Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 16:23:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524684.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_SRR10524684 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524684.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 16:23:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524684.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,349,428
Mapped reads	1,243,237 / 92.13%
Unmapped reads	106,191 / 7.87%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,152 / 0.38%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	38,813 / 2.88%
Duplication rate	2.27%
Clipped reads	1,246,642 / 92.38%

2.2. ACGT Content

Number/percentage of A's	19,239,113 / 25.88%
Number/percentage of C's	14,029,129 / 18.87%
Number/percentage of T's	22,404,052 / 30.13%
Number/percentage of G's	18,663,622 / 25.1%
Number/percentage of N's	9,748 / 0.01%
GC Percentage	43.97%

2.3. Coverage

Mean	0.024

Standard Deviation	0.2354

2.4. Mapping Quality

Mean Mapping Quality	46.21

2.5. Mismatches and indels

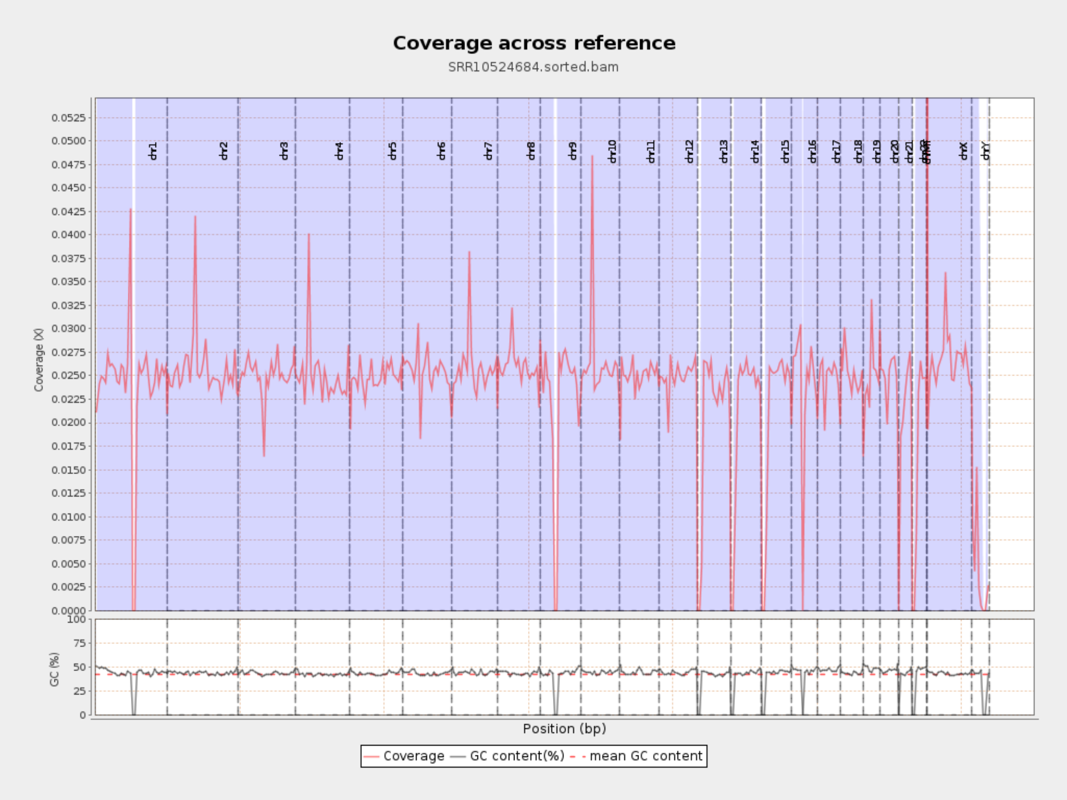
General error rate	0.52%
Mismatches	375,509
Insertions	4,515
Mapped reads with at least one insertion	0.36%
Deletions	13,891
Mapped reads with at least one deletion	1.11%
Homopolymer indels	45.39%

2.6. Chromosome stats

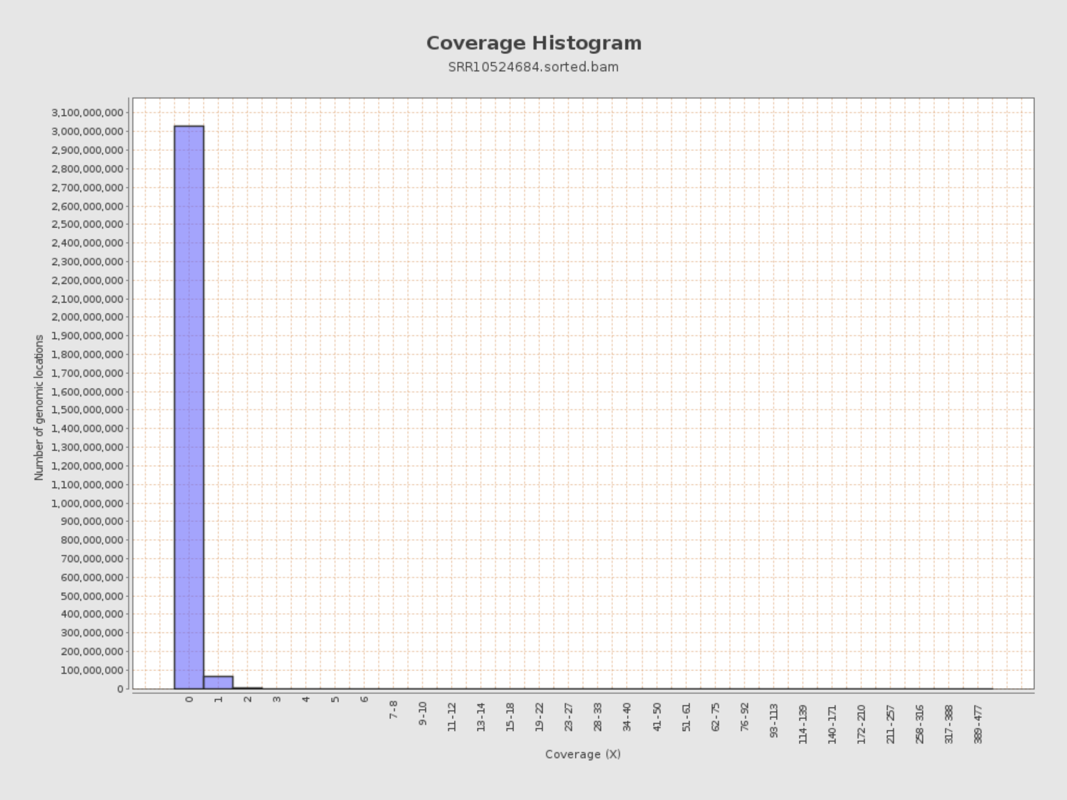
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5969978	0.024	0.4064
chr2	243199373	6275231	0.0258	0.2834
chr3	198022430	4953203	0.025	0.1699
chr4	191154276	4799293	0.0251	0.1853
chr5	180915260	4505940	0.0249	0.1691
chr6	171115067	4358350	0.0255	0.1862
chr7	159138663	4120950	0.0259	0.2696

chr8	146364022	3816444	0.0261	0.2735
chr9	141213431	3135919	0.0222	0.2024
chr10	135534747	3602572	0.0266	0.256
chr11	135006516	3392414	0.0251	0.2084
chr12	133851895	3337969	0.0249	0.1703
chr13	115169878	2349551	0.0204	0.153
chr14	107349540	2234543	0.0208	0.1567
chr15	102531392	2117802	0.0207	0.1536
chr16	90354753	2124308	0.0235	0.1759
chr17	81195210	1996657	0.0246	0.1745
chr18	78077248	1972344	0.0253	0.3668
chr19	59128983	1482013	0.0251	0.3195
chr20	63025520	1558582	0.0247	0.1709
chr21	48129895	1000157	0.0208	0.1713
chr22	51304566	871537	0.017	0.1388
chrMT	16571	16233	0.9796	1.0858
chrX	155270560	4135199	0.0266	0.1869
chrY	59373566	240702	0.0041	0.1405

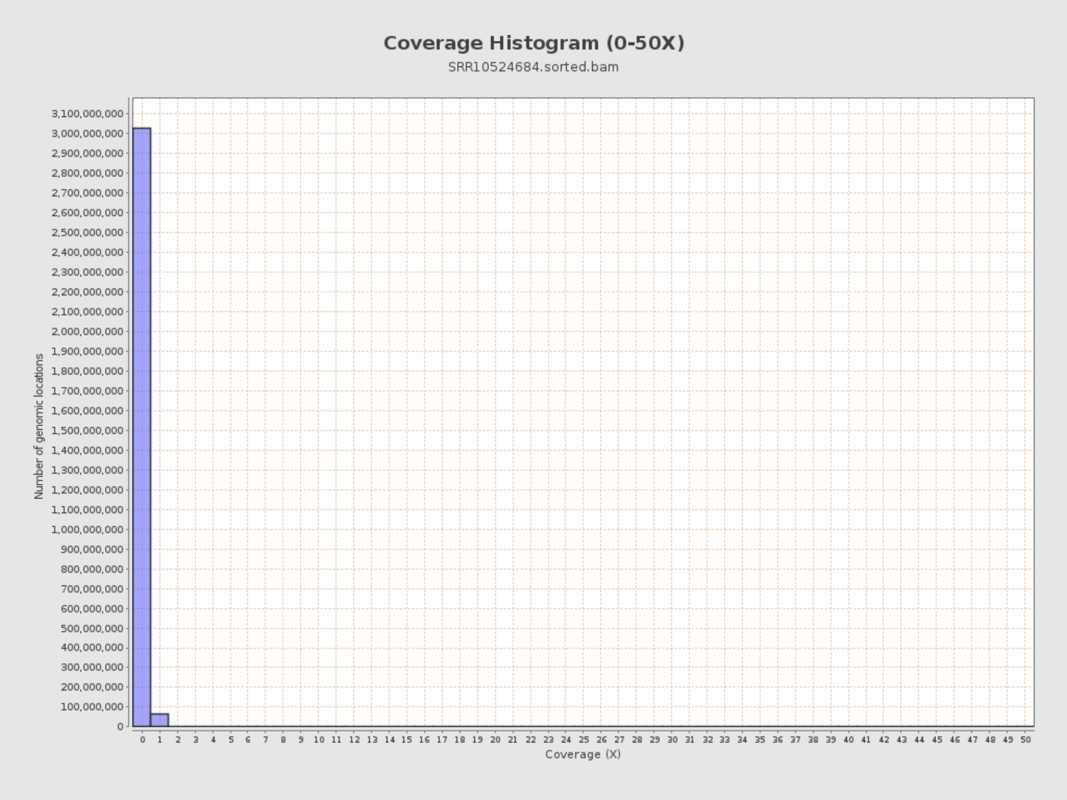
3. Results : Coverage across reference



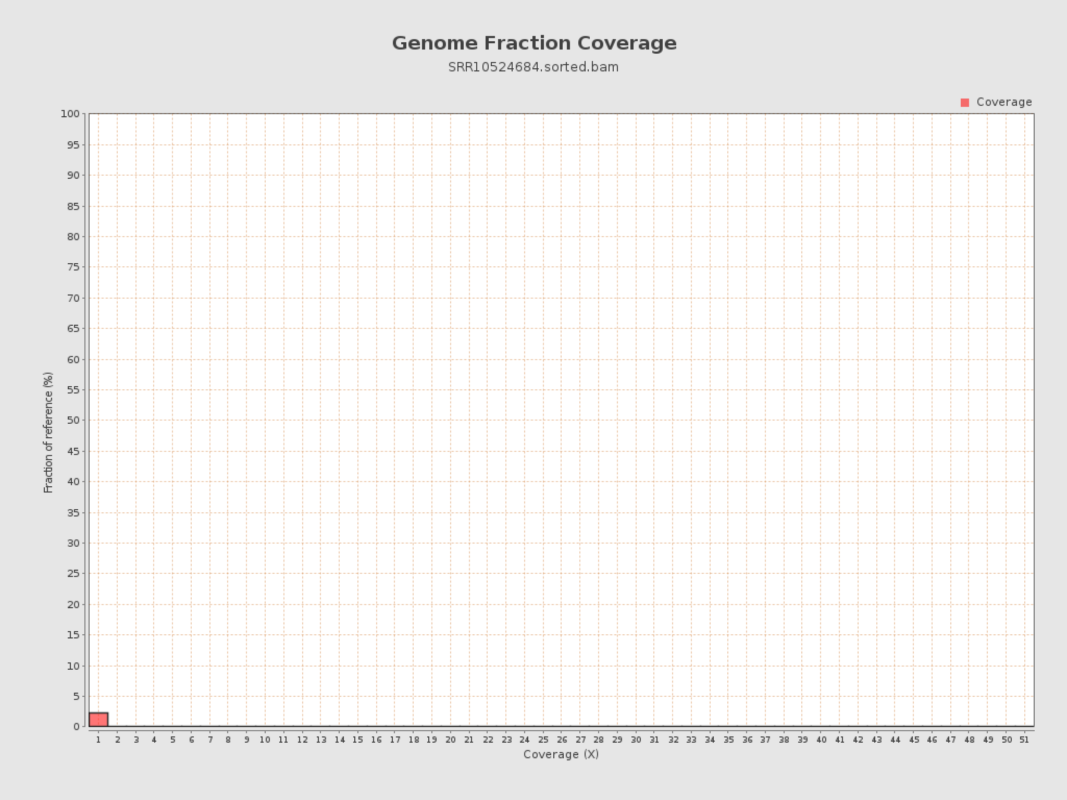
4. Results : Coverage Histogram



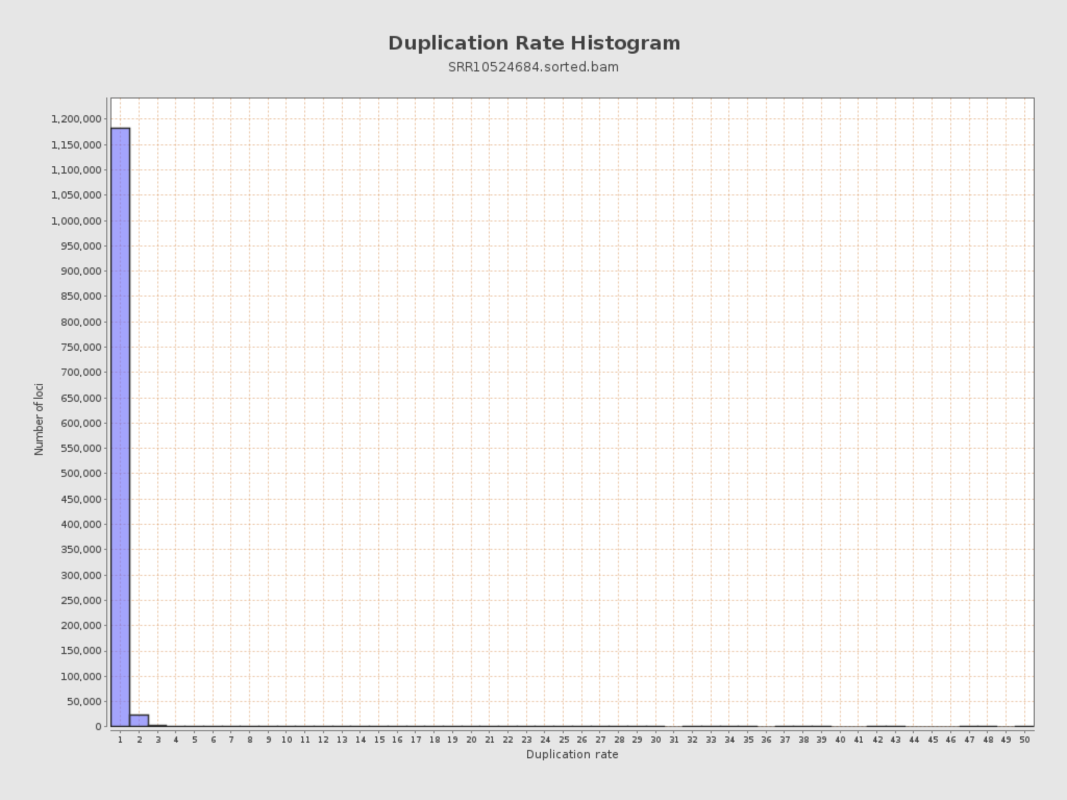
5. Results : Coverage Histogram (0-50X)



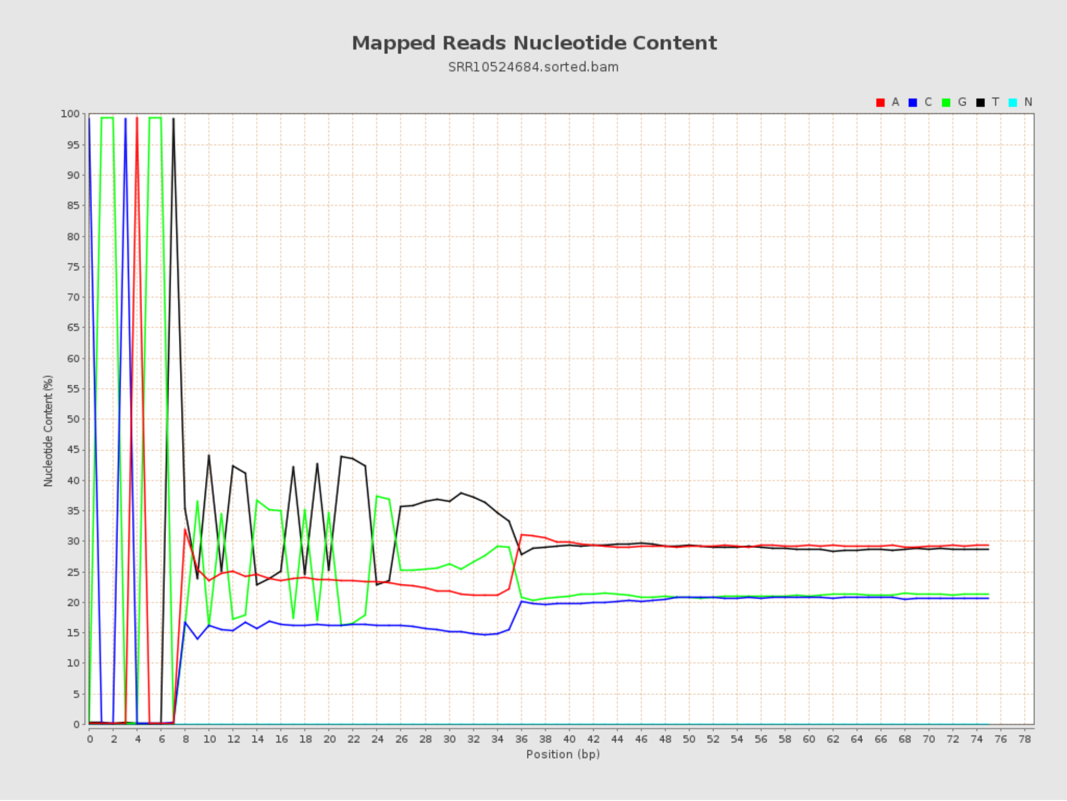
6. Results : Genome Fraction Coverage



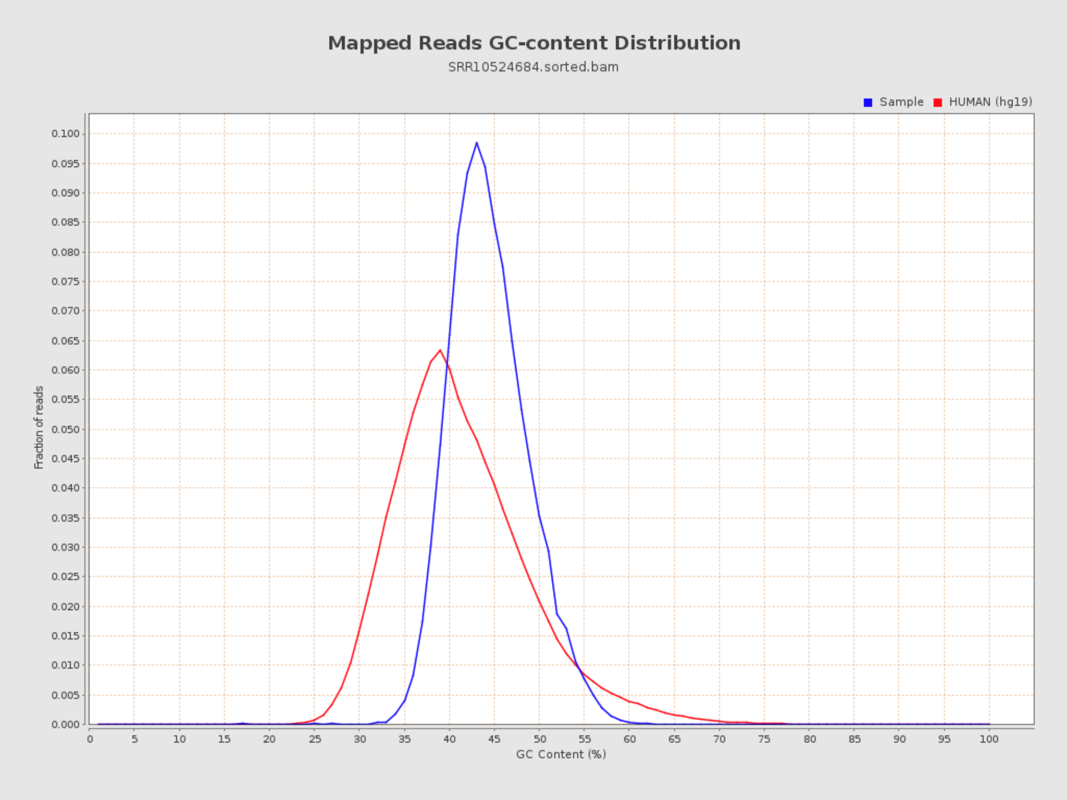
7. Results : Duplication Rate Histogram



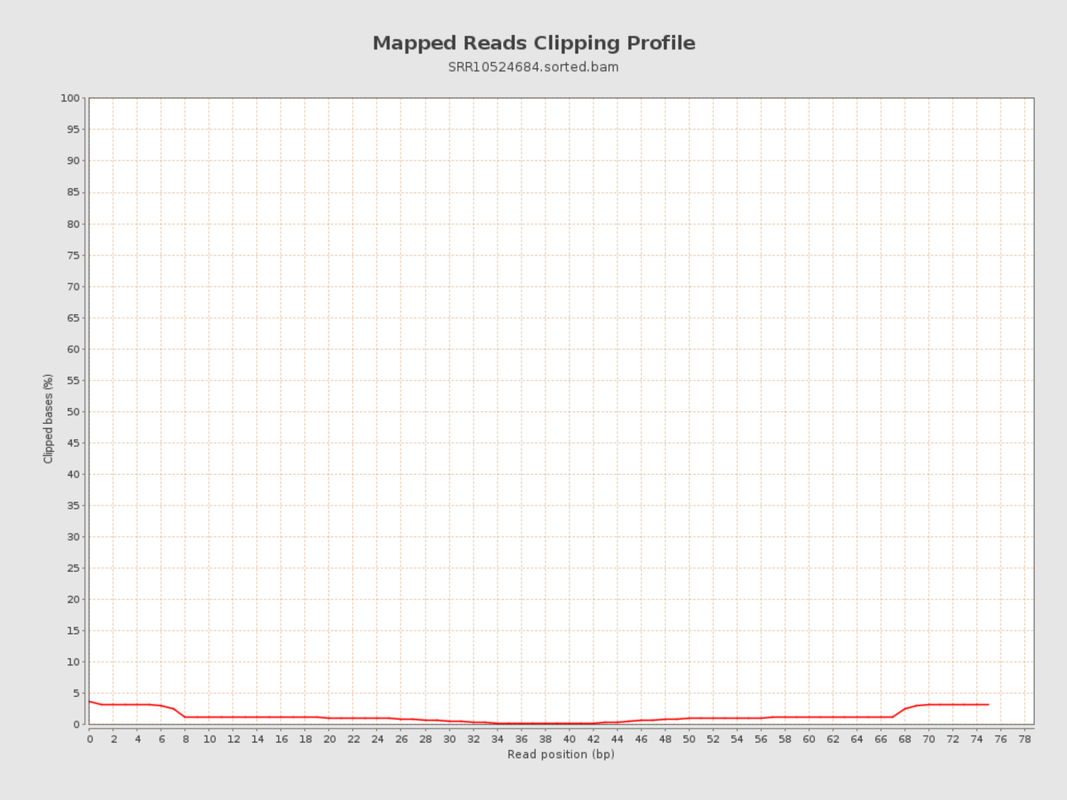
8. Results : Mapped Reads Nucleotide Content



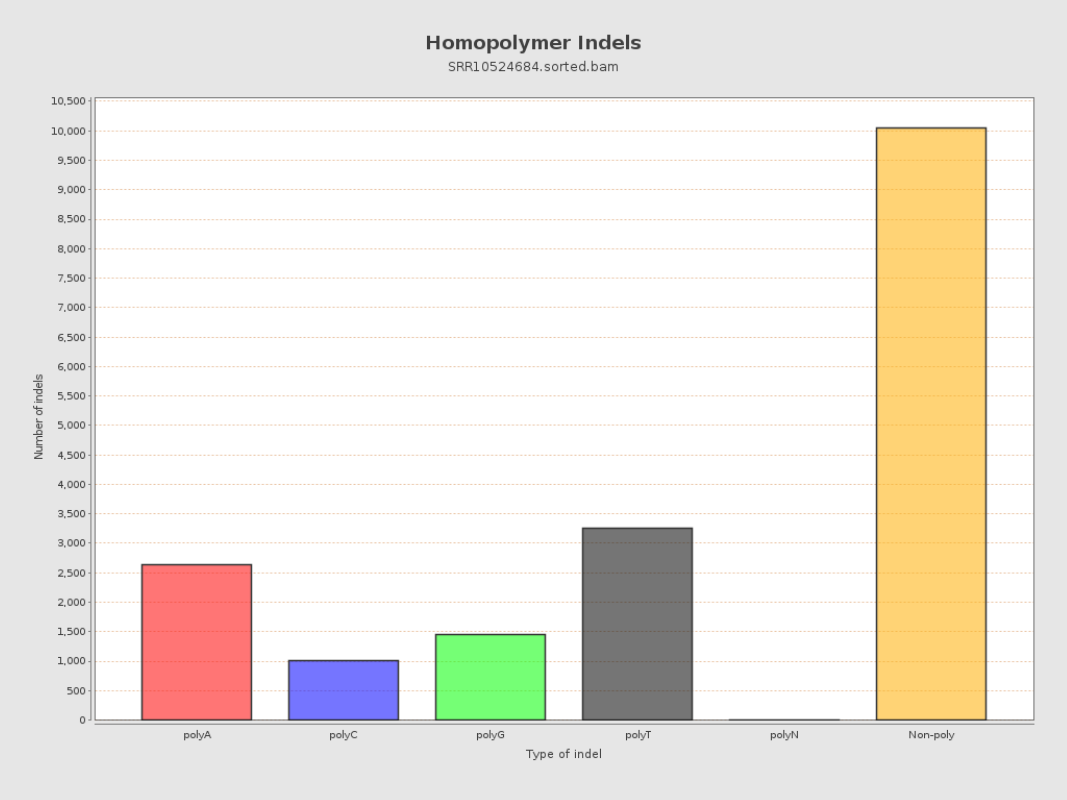
9. Results : Mapped Reads GC-content Distribution



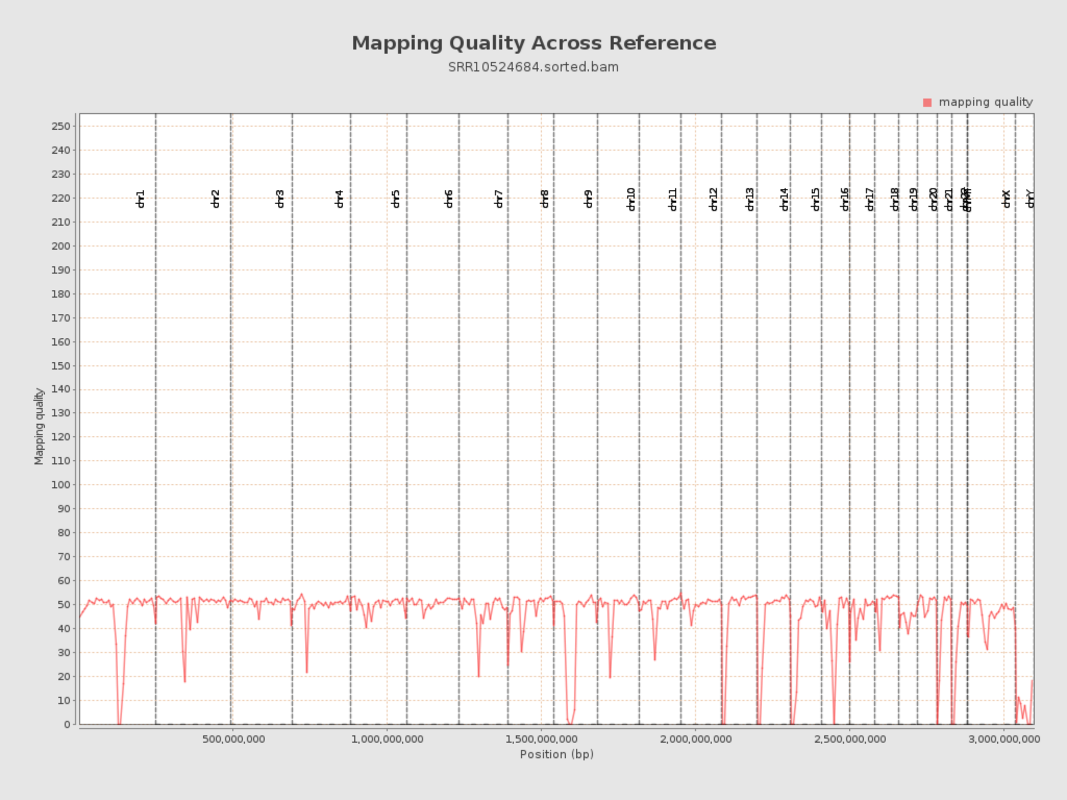
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram