4. Results : Coverage Histogram



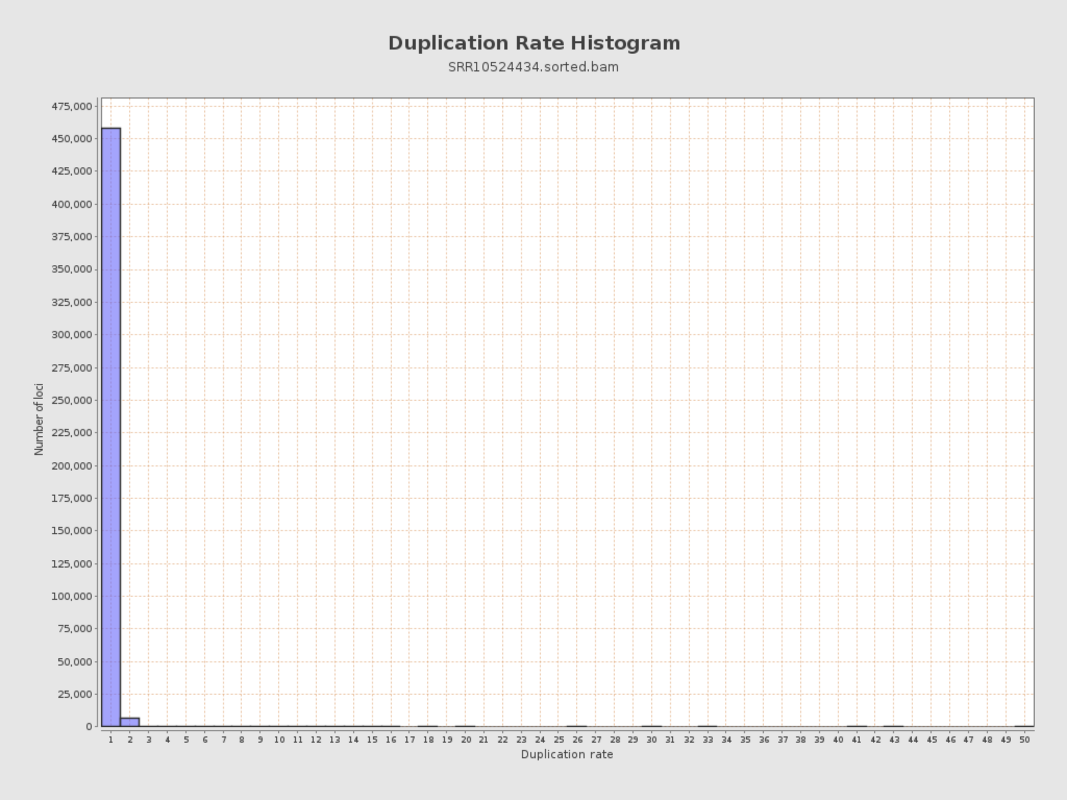
5. Results : Coverage Histogram (0-50X)



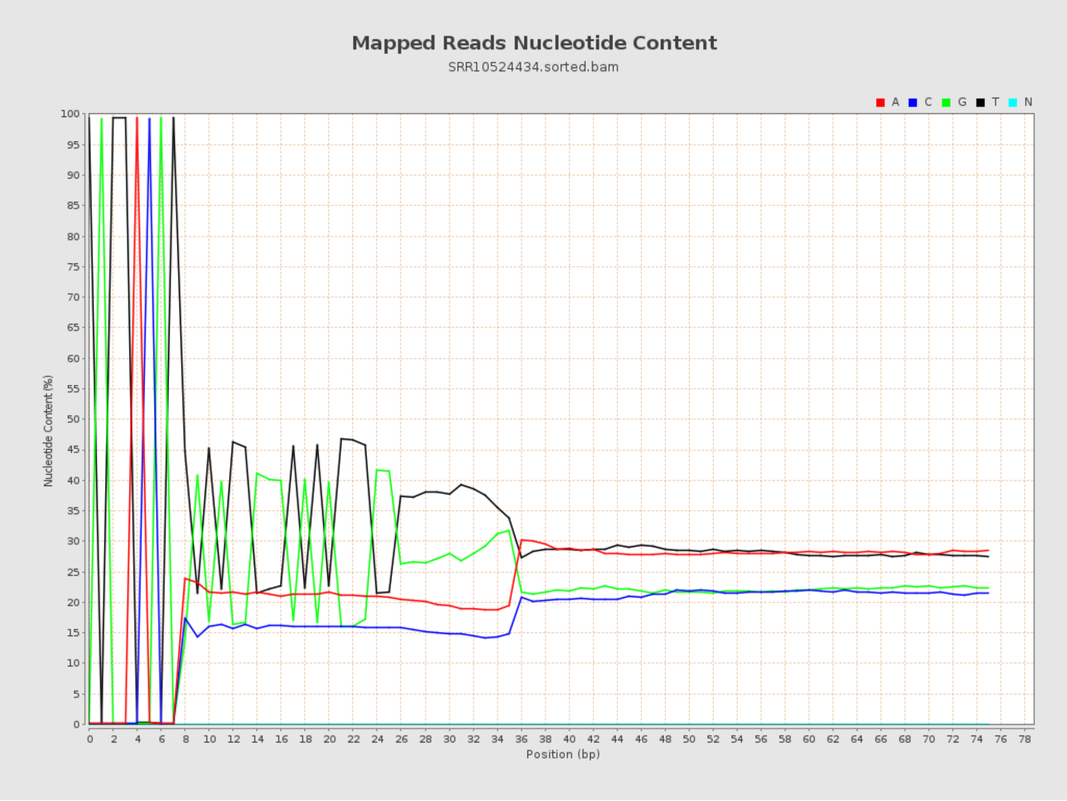
6. Results : Genome Fraction Coverage



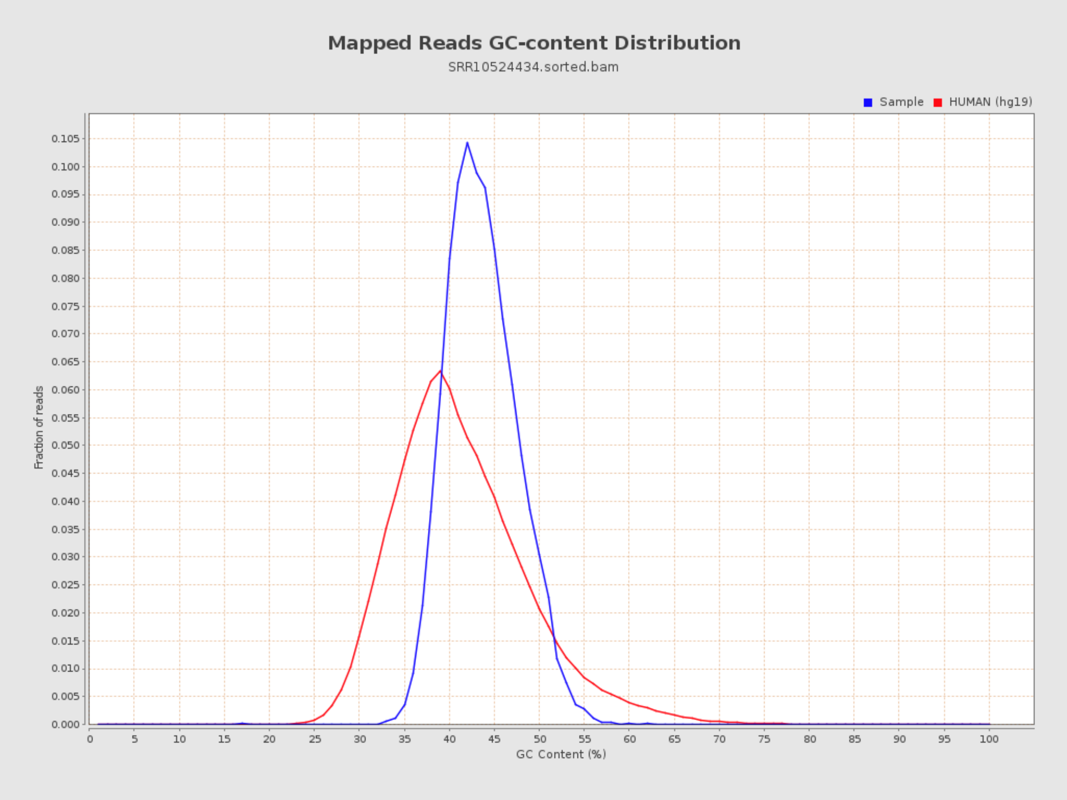
7. Results : Duplication Rate Histogram



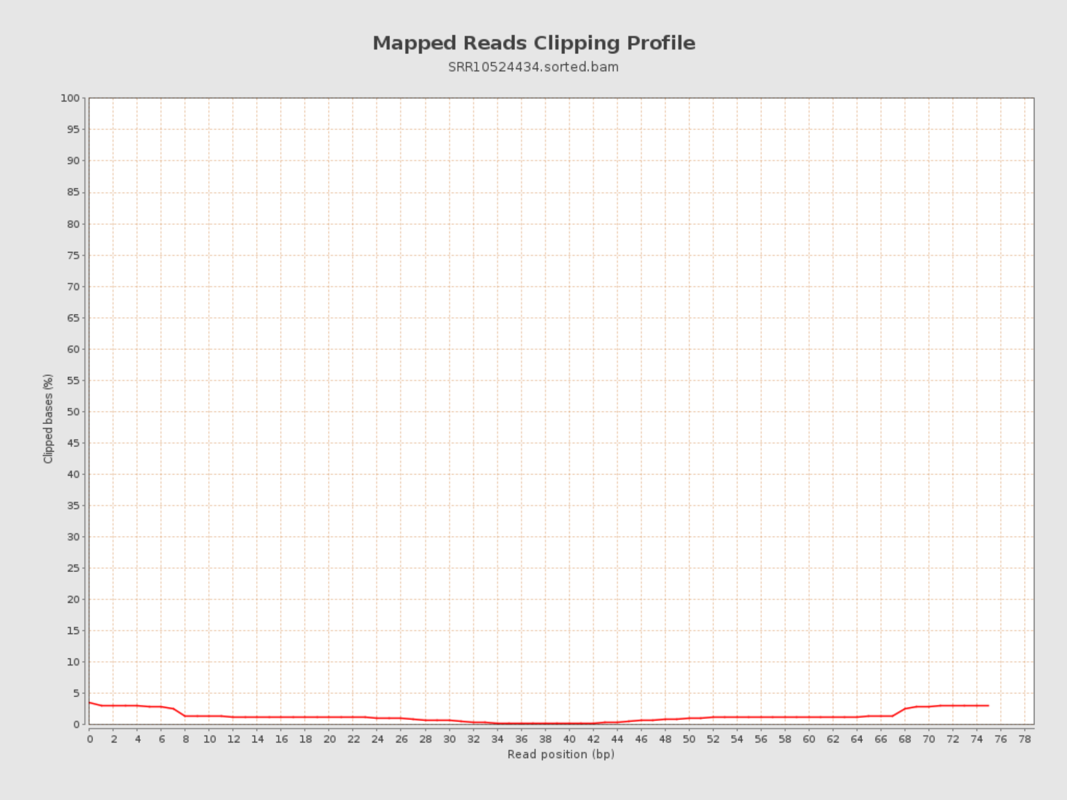
8. Results : Mapped Reads Nucleotide Content



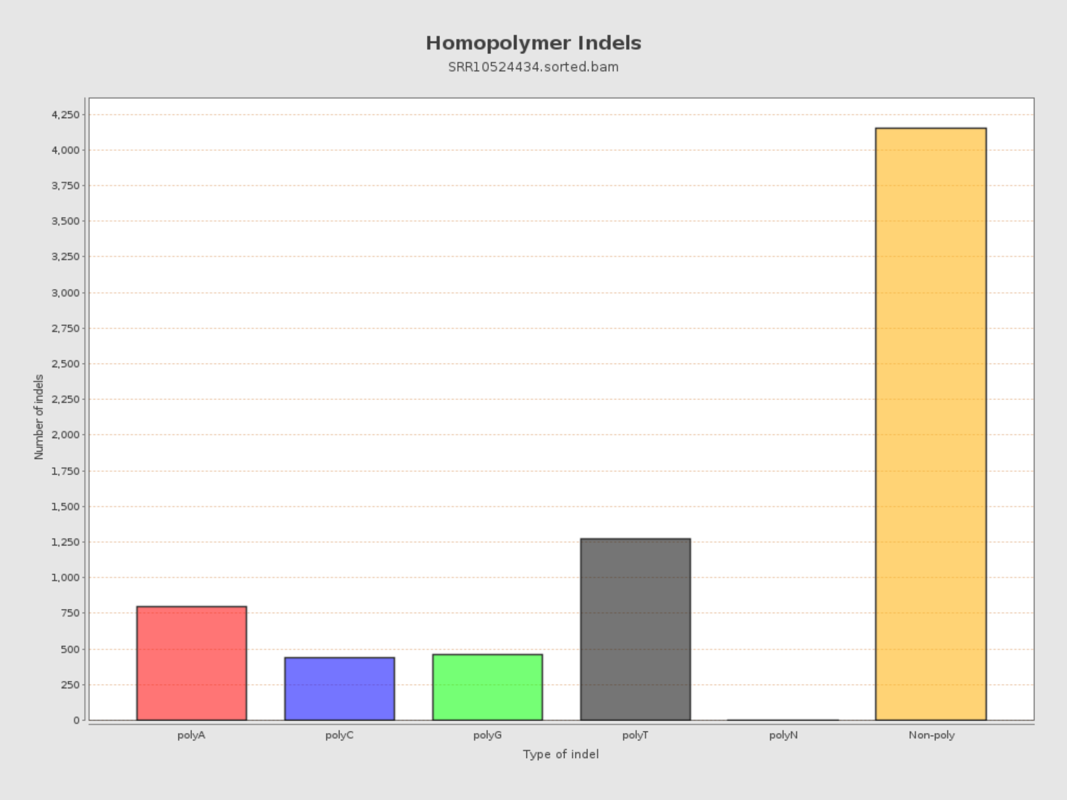
9. Results : Mapped Reads GC-content Distribution



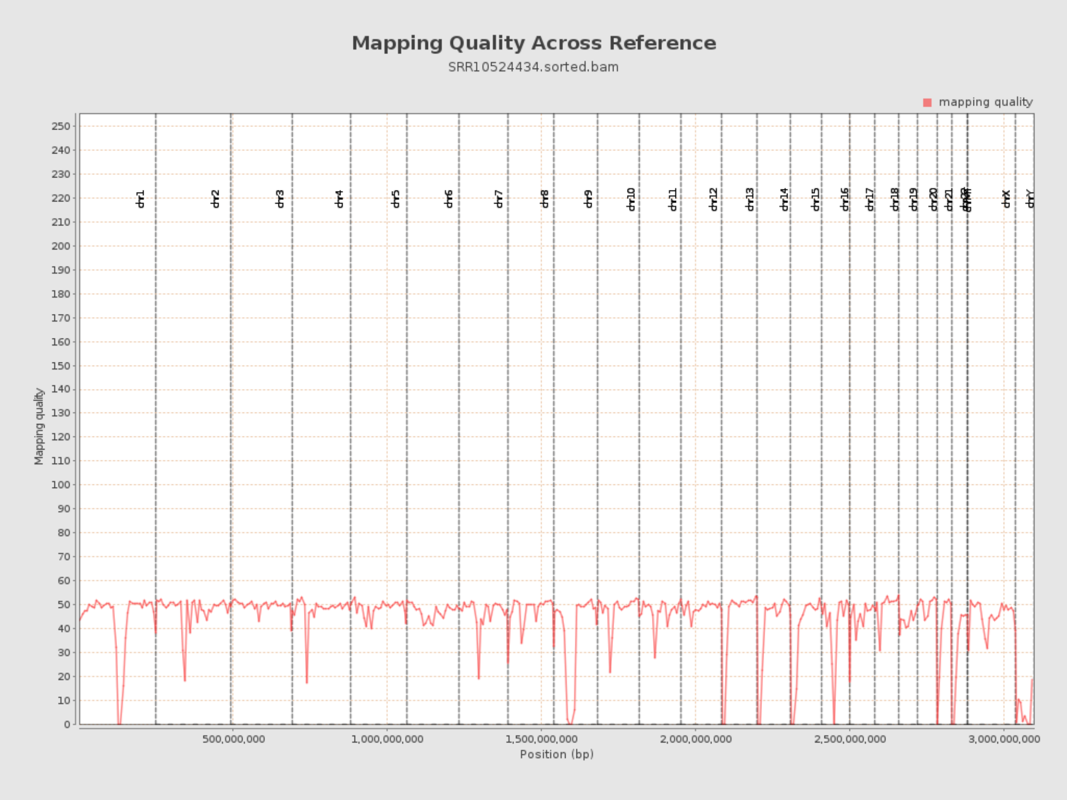
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram