Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 20:20:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524779.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_SRR10524779 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524779.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 20:20:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524779.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,503,592
Mapped reads	1,363,773 / 90.7%
Unmapped reads	139,819 / 9.3%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,834 / 0.32%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	55,882 / 3.72%
Duplication rate	3.16%
Clipped reads	1,365,383 / 90.81%

2.2. ACGT Content

Number/percentage of A's	18,977,969 / 24.6%
Number/percentage of C's	14,031,270 / 18.19%
Number/percentage of T's	25,290,795 / 32.78%
Number/percentage of G's	18,849,245 / 24.43%
Number/percentage of N's	9,006 / 0.01%
GC Percentage	42.61%

2.3. Coverage

Mean	0.0249

Standard Deviation	0.2341

2.4. Mapping Quality

Mean Mapping Quality	44.29

2.5. Mismatches and indels

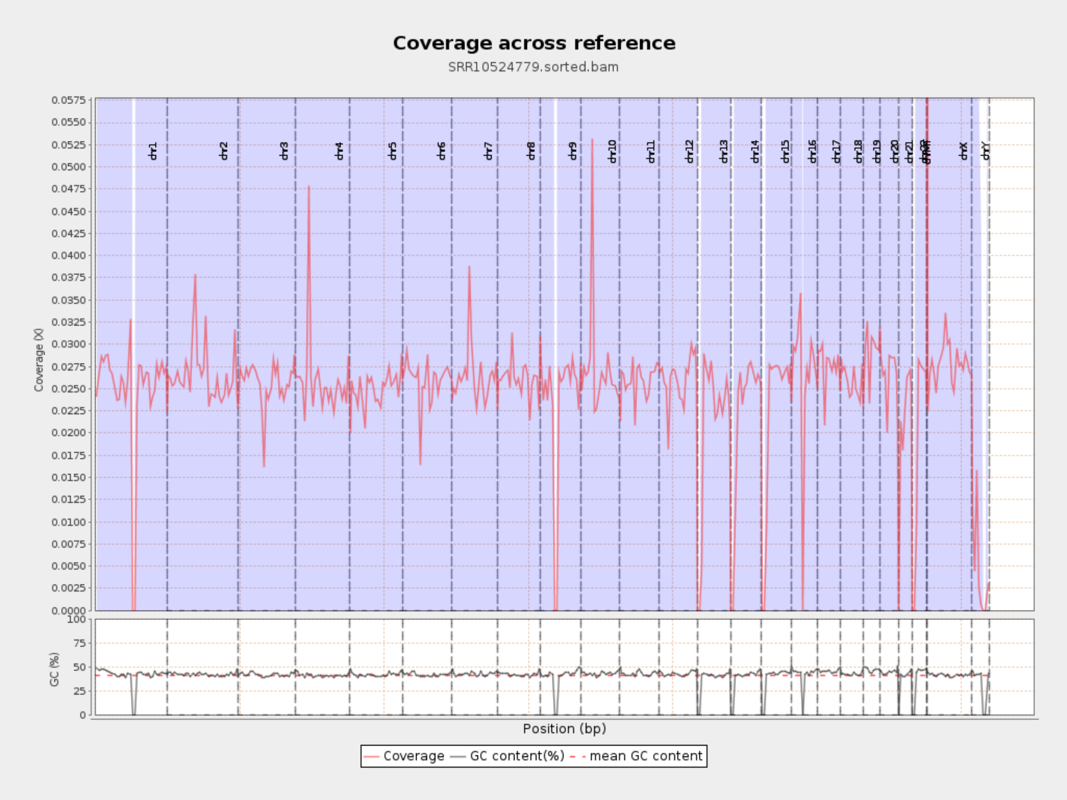
General error rate	0.53%
Mismatches	393,385
Insertions	5,862
Mapped reads with at least one insertion	0.43%
Deletions	15,033
Mapped reads with at least one deletion	1.09%
Homopolymer indels	41.98%

2.6. Chromosome stats

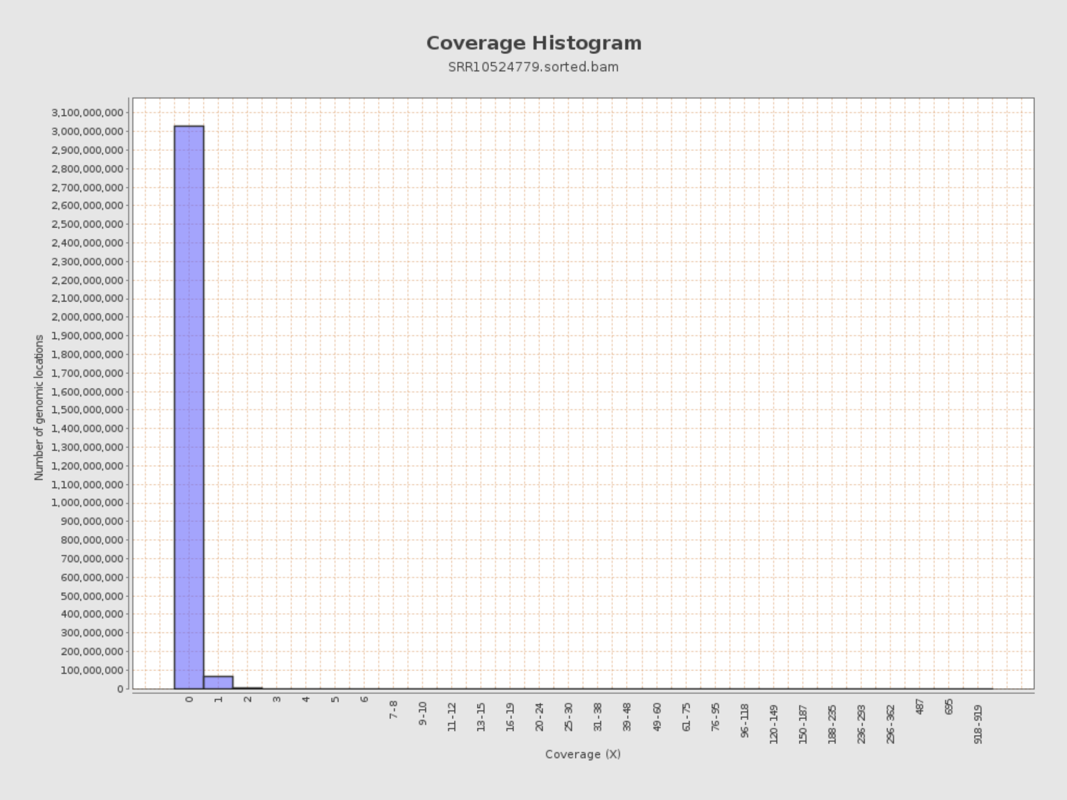
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6164124	0.0247	0.2983
chr2	243199373	6483715	0.0267	0.4103
chr3	198022430	5062454	0.0256	0.1775
chr4	191154276	4961040	0.026	0.2029
chr5	180915260	4532758	0.0251	0.1735
chr6	171115067	4432925	0.0259	0.1987
chr7	159138663	4218849	0.0265	0.2644

chr8	146364022	3818860	0.0261	0.2085
chr9	141213431	3271068	0.0232	0.1977
chr10	135534747	3711588	0.0274	0.2679
chr11	135006516	3503374	0.0259	0.2069
chr12	133851895	3483398	0.026	0.1788
chr13	115169878	2398825	0.0208	0.1597
chr14	107349540	2315651	0.0216	0.1654
chr15	102531392	2240441	0.0219	0.1641
chr16	90354753	2352373	0.026	0.1938
chr17	81195210	2239408	0.0276	0.1899
chr18	78077248	2009900	0.0257	0.2915
chr19	59128983	1728611	0.0292	0.2597
chr20	63025520	1667085	0.0265	0.1881
chr21	48129895	1016584	0.0211	0.1783
chr22	51304566	966493	0.0188	0.1534
chrMT	16571	23396	1.4119	1.3274
chrX	155270560	4316410	0.0278	0.1947
chrY	59373566	263293	0.0044	0.1243

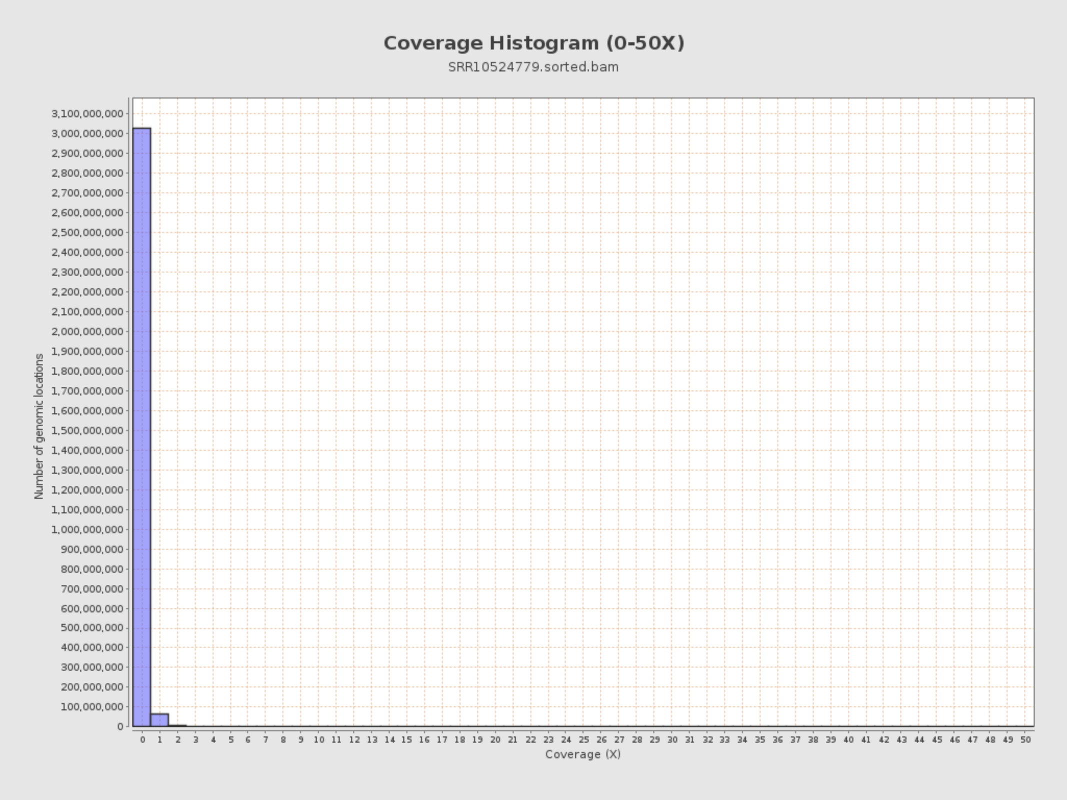
3. Results : Coverage across reference



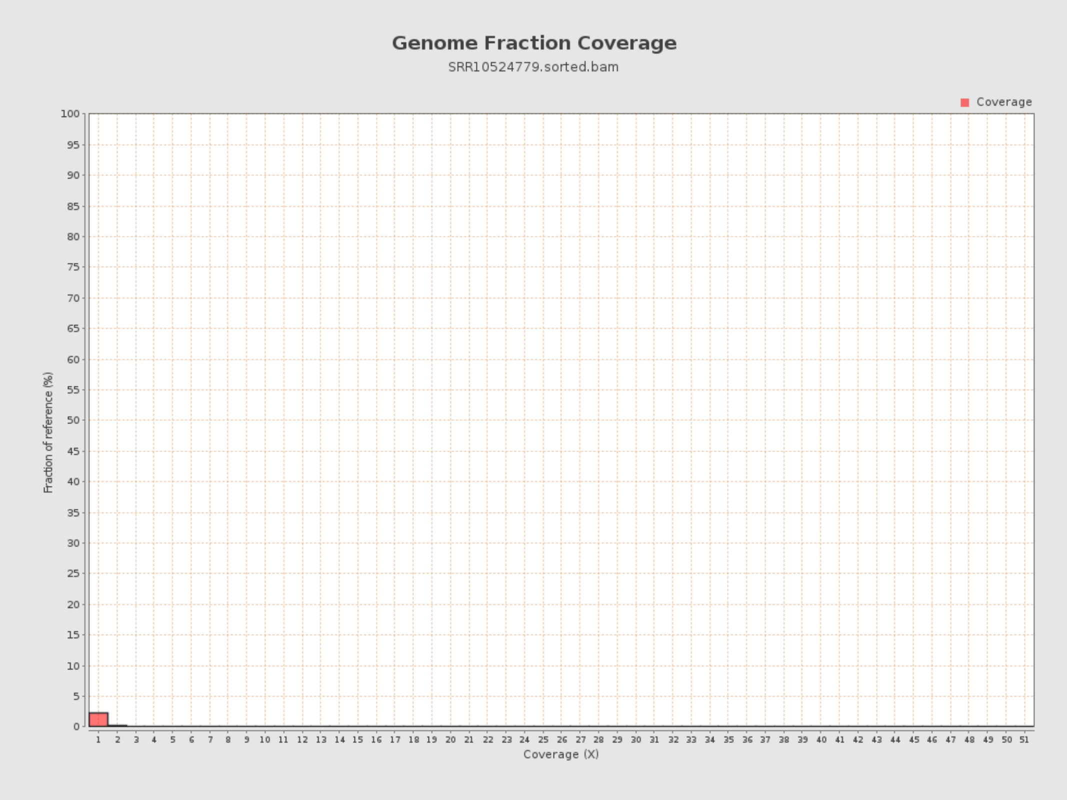
4. Results : Coverage Histogram



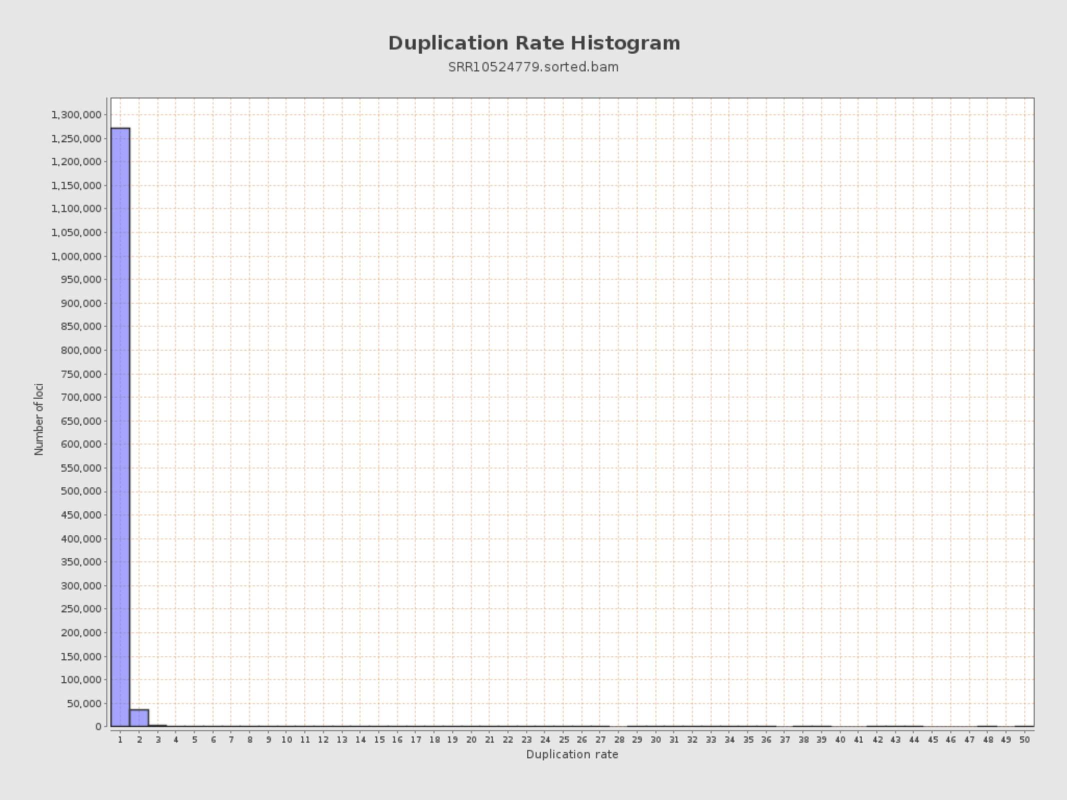
5. Results : Coverage Histogram (0-50X)



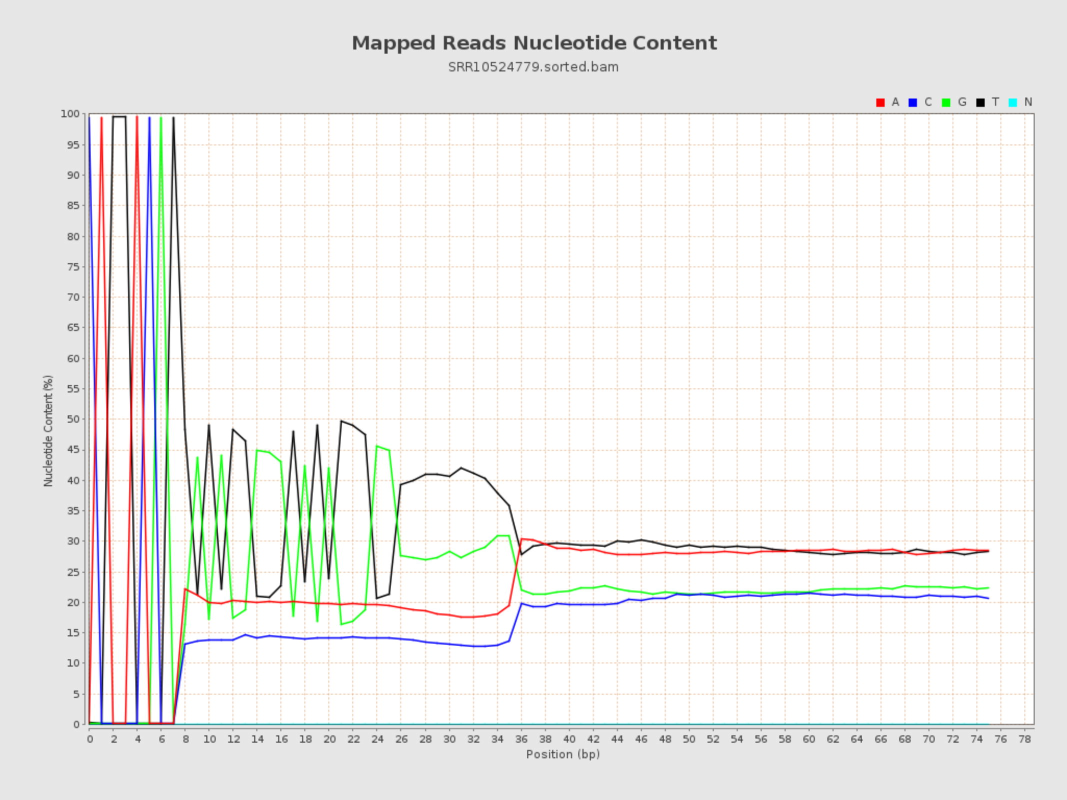
6. Results : Genome Fraction Coverage



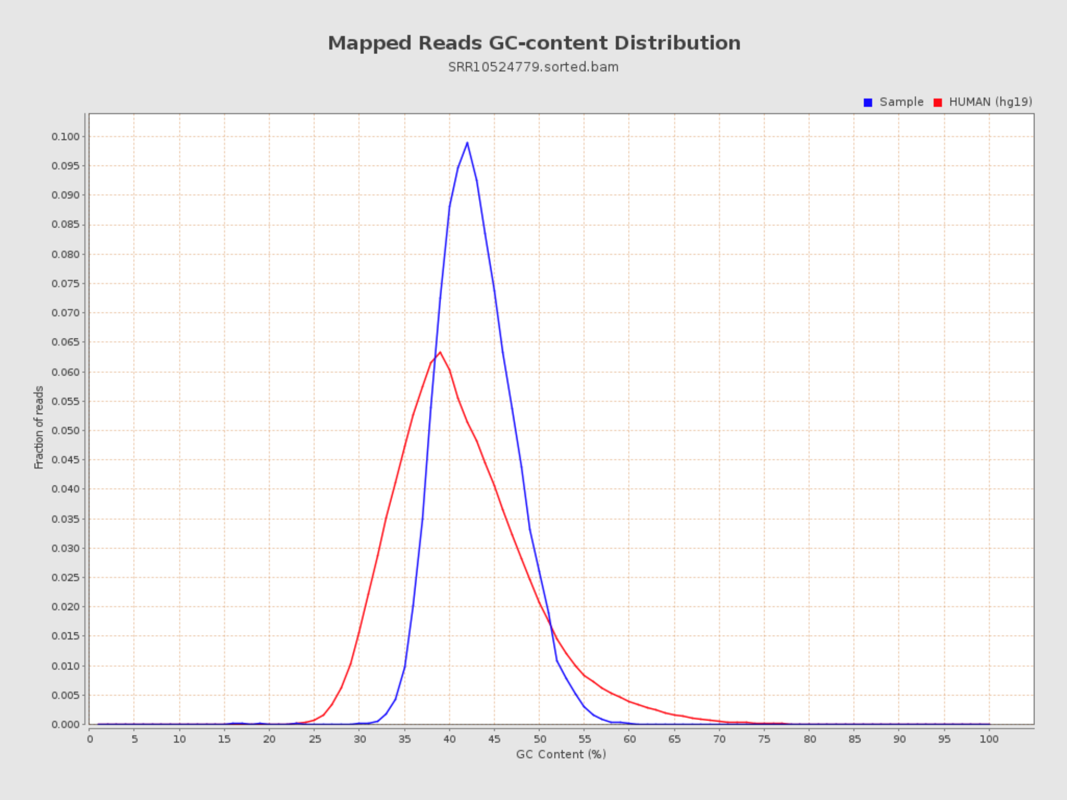
7. Results : Duplication Rate Histogram



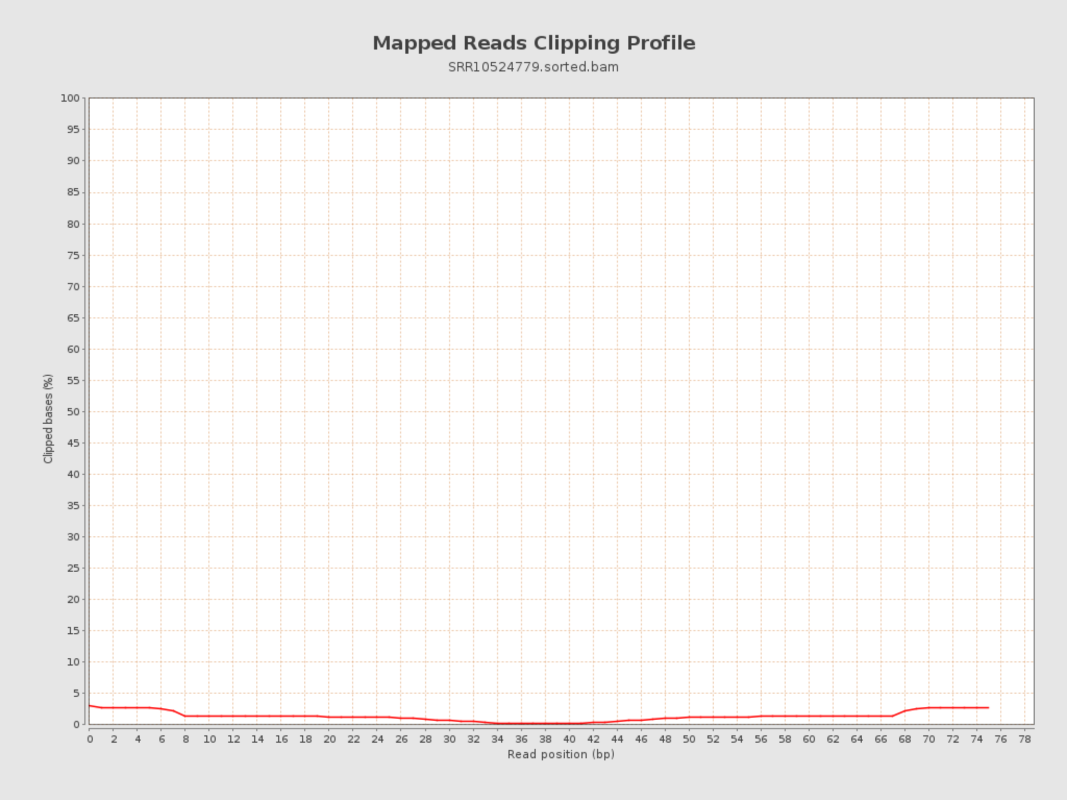
8. Results : Mapped Reads Nucleotide Content



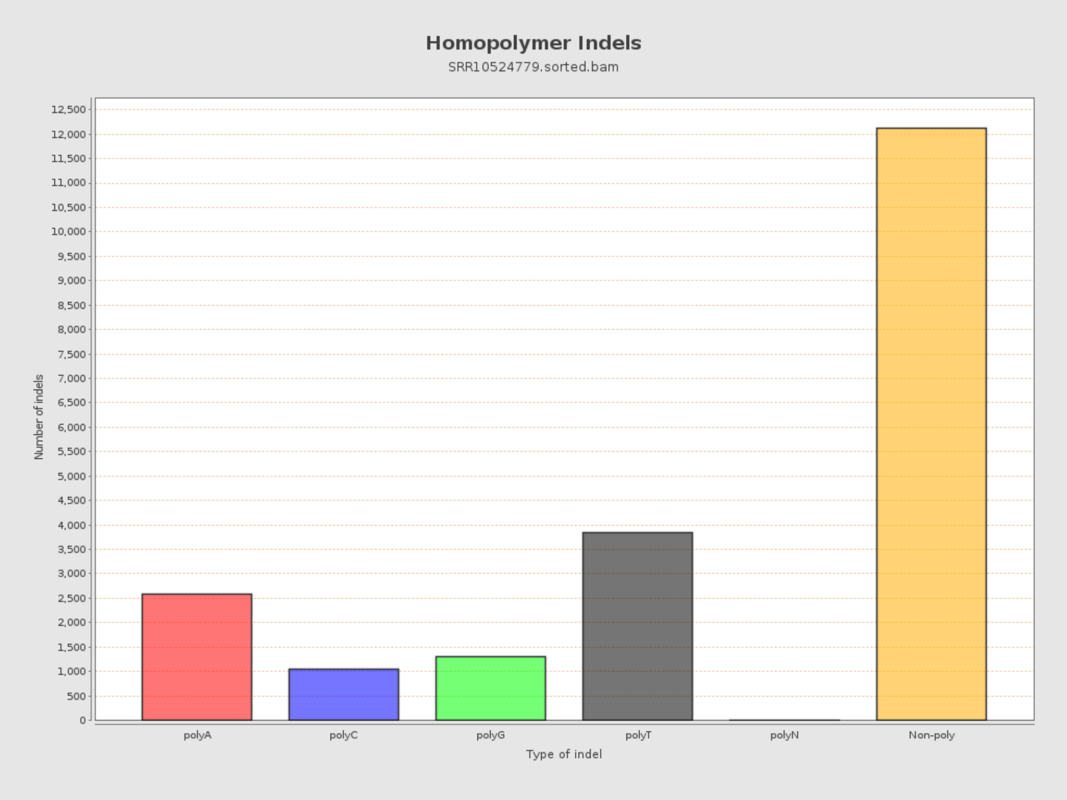
9. Results : Mapped Reads GC-content Distribution



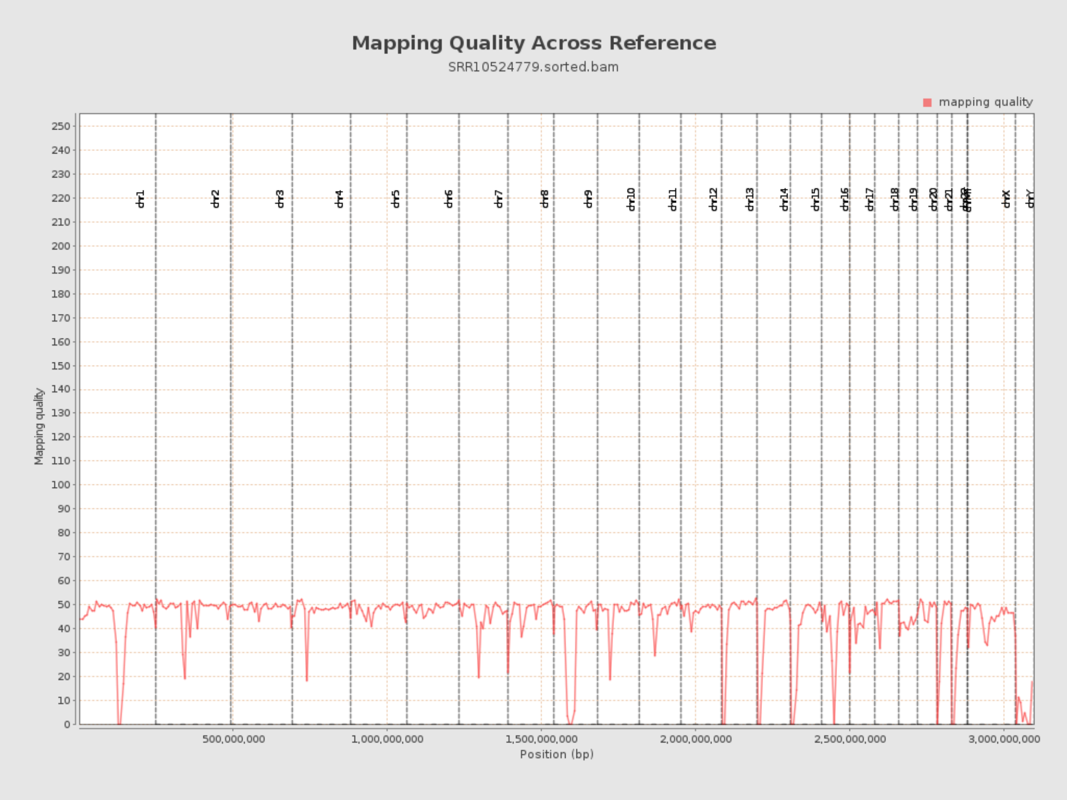
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram