Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 15:27:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524661.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_SRR10524661 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524661.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 15:27:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524661.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,369,443
Mapped reads	2,193,381 / 92.57%
Unmapped reads	176,062 / 7.43%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,678 / 0.41%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	109,516 / 4.62%
Duplication rate	3.7%
Clipped reads	2,201,411 / 92.91%

2.2. ACGT Content

Number/percentage of A's	33,609,972 / 25.95%
Number/percentage of C's	23,229,151 / 17.93%
Number/percentage of T's	40,277,846 / 31.1%
Number/percentage of G's	32,384,568 / 25%
Number/percentage of N's	17,579 / 0.01%
GC Percentage	42.94%

2.3. Coverage

Mean	0.0419

Standard Deviation	0.3744

2.4. Mapping Quality

Mean Mapping Quality	45.82

2.5. Mismatches and indels

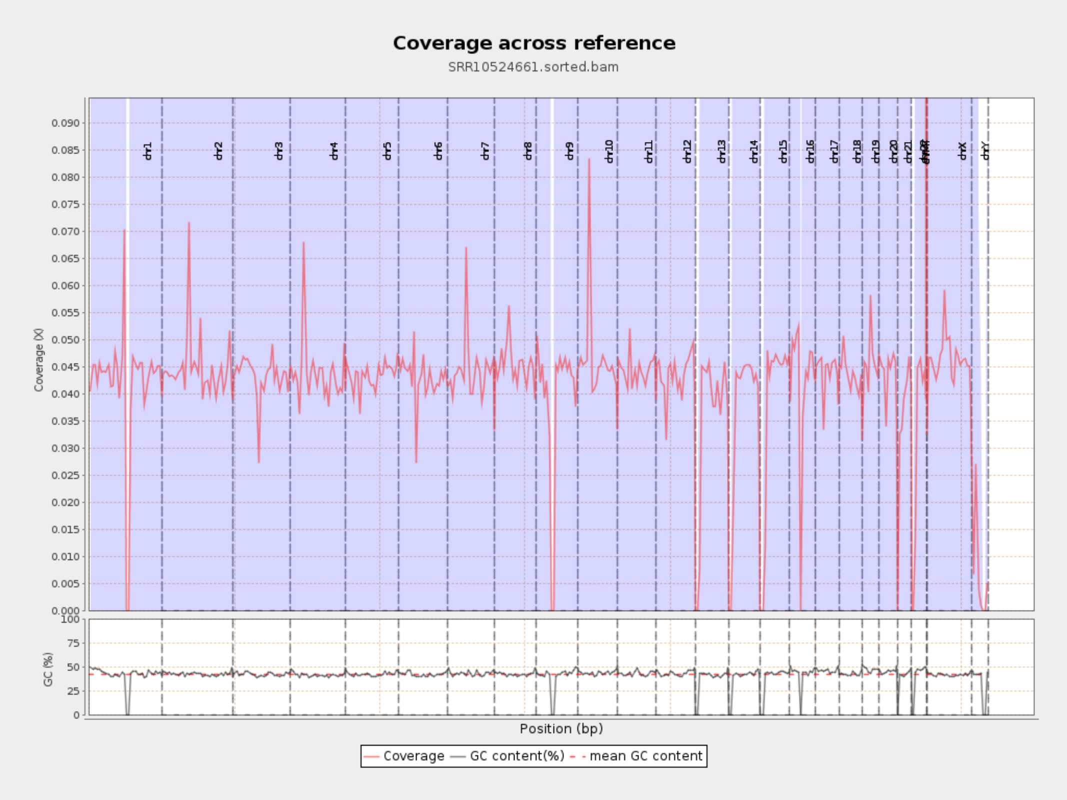
General error rate	0.5%
Mismatches	634,420
Insertions	7,703
Mapped reads with at least one insertion	0.35%
Deletions	23,770
Mapped reads with at least one deletion	1.08%
Homopolymer indels	44.57%

2.6. Chromosome stats

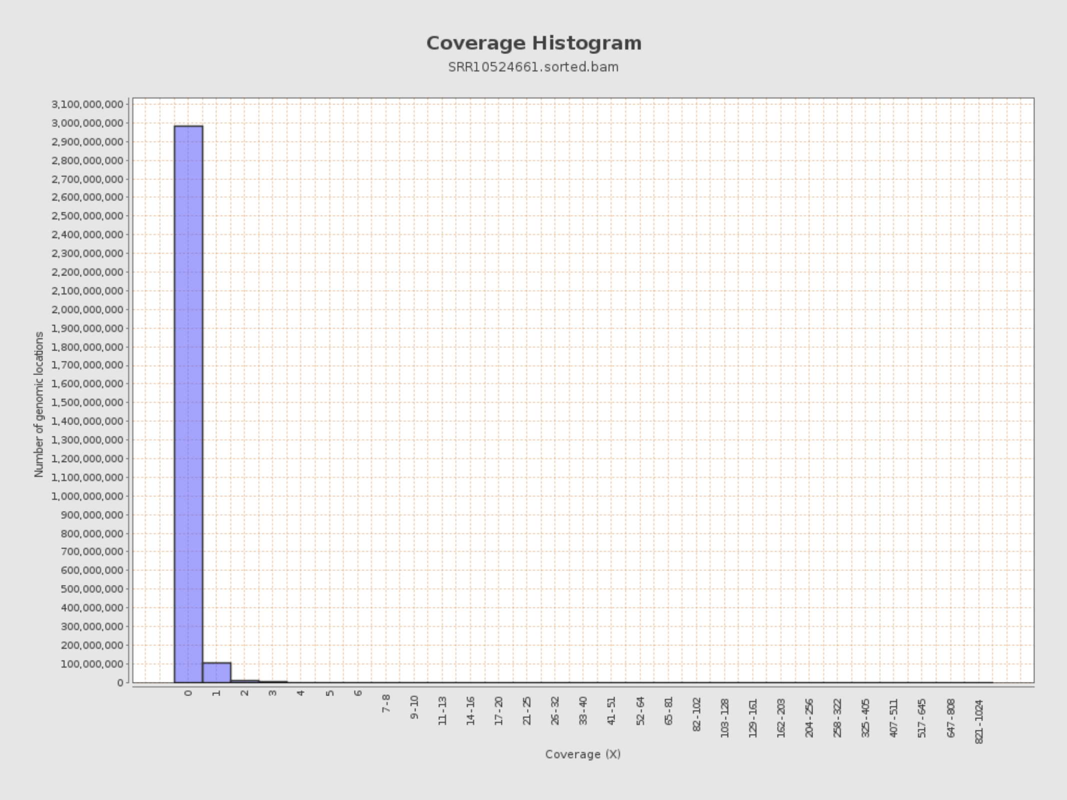
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10431483	0.0419	0.7002
chr2	243199373	10895764	0.0448	0.5198
chr3	198022430	8551386	0.0432	0.2331
chr4	191154276	8354358	0.0437	0.2708
chr5	180915260	7834608	0.0433	0.2339
chr6	171115067	7352854	0.043	0.2699
chr7	159138663	7081371	0.0445	0.4334

chr8	146364022	6641298	0.0454	0.3949
chr9	141213431	5444073	0.0386	0.3075
chr10	135534747	6320643	0.0466	0.3937
chr11	135006516	5962327	0.0442	0.3196
chr12	133851895	5818270	0.0435	0.2364
chr13	115169878	4026530	0.035	0.2091
chr14	107349540	3882177	0.0362	0.2203
chr15	102531392	3792112	0.037	0.2161
chr16	90354753	3788305	0.0419	0.2511
chr17	81195210	3550230	0.0437	0.2548
chr18	78077248	3413488	0.0437	0.5722
chr19	59128983	2710272	0.0458	0.4926
chr20	63025520	2763187	0.0438	0.2384
chr21	48129895	1711905	0.0356	0.2547
chr22	51304566	1555272	0.0303	0.1954
chrMT	16571	82044	4.9511	3.4562
chrX	155270560	7165077	0.0461	0.2693
chrY	59373566	428067	0.0072	0.2631

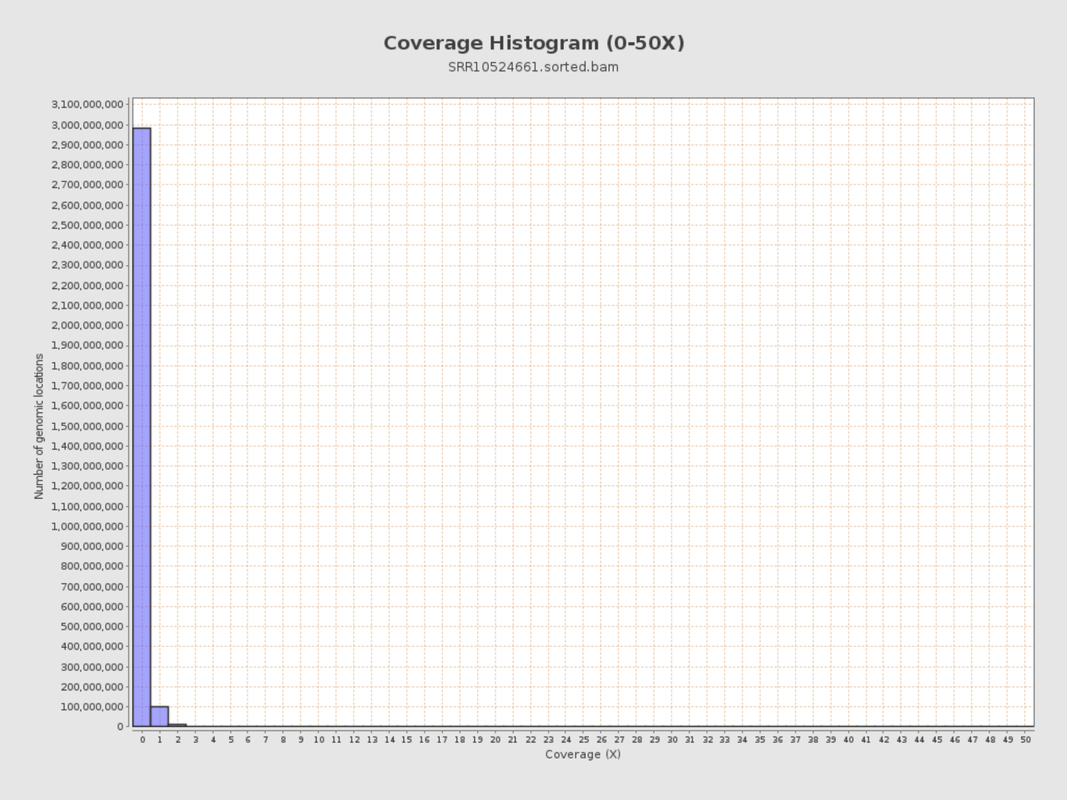
3. Results : Coverage across reference



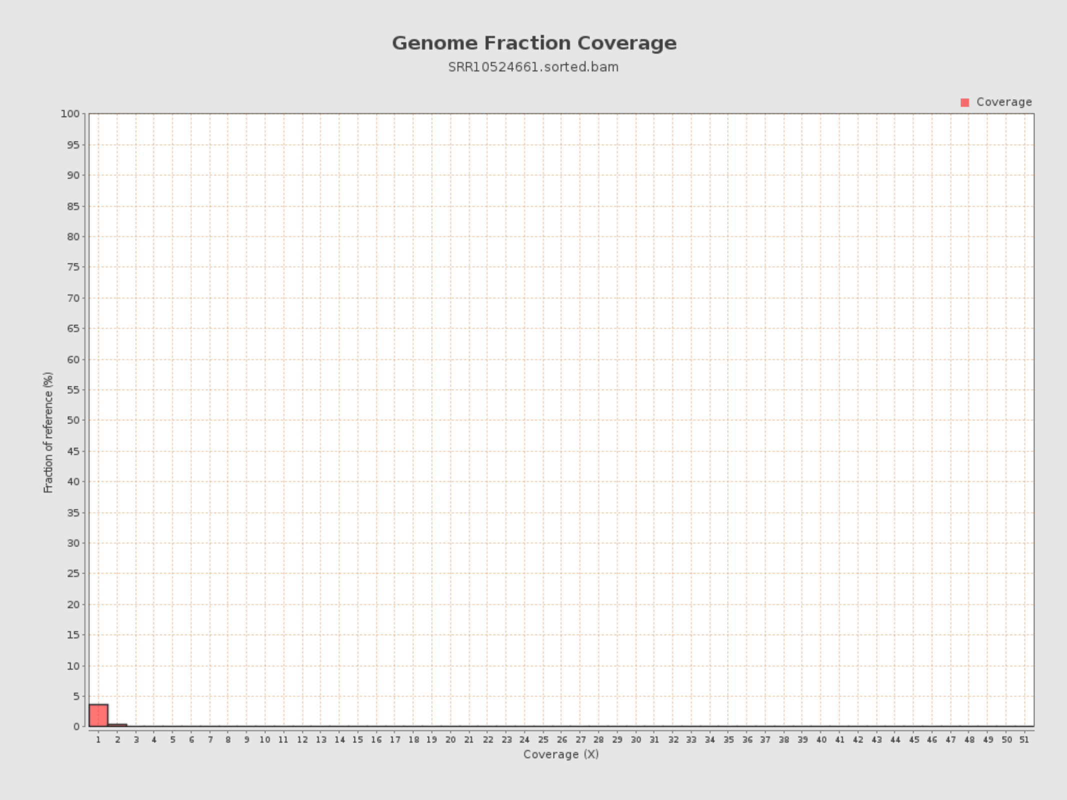
4. Results : Coverage Histogram



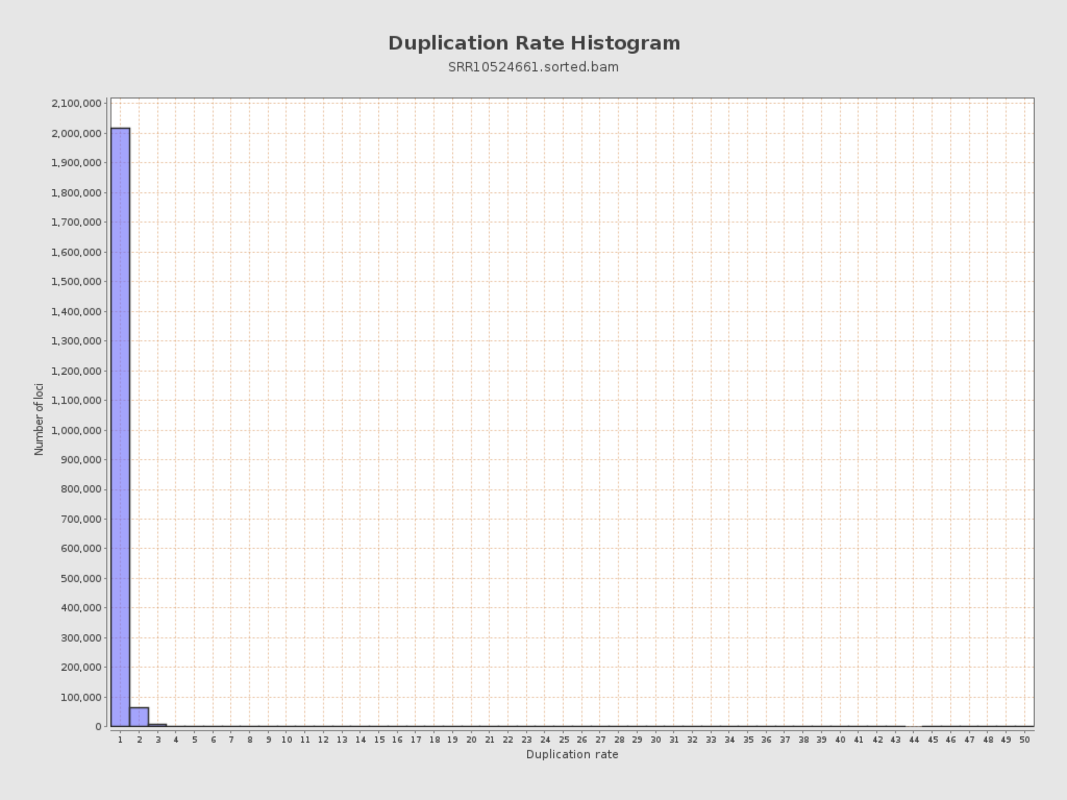
5. Results : Coverage Histogram (0-50X)



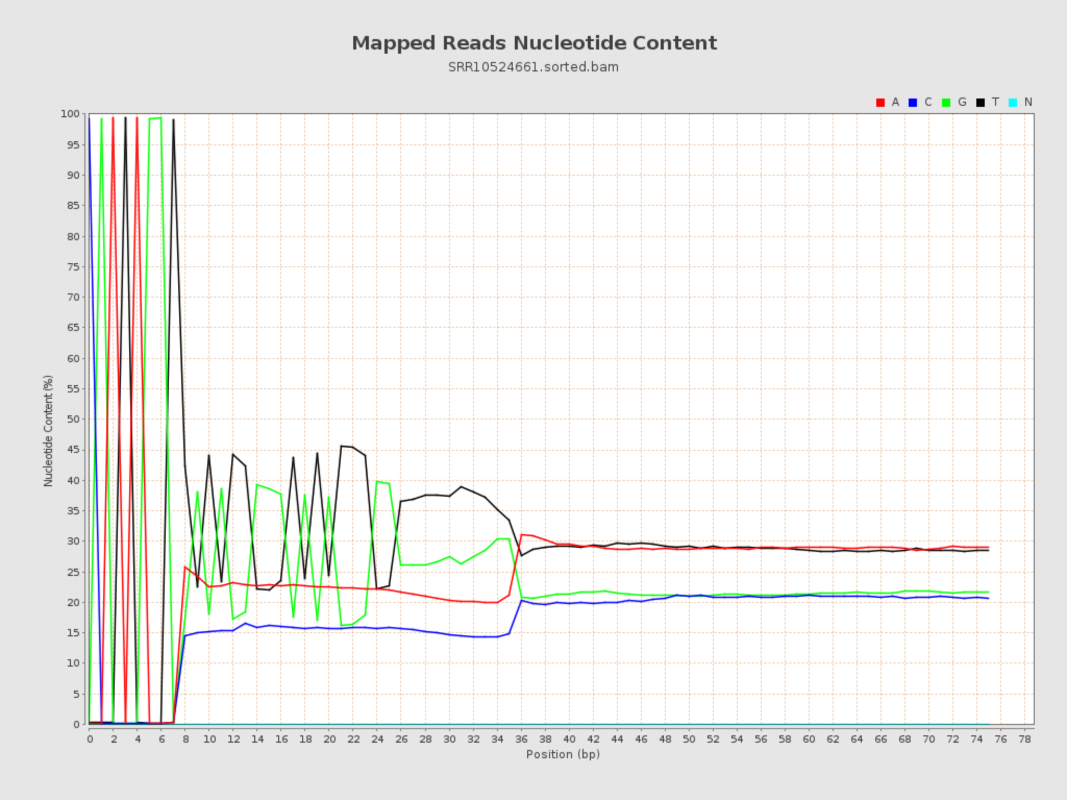
6. Results : Genome Fraction Coverage



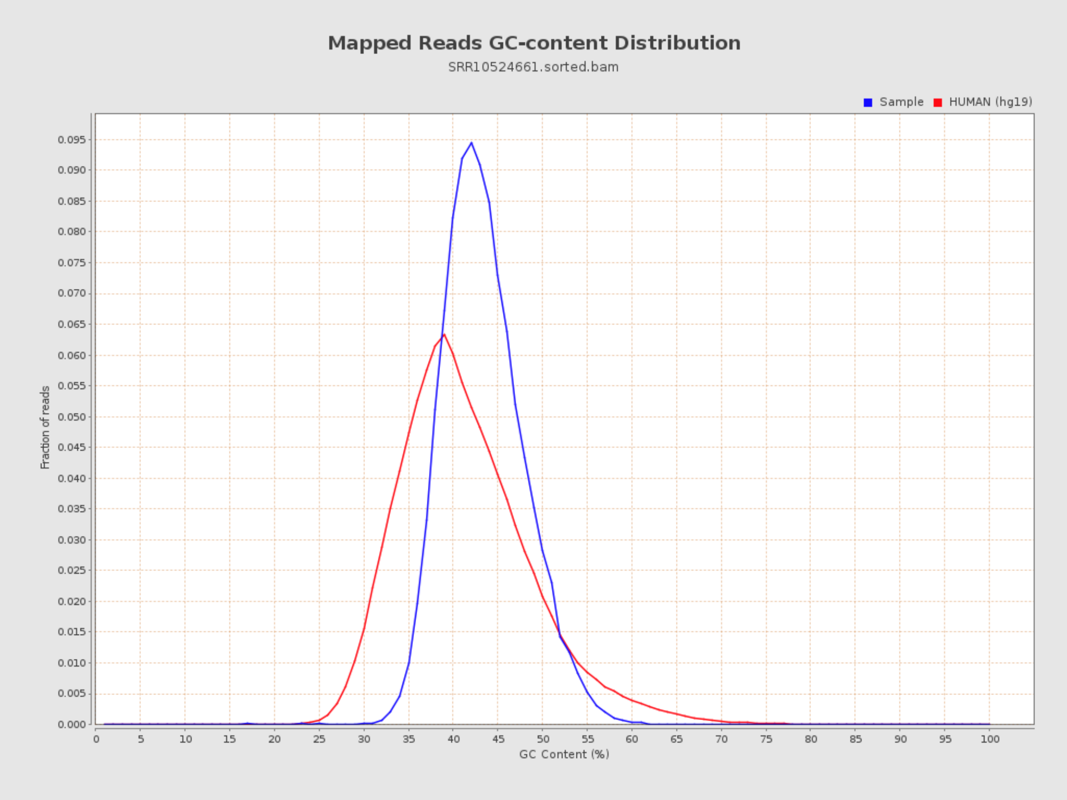
7. Results : Duplication Rate Histogram



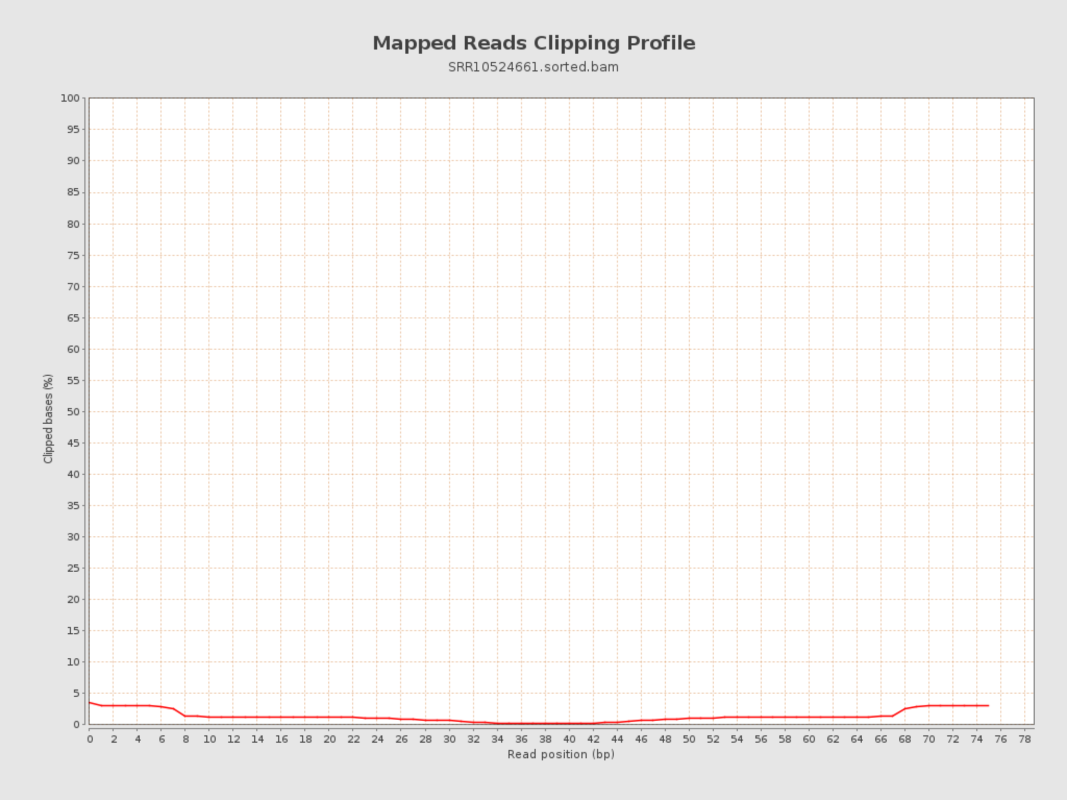
8. Results : Mapped Reads Nucleotide Content



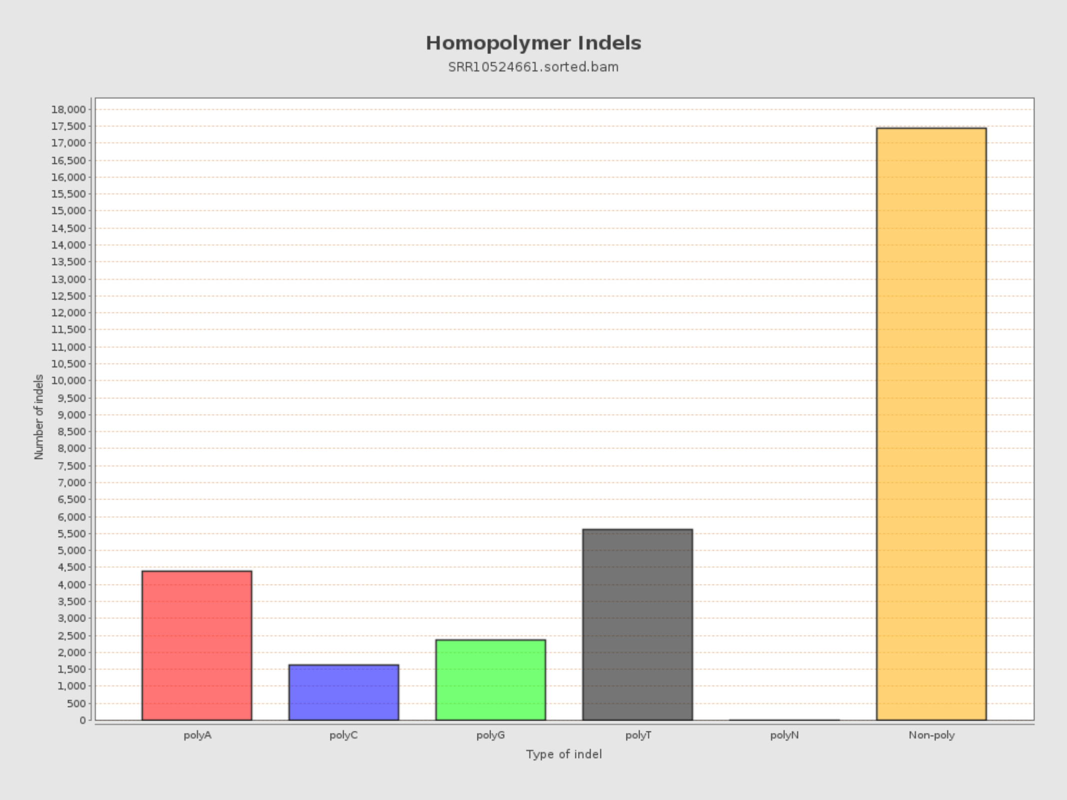
9. Results : Mapped Reads GC-content Distribution



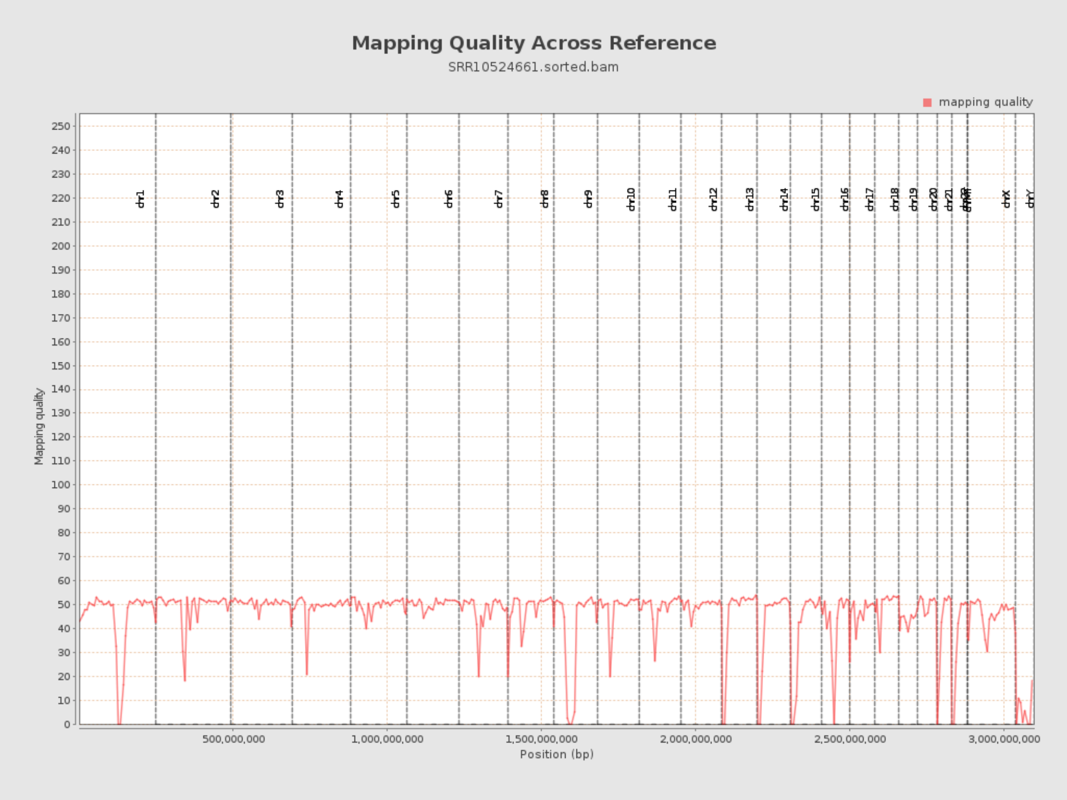
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram