Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 00:47:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524367.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_SRR10524367 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524367.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 00:47:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524367.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,036,254
Mapped reads	1,880,425 / 92.35%
Unmapped reads	155,829 / 7.65%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,476 / 0.42%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	84,859 / 4.17%
Duplication rate	3.3%
Clipped reads	1,883,176 / 92.48%

2.2. ACGT Content

Number/percentage of A's	28,597,873 / 26.04%
Number/percentage of C's	20,618,852 / 18.78%
Number/percentage of T's	33,511,673 / 30.52%
Number/percentage of G's	27,089,514 / 24.67%
Number/percentage of N's	2,072 / 0%
GC Percentage	43.44%

2.3. Coverage

Mean	0.0355

Standard Deviation	0.3176

2.4. Mapping Quality

Mean Mapping Quality	44.73

2.5. Mismatches and indels

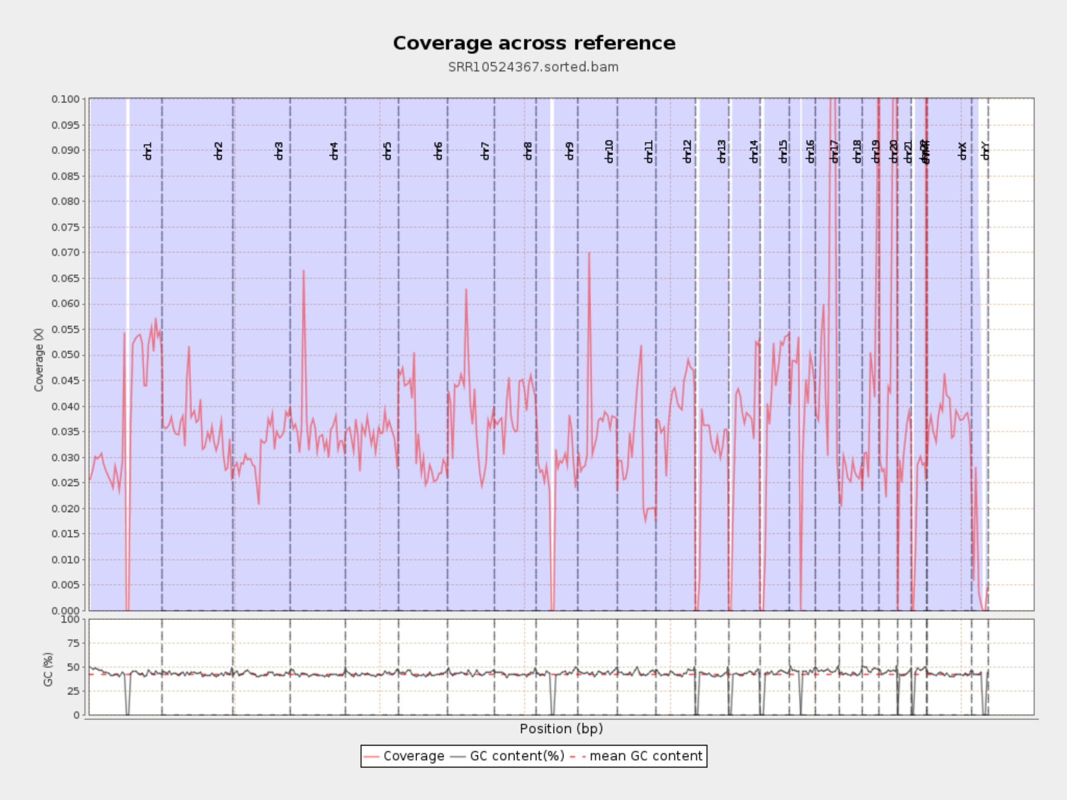
General error rate	0.52%
Mismatches	549,064
Insertions	9,024
Mapped reads with at least one insertion	0.48%
Deletions	20,664
Mapped reads with at least one deletion	1.09%
Homopolymer indels	41.13%

2.6. Chromosome stats

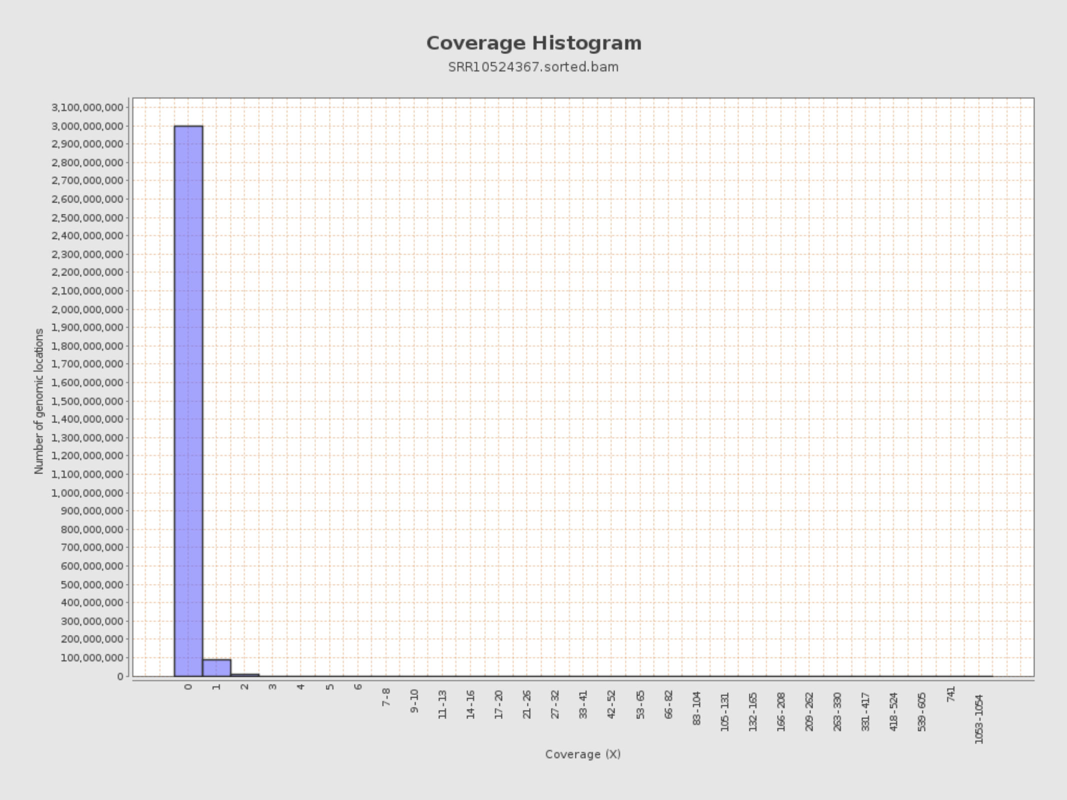
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9225560	0.037	0.4856
chr2	243199373	8620211	0.0354	0.4823
chr3	198022430	6263798	0.0316	0.1972
chr4	191154276	6796531	0.0356	0.2649
chr5	180915260	6221625	0.0344	0.2046
chr6	171115067	5818811	0.034	0.2371
chr7	159138663	6219400	0.0391	0.3953

chr8	146364022	5839224	0.0399	0.4202
chr9	141213431	3652269	0.0259	0.2279
chr10	135534747	4894906	0.0361	0.3427
chr11	135006516	3956699	0.0293	0.2484
chr12	133851895	5440128	0.0406	0.2256
chr13	115169878	3293505	0.0286	0.1876
chr14	107349540	3722436	0.0347	0.2121
chr15	102531392	3927759	0.0383	0.2209
chr16	90354753	3761326	0.0416	0.2402
chr17	81195210	4847038	0.0597	0.2875
chr18	78077248	2071203	0.0265	0.3876
chr19	59128983	2860813	0.0484	0.3877
chr20	63025520	3680687	0.0584	0.2847
chr21	48129895	1417442	0.0295	0.2443
chr22	51304566	1033354	0.0201	0.1559
chrMT	16571	53896	3.2524	2.613
chrX	155270560	5829949	0.0375	0.2311
chrY	59373566	404855	0.0068	0.2927

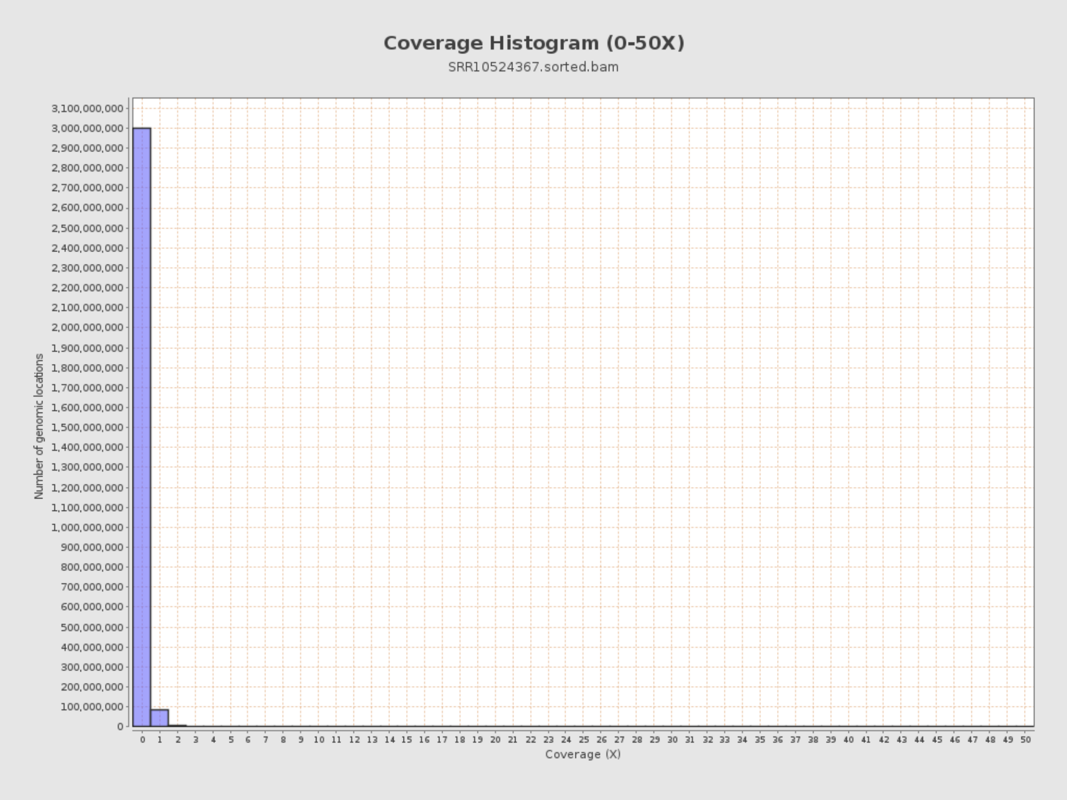
3. Results : Coverage across reference



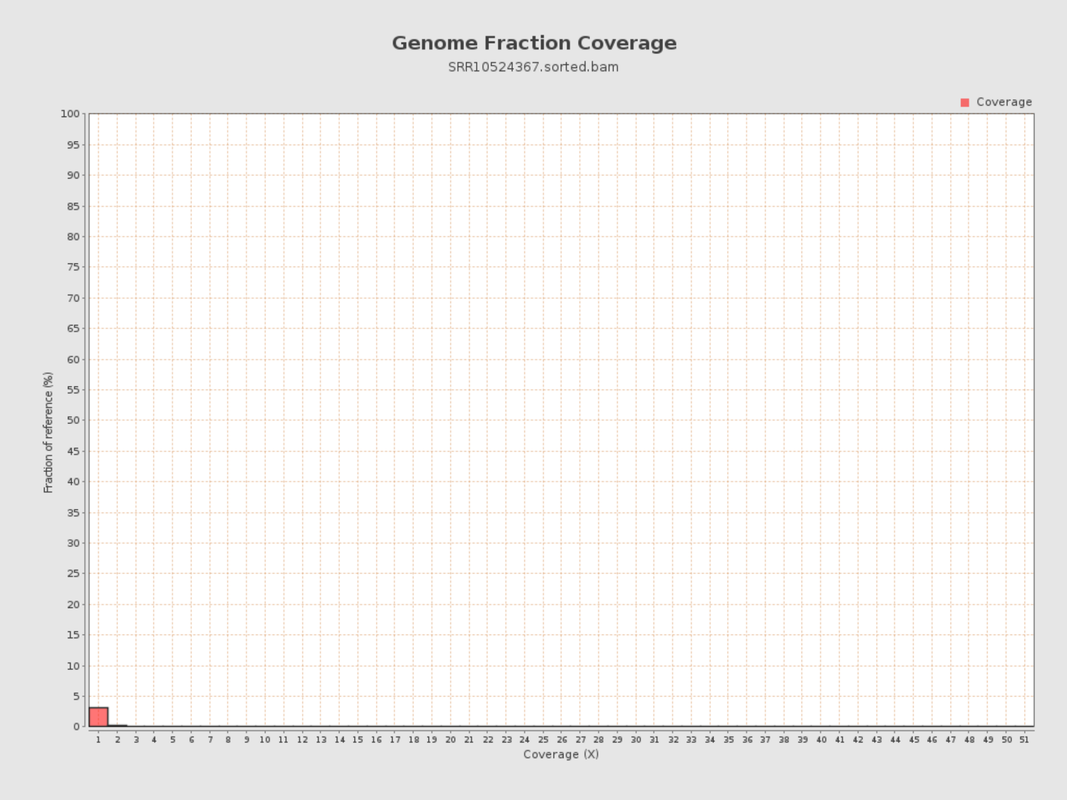
4. Results : Coverage Histogram



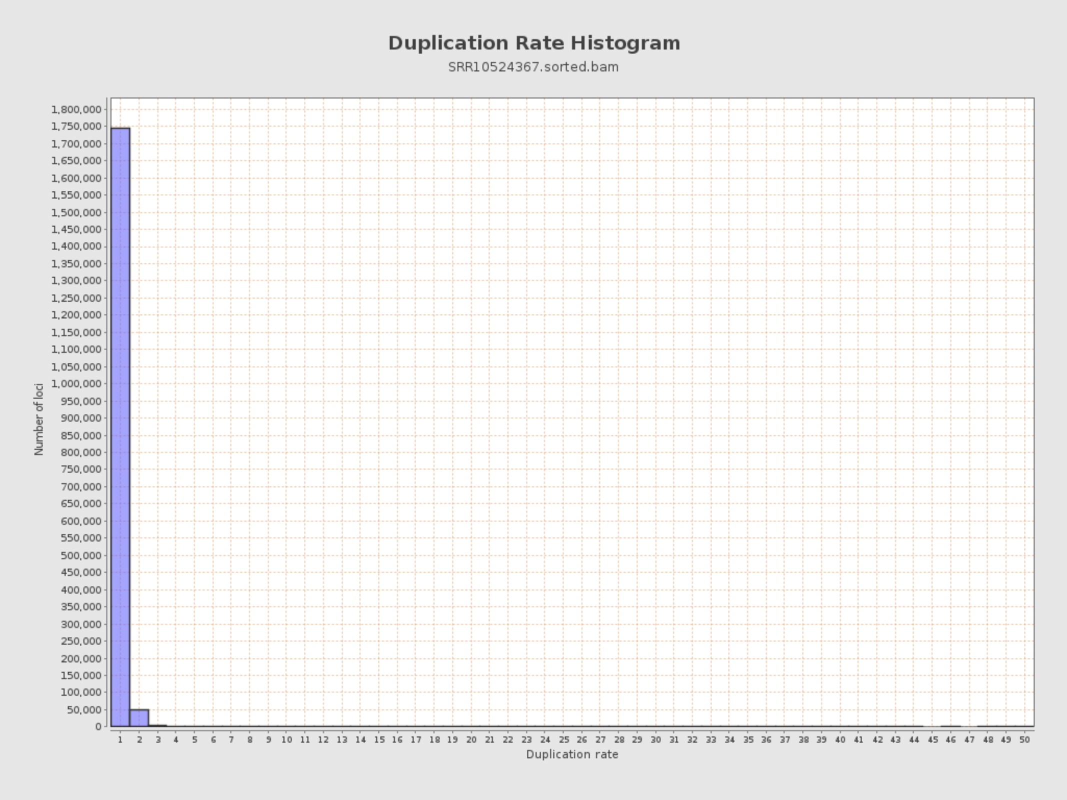
5. Results : Coverage Histogram (0-50X)



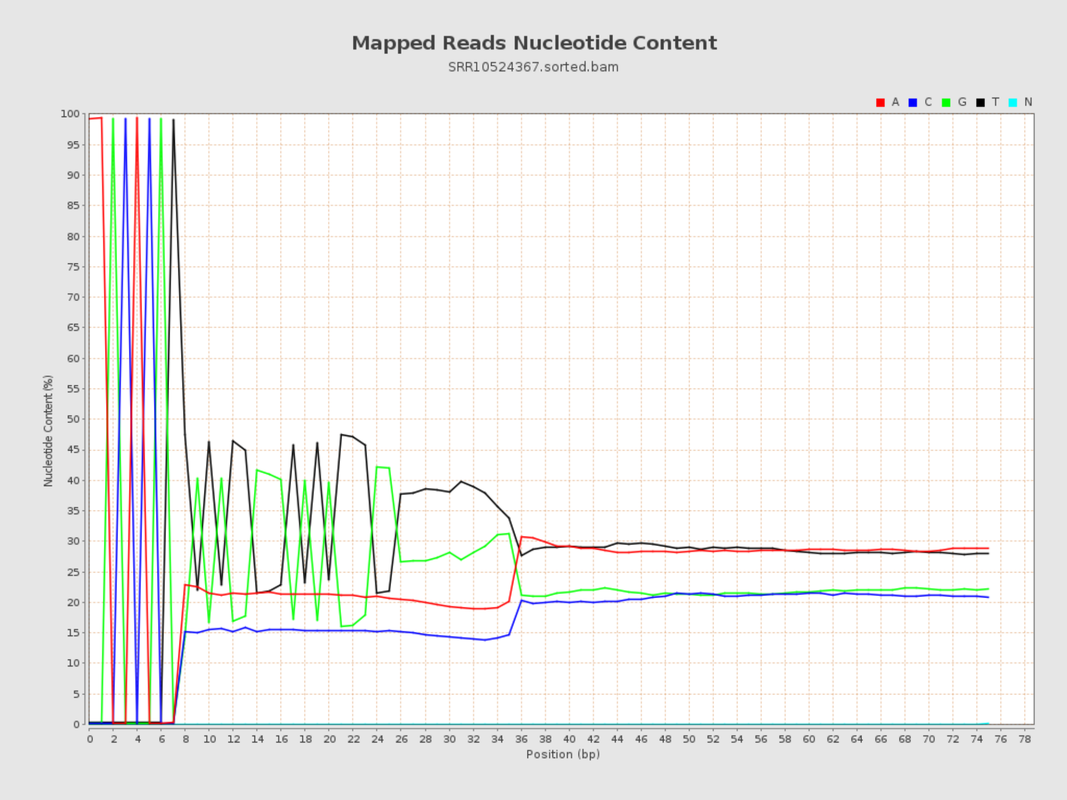
6. Results : Genome Fraction Coverage



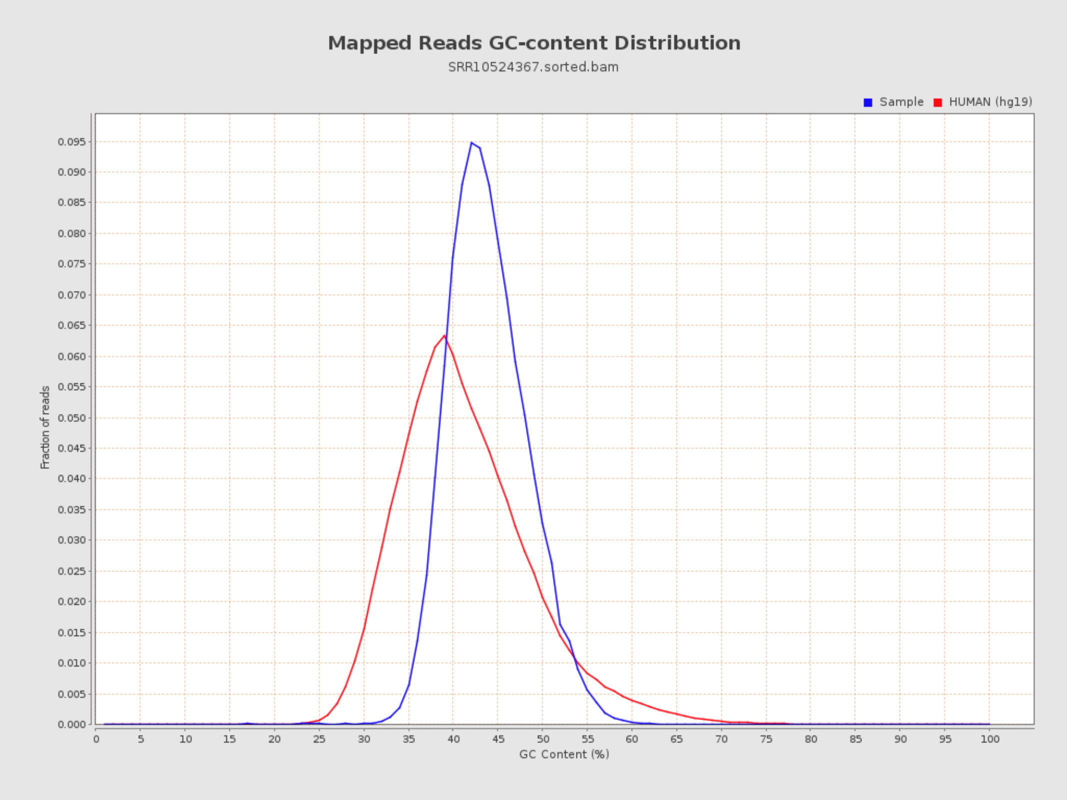
7. Results : Duplication Rate Histogram



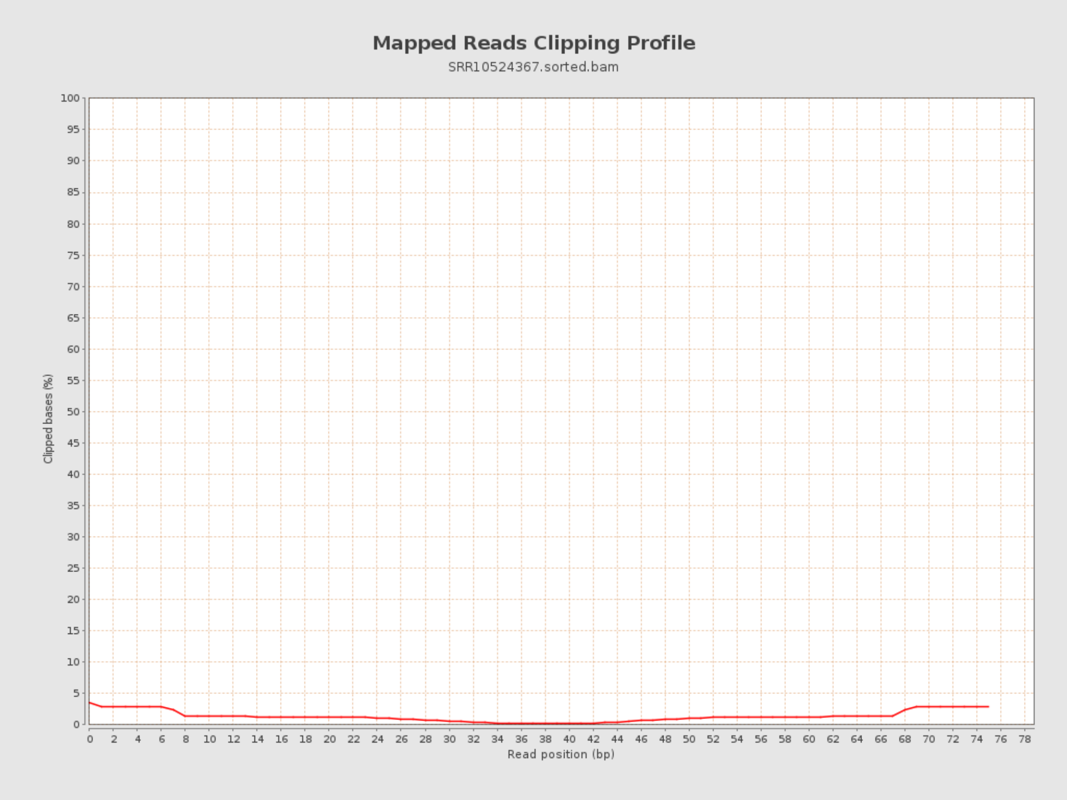
8. Results : Mapped Reads Nucleotide Content



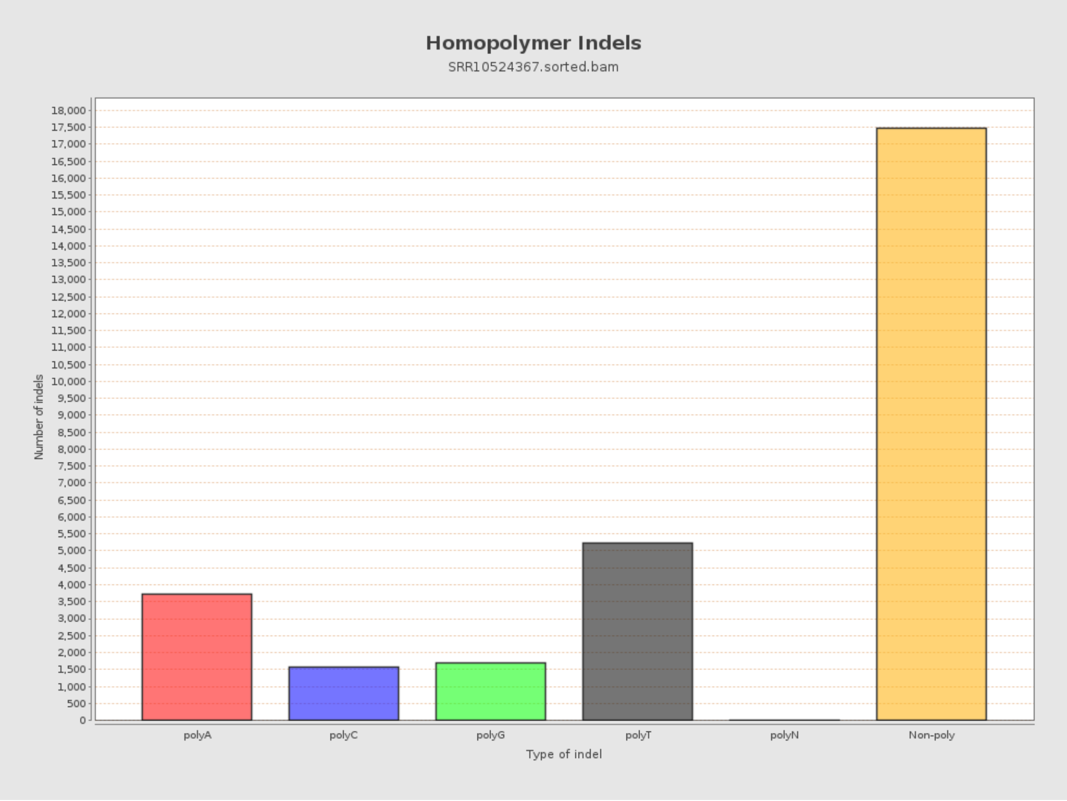
9. Results : Mapped Reads GC-content Distribution



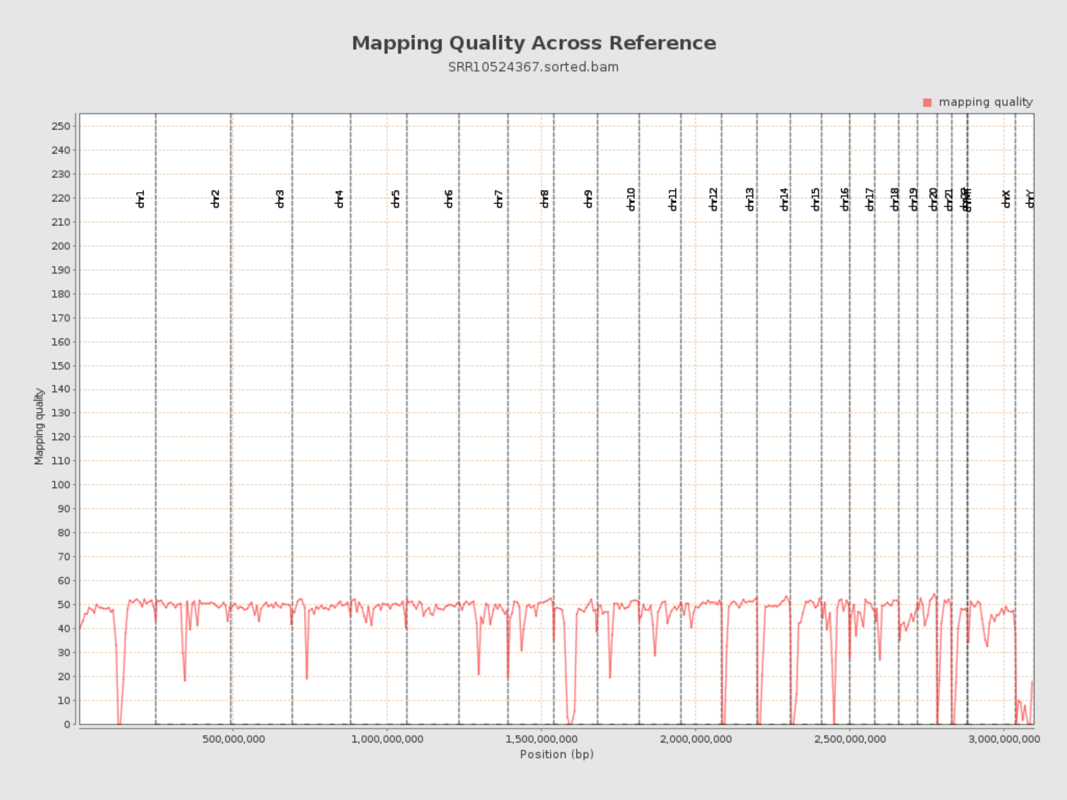
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram