Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/01 20:04:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524607.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_SRR10524607 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524607.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 01 20:04:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524607.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,427,658
Mapped reads	1,335,617 / 93.55%
Unmapped reads	92,041 / 6.45%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,728 / 0.19%
Read min/max/mean length	30 / 76 / 76.06
Duplicated reads (estimated)	55,636 / 3.9%
Duplication rate	3.26%
Clipped reads	1,335,779 / 93.56%

2.2. ACGT Content

Number/percentage of A's	18,446,060 / 23.77%
Number/percentage of C's	14,324,018 / 18.46%
Number/percentage of T's	25,045,734 / 32.27%
Number/percentage of G's	19,785,941 / 25.5%
Number/percentage of N's	482 / 0%
GC Percentage	43.95%

2.3. Coverage

Mean	0.0251

Standard Deviation	0.2296

2.4. Mapping Quality

Mean Mapping Quality	45.42

2.5. Mismatches and indels

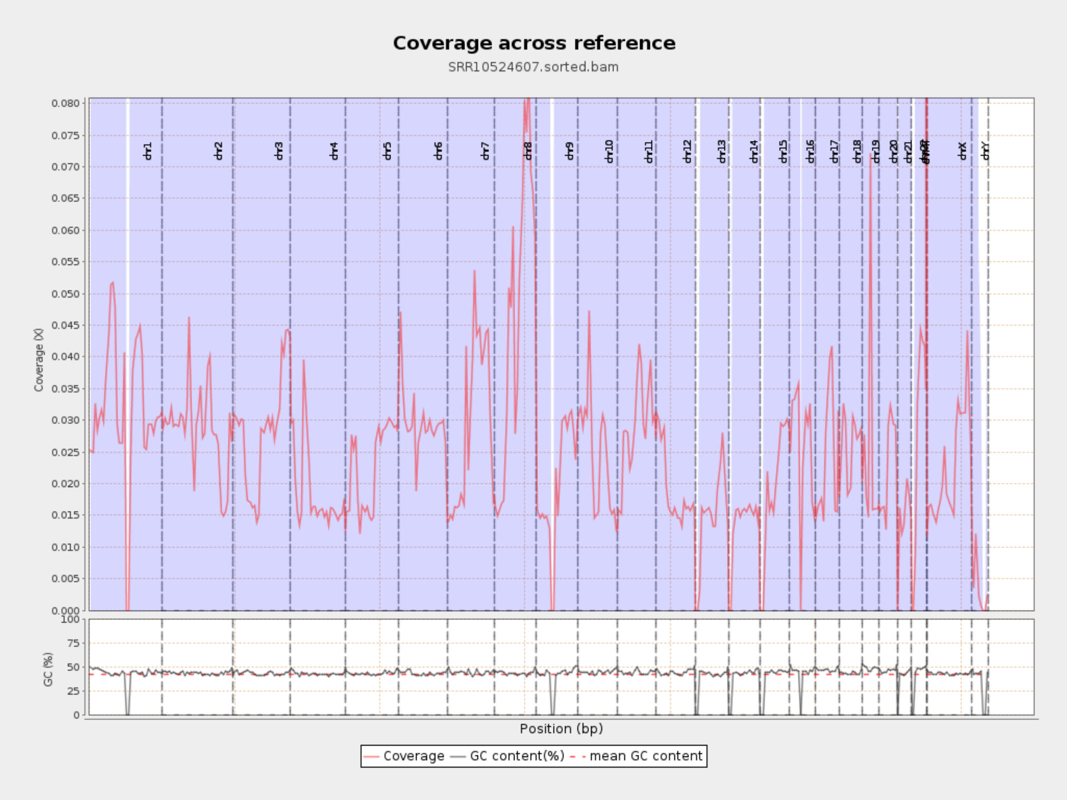
General error rate	0.46%
Mismatches	350,905
Insertions	4,668
Mapped reads with at least one insertion	0.35%
Deletions	14,689
Mapped reads with at least one deletion	1.09%
Homopolymer indels	43.87%

2.6. Chromosome stats

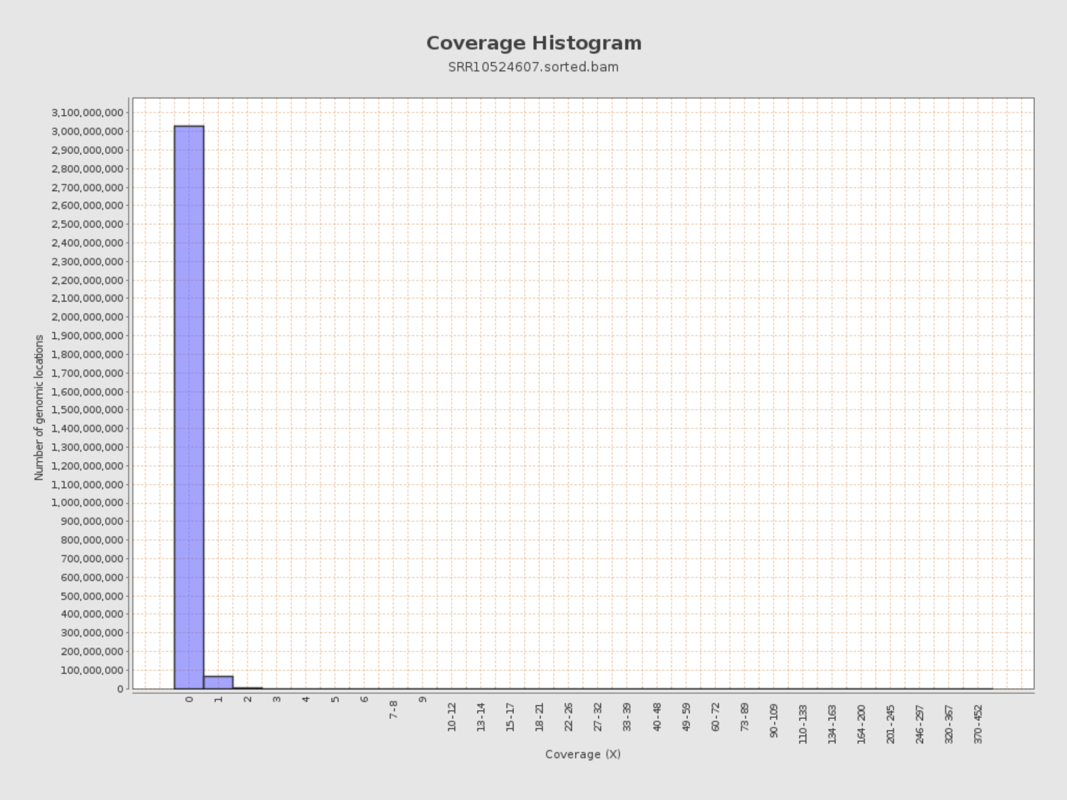
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7945543	0.0319	0.3675
chr2	243199373	6978738	0.0287	0.2747
chr3	198022430	5595746	0.0283	0.1843
chr4	191154276	3552560	0.0186	0.1704
chr5	180915260	4098552	0.0227	0.1654
chr6	171115067	5083744	0.0297	0.2016
chr7	159138663	4750763	0.0299	0.3152

chr8	146364022	6820415	0.0466	0.2923
chr9	141213431	2762647	0.0196	0.202
chr10	135534747	3341907	0.0247	0.2368
chr11	135006516	3916679	0.029	0.2295
chr12	133851895	2538773	0.019	0.1554
chr13	115169878	1708251	0.0148	0.1337
chr14	107349540	1441582	0.0134	0.1304
chr15	102531392	1969132	0.0192	0.1579
chr16	90354753	2333204	0.0258	0.1844
chr17	81195210	1972580	0.0243	0.1766
chr18	78077248	2060982	0.0264	0.3198
chr19	59128983	1487972	0.0252	0.2657
chr20	63025520	1442352	0.0229	0.1707
chr21	48129895	698405	0.0145	0.1472
chr22	51304566	1388753	0.0271	0.1805
chrMT	16571	14835	0.8952	1.0585
chrX	155270560	3526211	0.0227	0.1862
chrY	59373566	196999	0.0033	0.1044

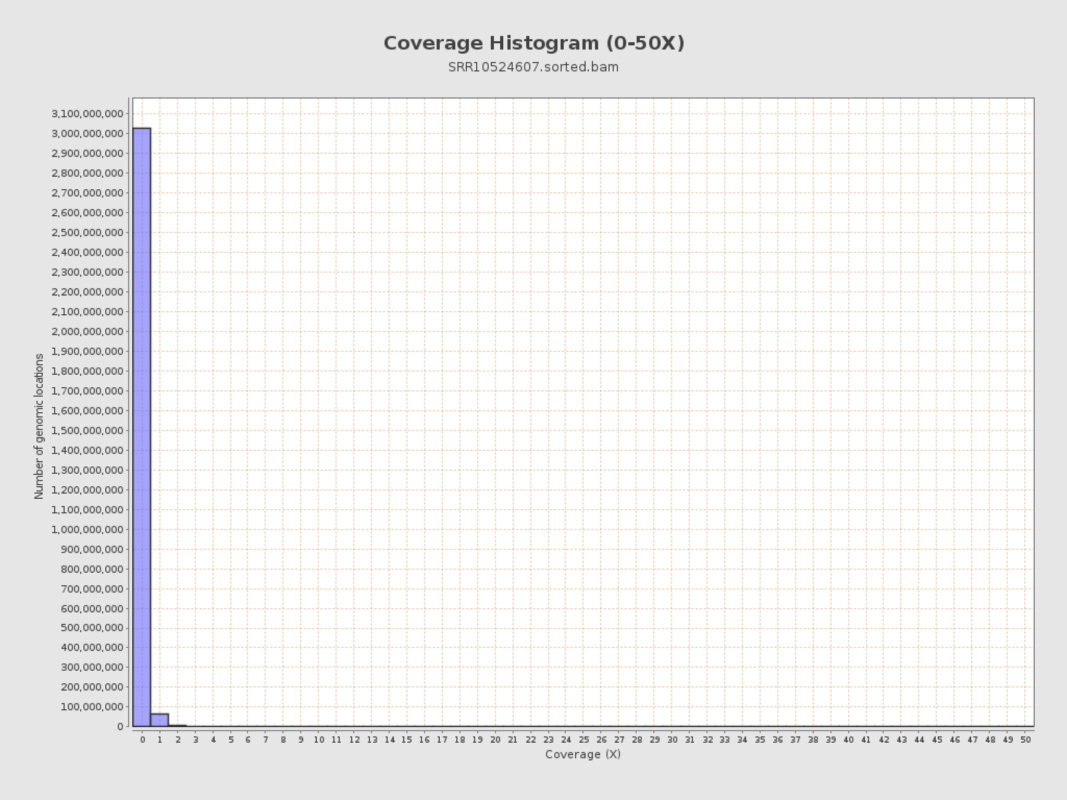
3. Results : Coverage across reference



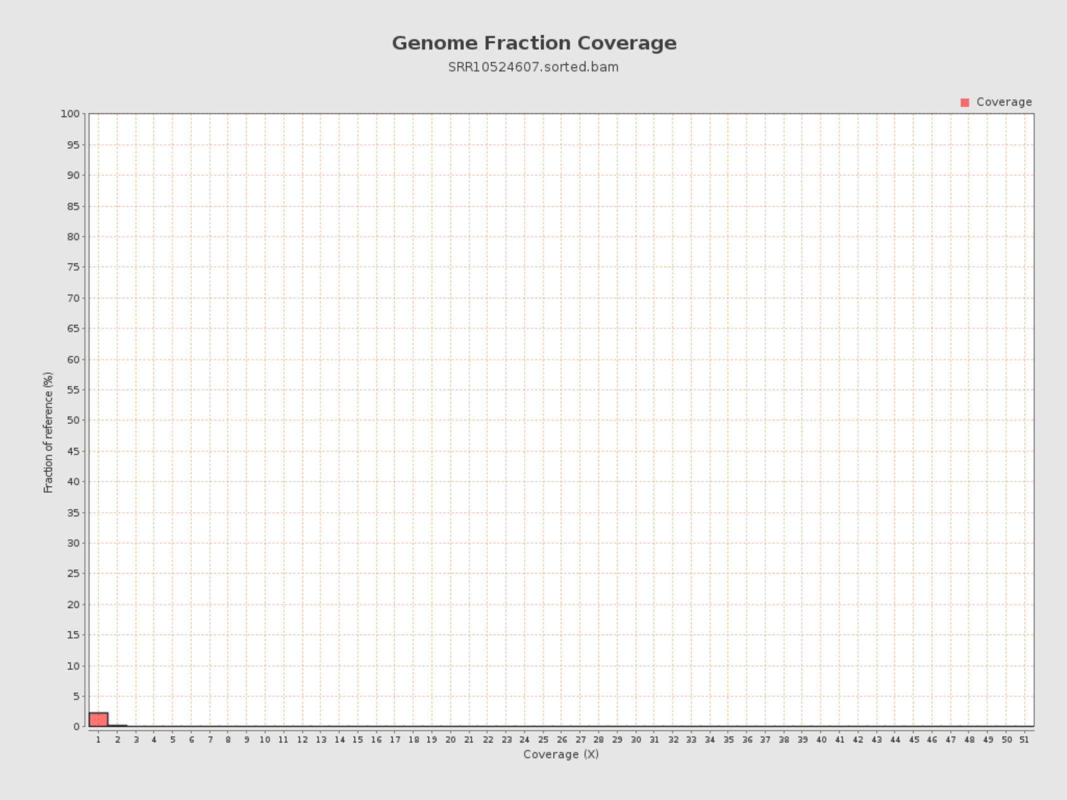
4. Results : Coverage Histogram



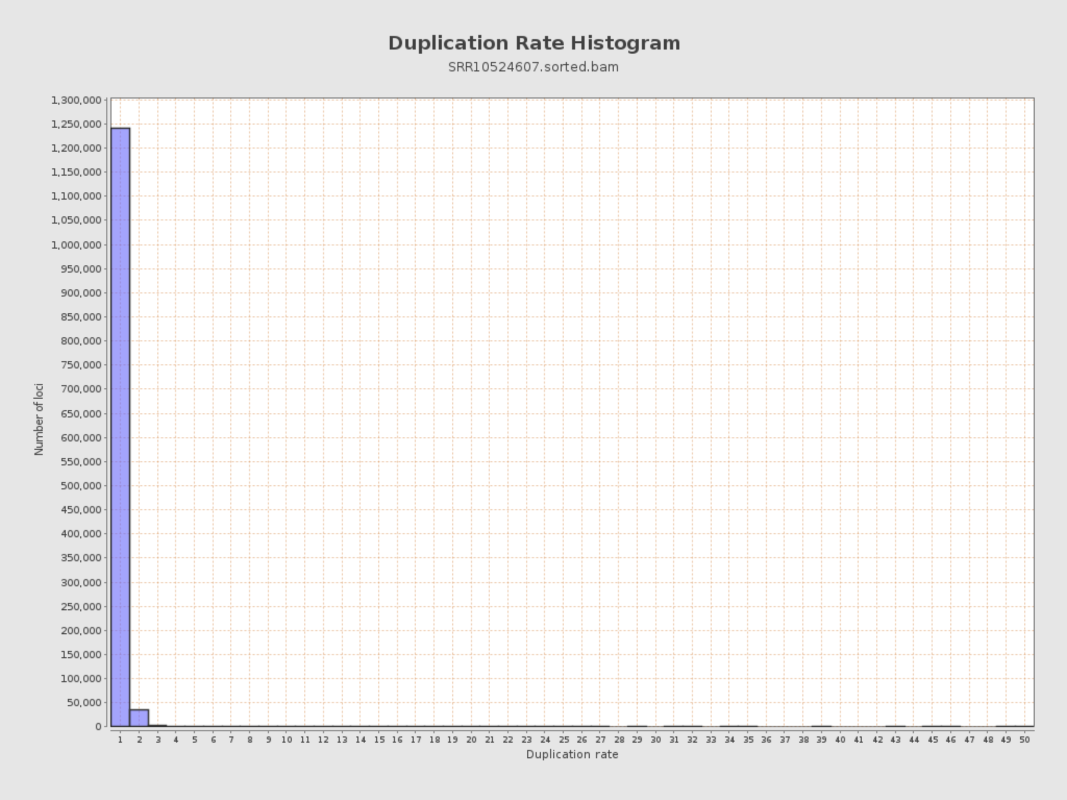
5. Results : Coverage Histogram (0-50X)



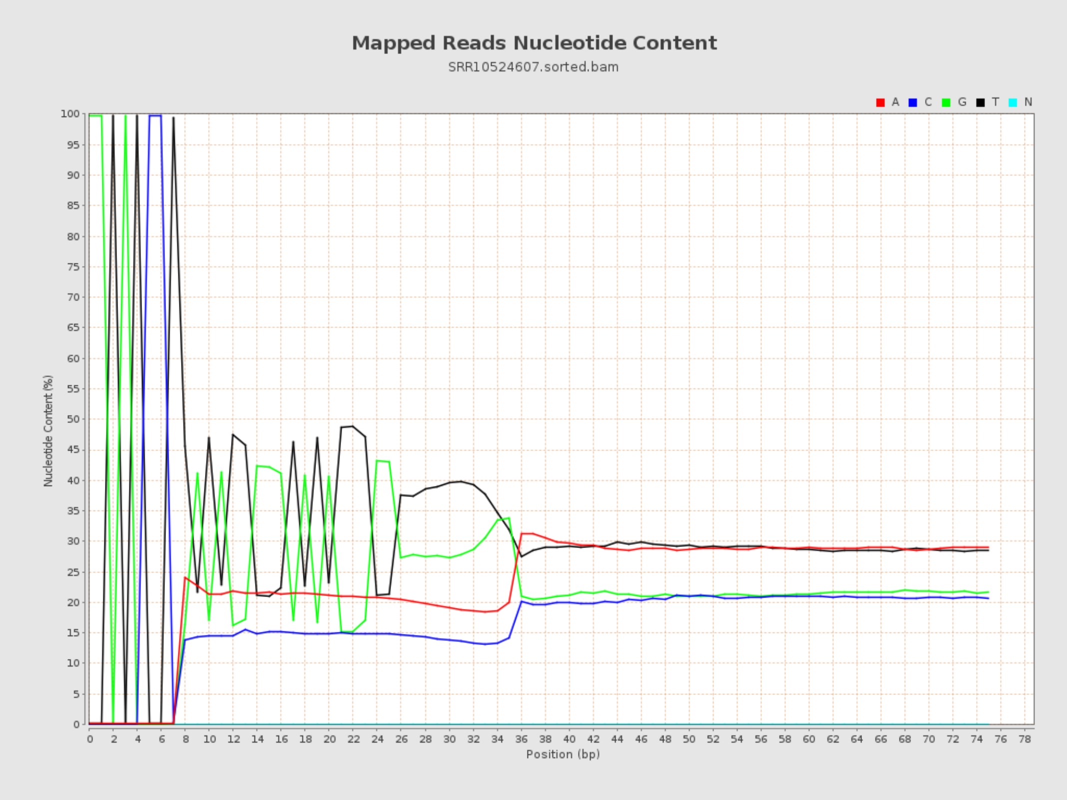
6. Results : Genome Fraction Coverage



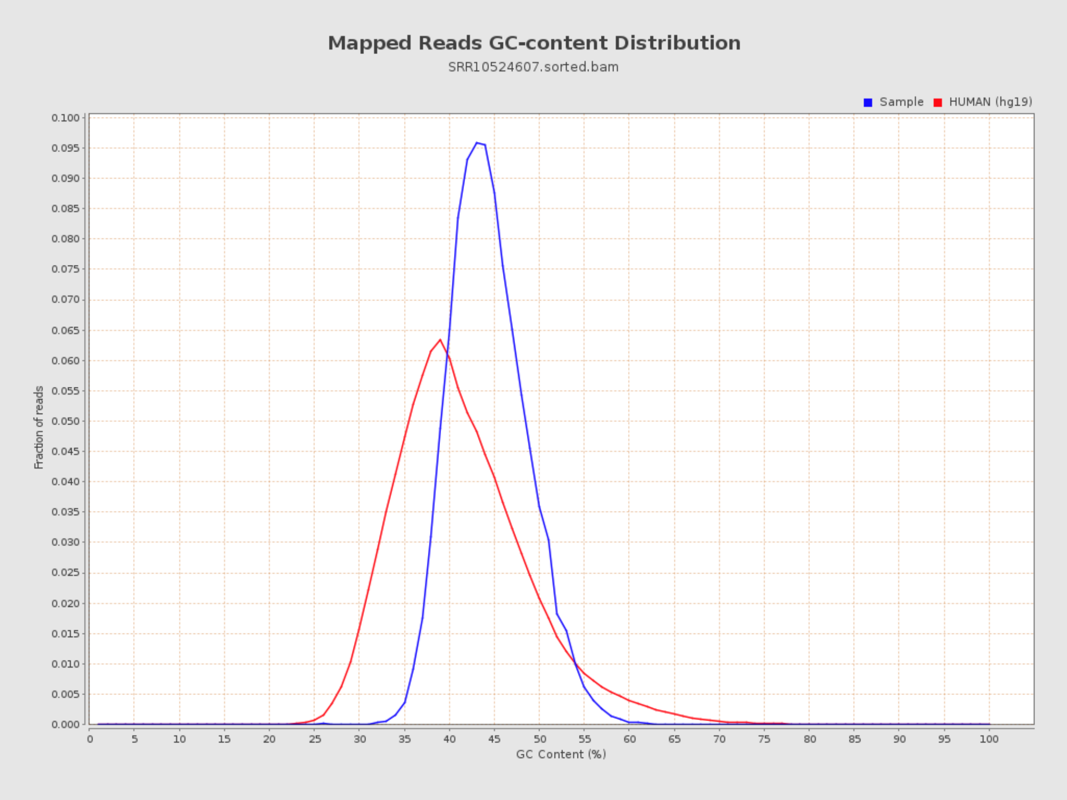
7. Results : Duplication Rate Histogram



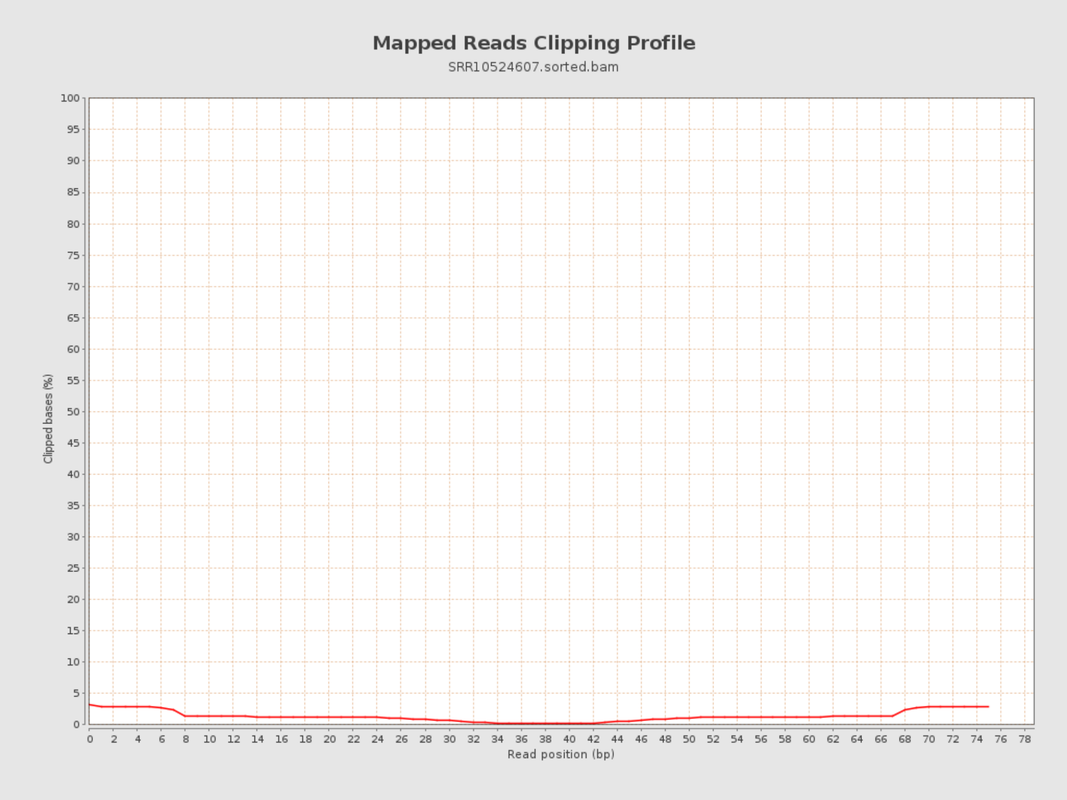
8. Results : Mapped Reads Nucleotide Content



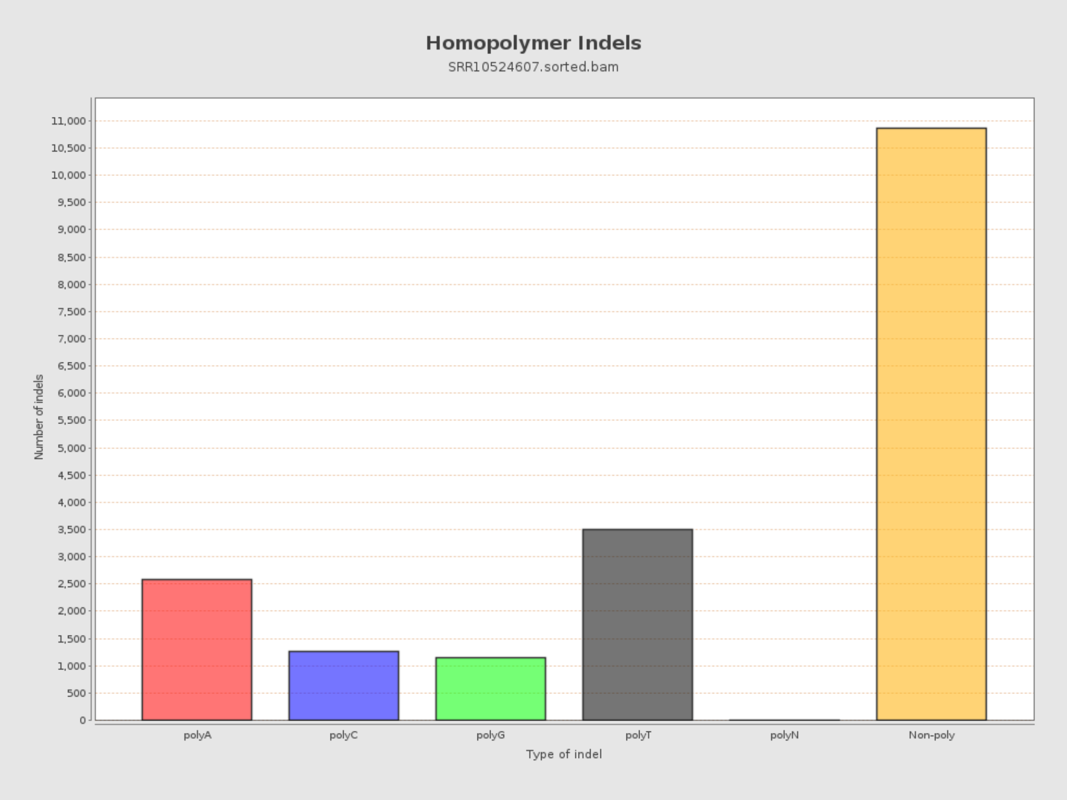
9. Results : Mapped Reads GC-content Distribution



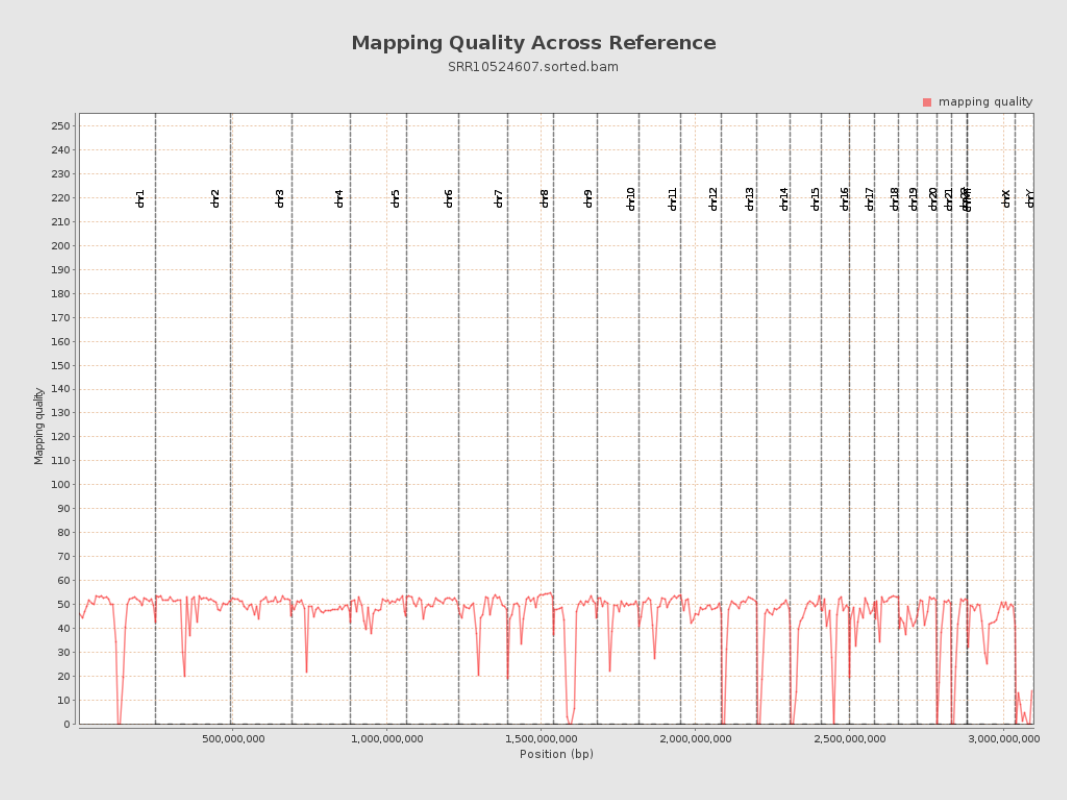
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram