Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 02:52:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524417.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_SRR10524417 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524417.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 02:52:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524417.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,778,619
Mapped reads	1,646,837 / 92.59%
Unmapped reads	131,782 / 7.41%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,687 / 0.38%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	75,091 / 4.22%
Duplication rate	3.44%
Clipped reads	1,647,468 / 92.63%

2.2. ACGT Content

Number/percentage of A's	24,850,742 / 25.77%
Number/percentage of C's	17,997,973 / 18.66%
Number/percentage of T's	30,909,452 / 32.05%
Number/percentage of G's	22,669,161 / 23.51%
Number/percentage of N's	12,555 / 0.01%
GC Percentage	42.17%

2.3. Coverage

Mean	0.0312

Standard Deviation	0.3187

2.4. Mapping Quality

Mean Mapping Quality	45.89

2.5. Mismatches and indels

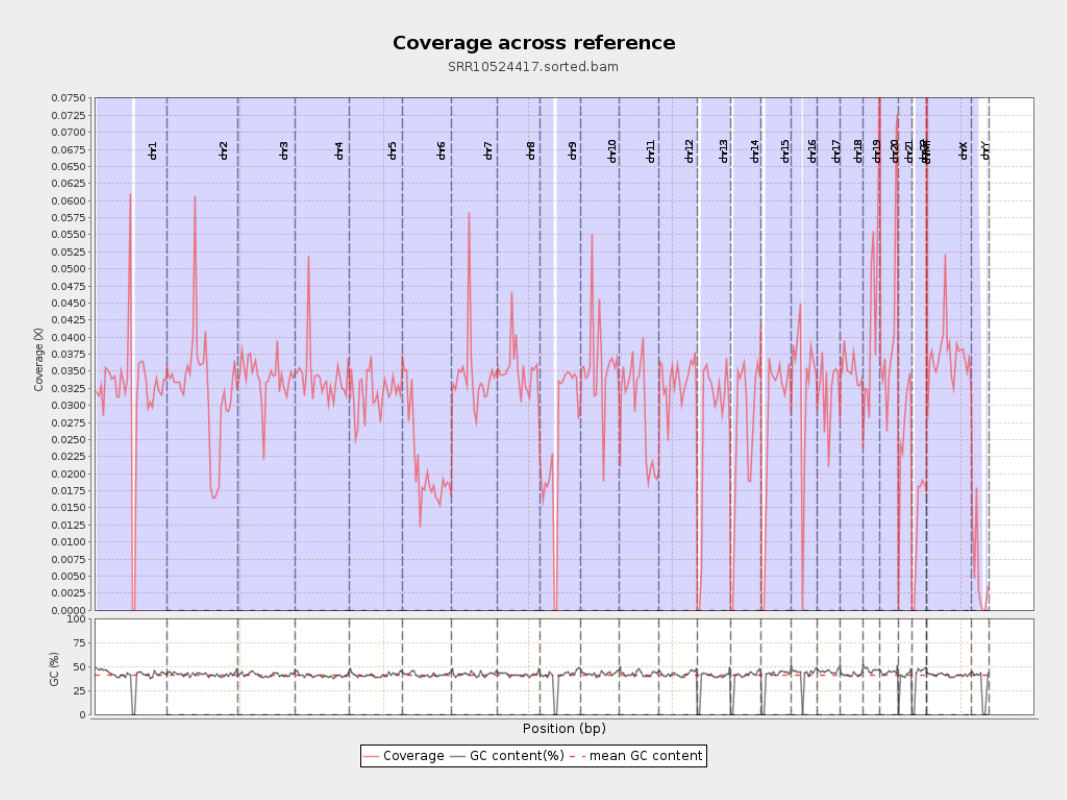
General error rate	0.51%
Mismatches	474,948
Insertions	7,845
Mapped reads with at least one insertion	0.47%
Deletions	18,099
Mapped reads with at least one deletion	1.09%
Homopolymer indels	42.78%

2.6. Chromosome stats

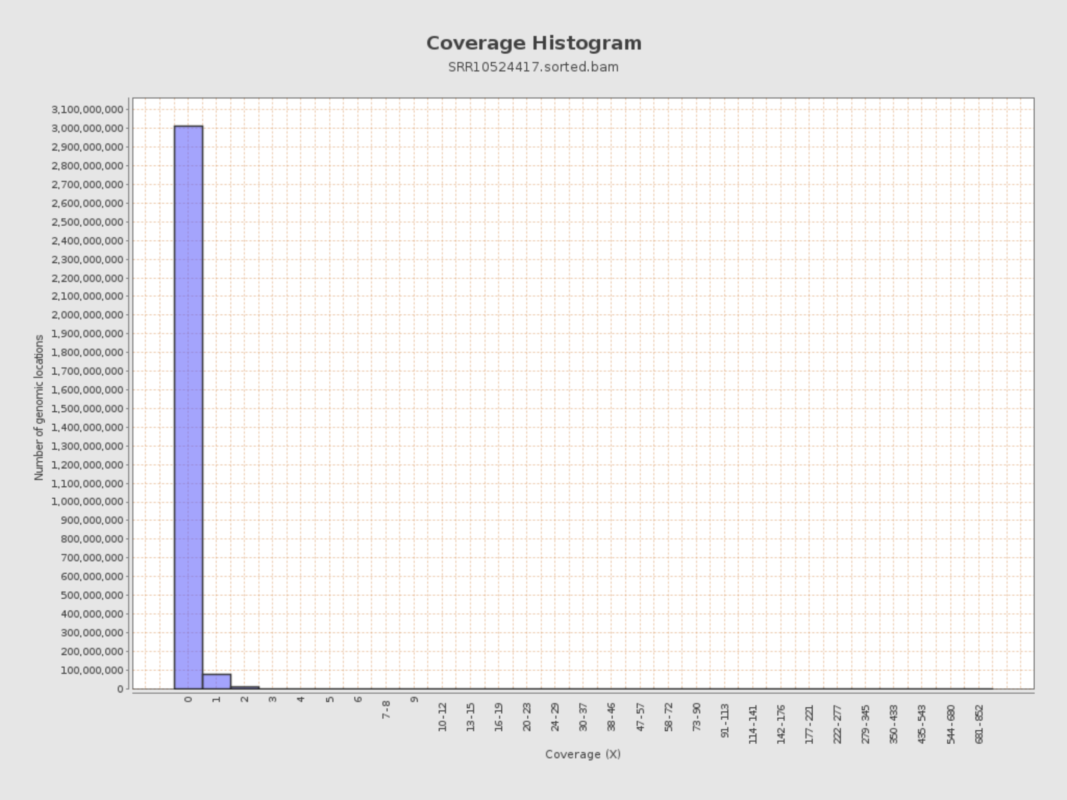
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7931799	0.0318	0.6827
chr2	243199373	7814505	0.0321	0.3421
chr3	198022430	6744985	0.0341	0.2014
chr4	191154276	6541992	0.0342	0.2318
chr5	180915260	5758719	0.0318	0.1958
chr6	171115067	3682719	0.0215	0.1779
chr7	159138663	5476581	0.0344	0.4439

chr8	146364022	5141435	0.0351	0.2991
chr9	141213431	3531234	0.025	0.2322
chr10	135534747	4841783	0.0357	0.2853
chr11	135006516	3947591	0.0292	0.2368
chr12	133851895	4506582	0.0337	0.2083
chr13	115169878	3143549	0.0273	0.1814
chr14	107349540	2805715	0.0261	0.1829
chr15	102531392	2880038	0.0281	0.184
chr16	90354753	2958329	0.0327	0.2079
chr17	81195210	2604323	0.0321	0.2161
chr18	78077248	2754889	0.0353	0.4061
chr19	59128983	2643803	0.0447	0.471
chr20	63025520	2598830	0.0412	0.2312
chr21	48129895	1251389	0.026	0.1965
chr22	51304566	664042	0.0129	0.1239
chrMT	16571	138791	8.3755	5.1648
chrX	155270560	5805703	0.0374	0.241
chrY	59373566	299254	0.005	0.1474

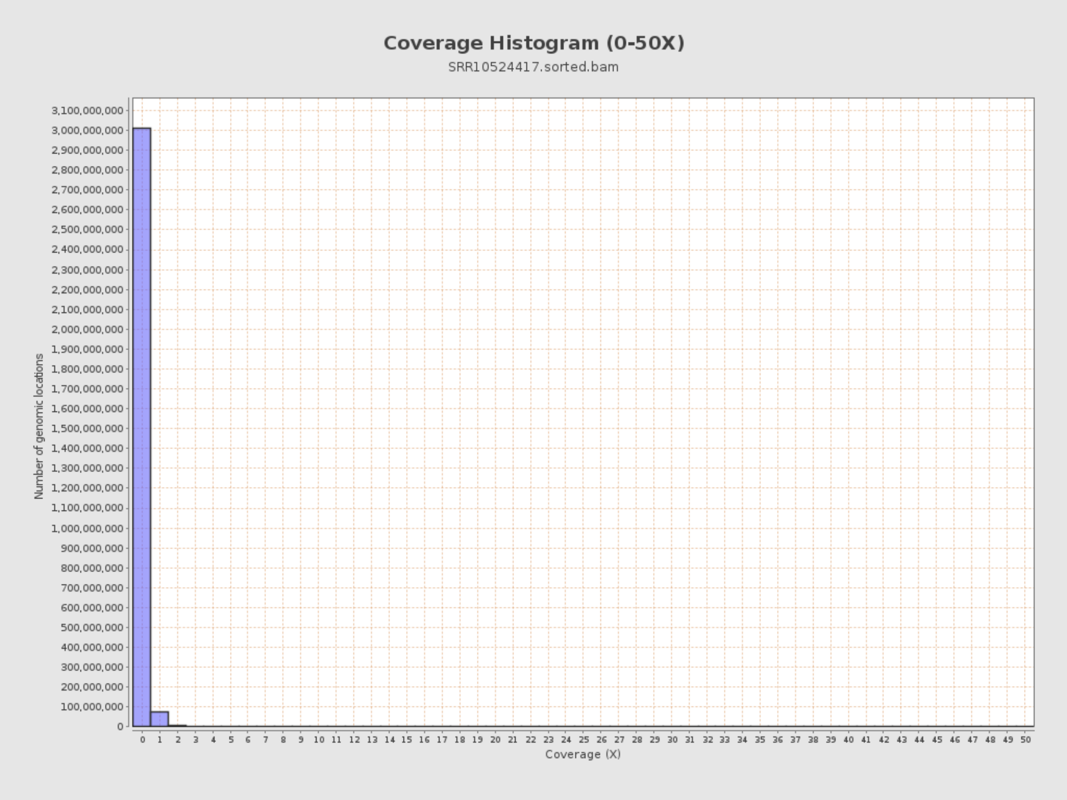
3. Results : Coverage across reference



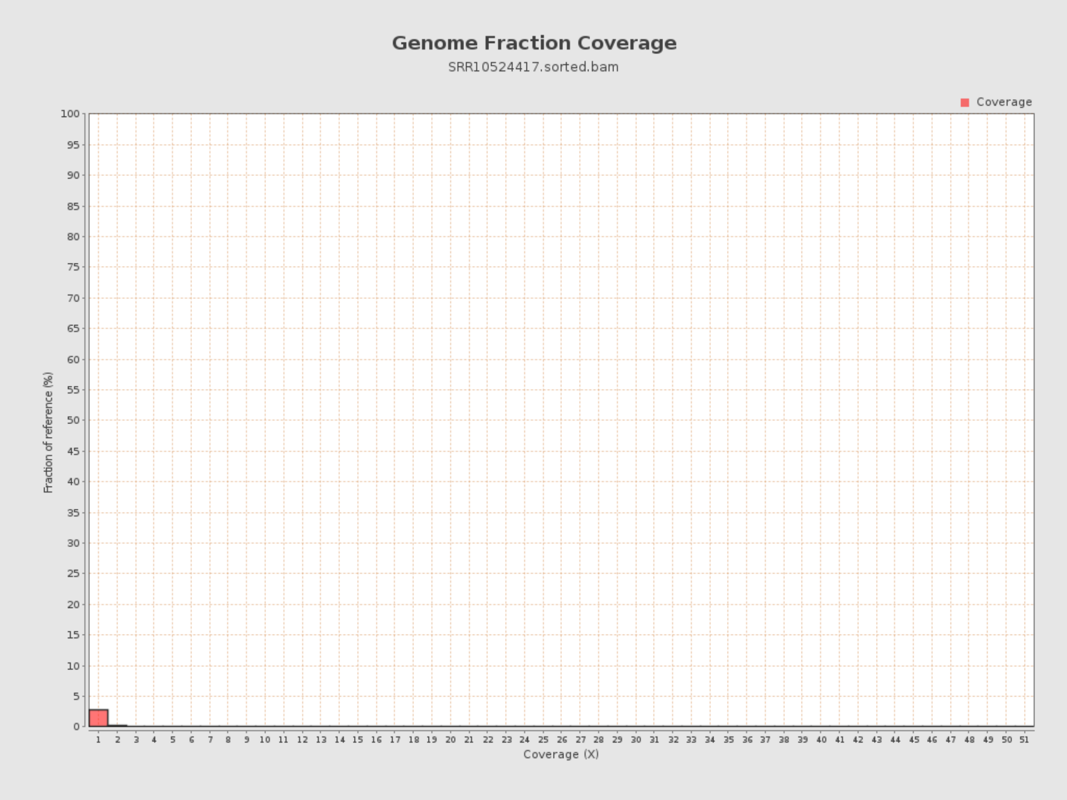
4. Results : Coverage Histogram



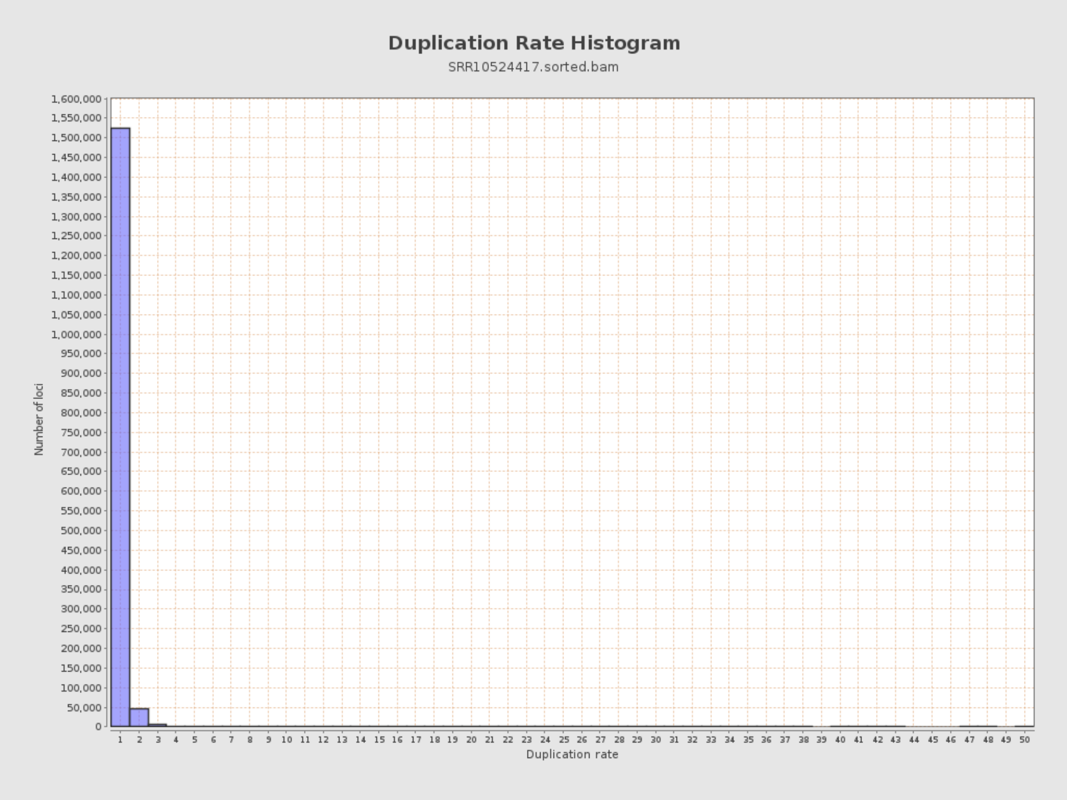
5. Results : Coverage Histogram (0-50X)



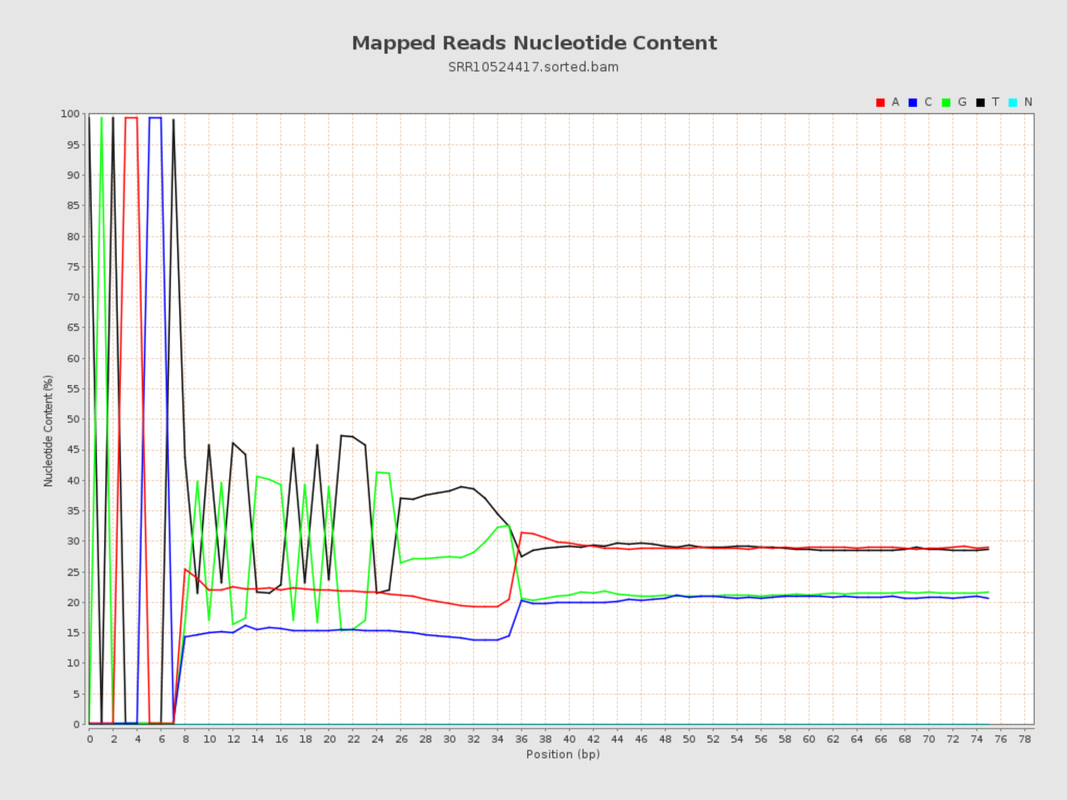
6. Results : Genome Fraction Coverage



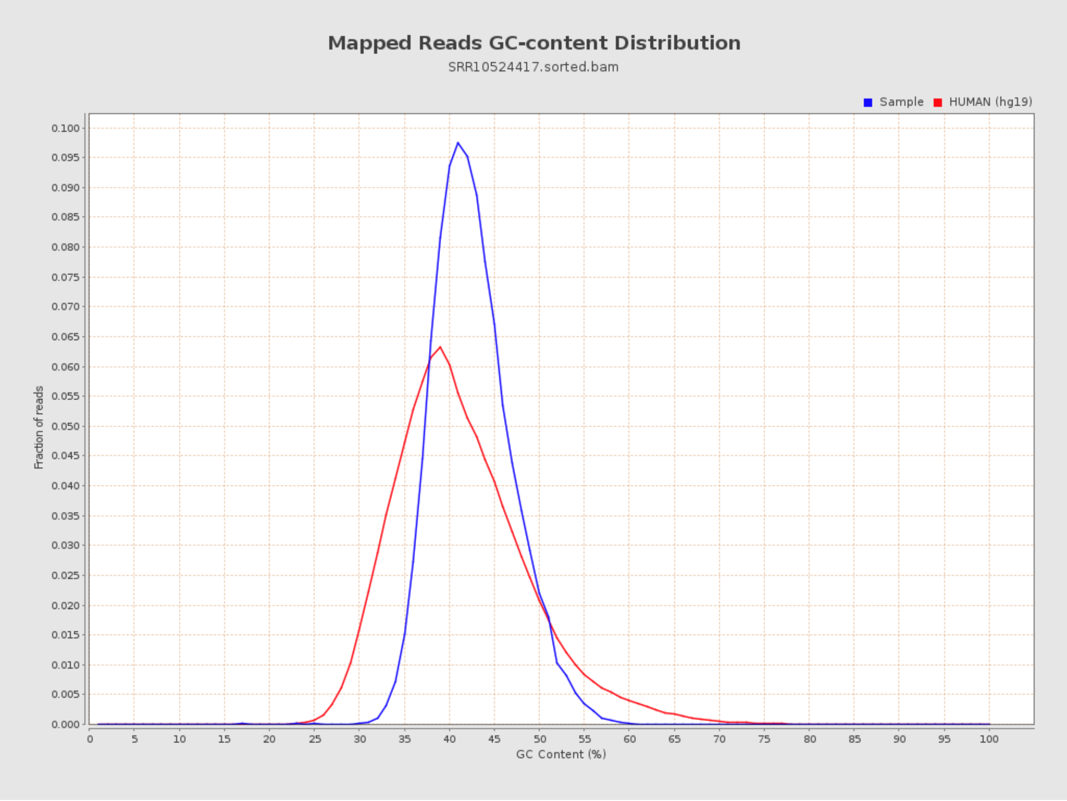
7. Results : Duplication Rate Histogram



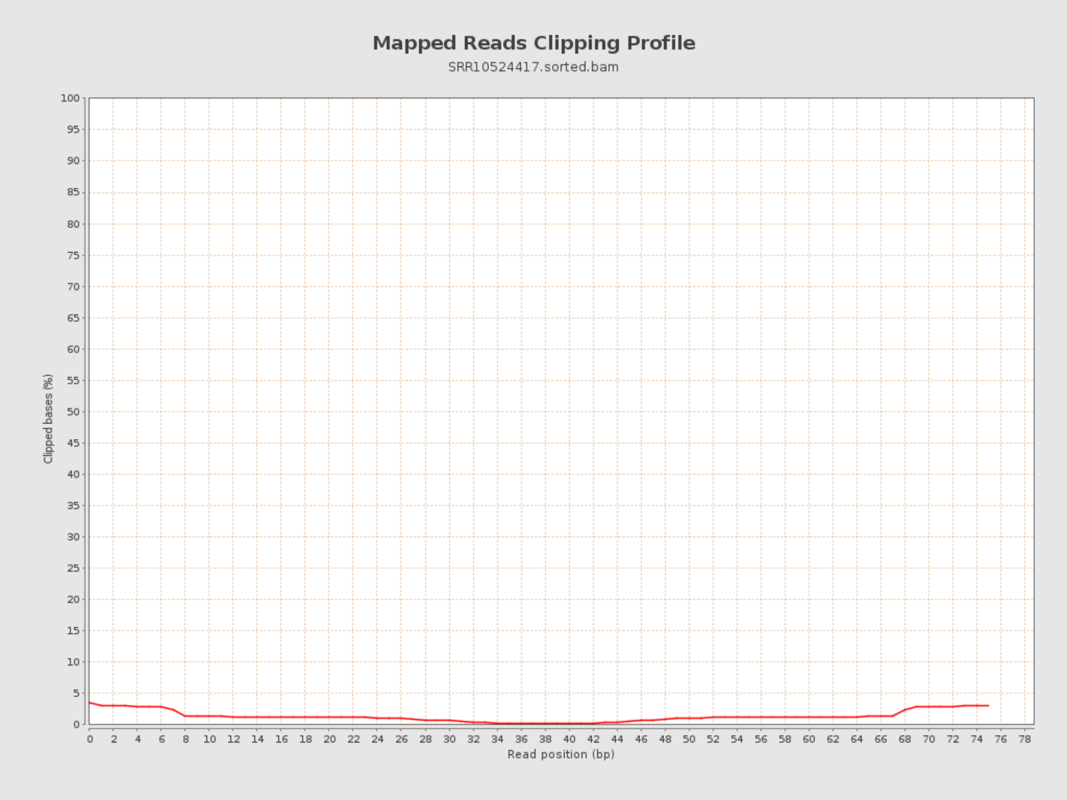
8. Results : Mapped Reads Nucleotide Content



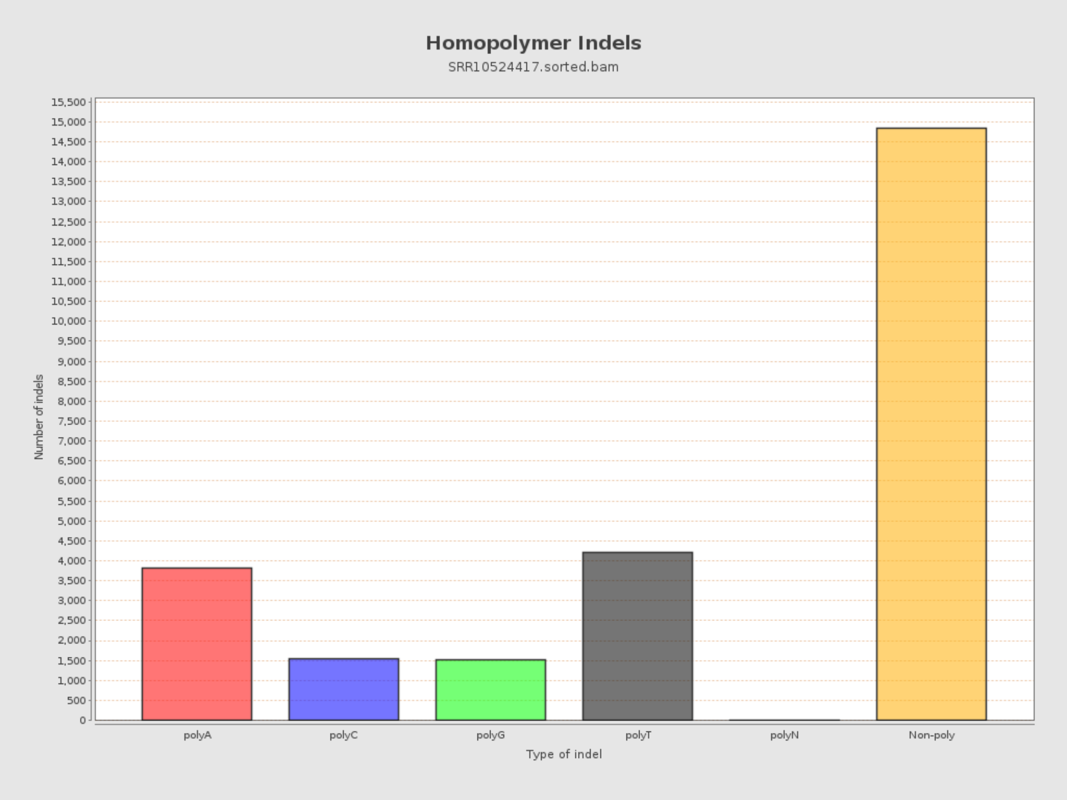
9. Results : Mapped Reads GC-content Distribution



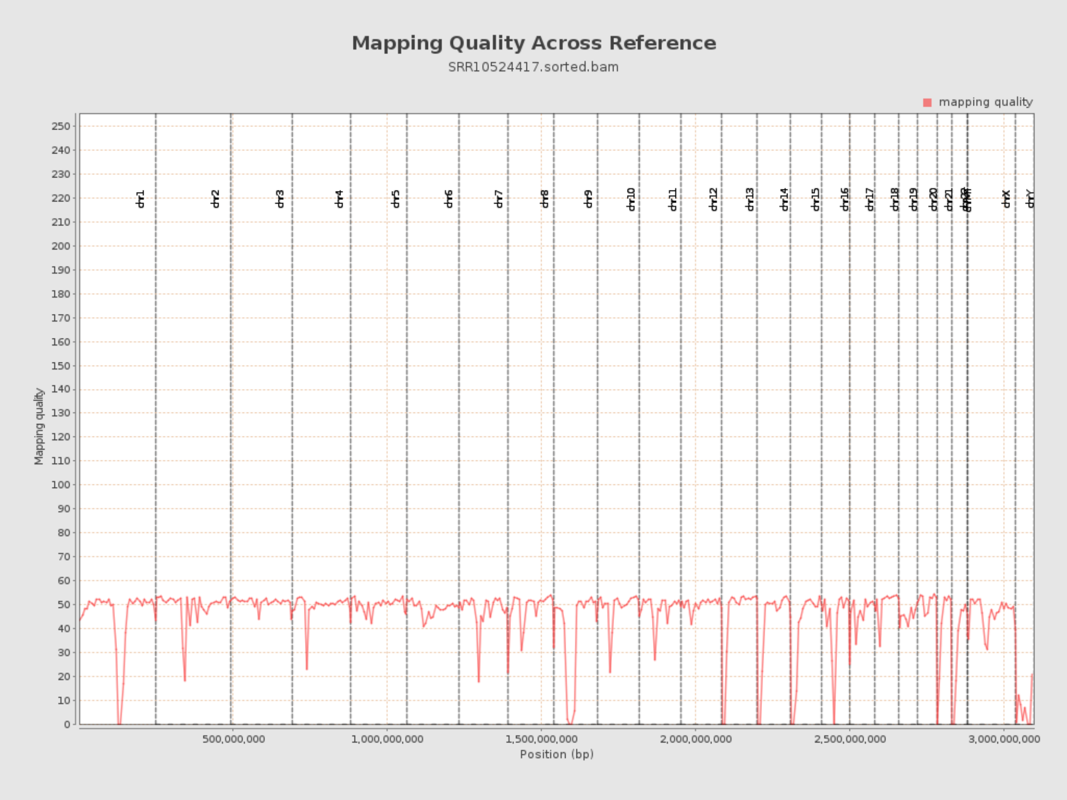
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram