Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 20:15:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524777.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_SRR10524777 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524777.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 20:15:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524777.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,471,586
Mapped reads	1,340,214 / 91.07%
Unmapped reads	131,372 / 8.93%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,842 / 0.33%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	53,214 / 3.62%
Duplication rate	3.02%
Clipped reads	1,341,167 / 91.14%

2.2. ACGT Content

Number/percentage of A's	17,829,651 / 23.3%
Number/percentage of C's	14,705,019 / 19.22%
Number/percentage of T's	25,518,538 / 33.35%
Number/percentage of G's	18,463,003 / 24.13%
Number/percentage of N's	9,530 / 0.01%
GC Percentage	43.34%

2.3. Coverage

Mean	0.0247

Standard Deviation	0.2314

2.4. Mapping Quality

Mean Mapping Quality	44.6

2.5. Mismatches and indels

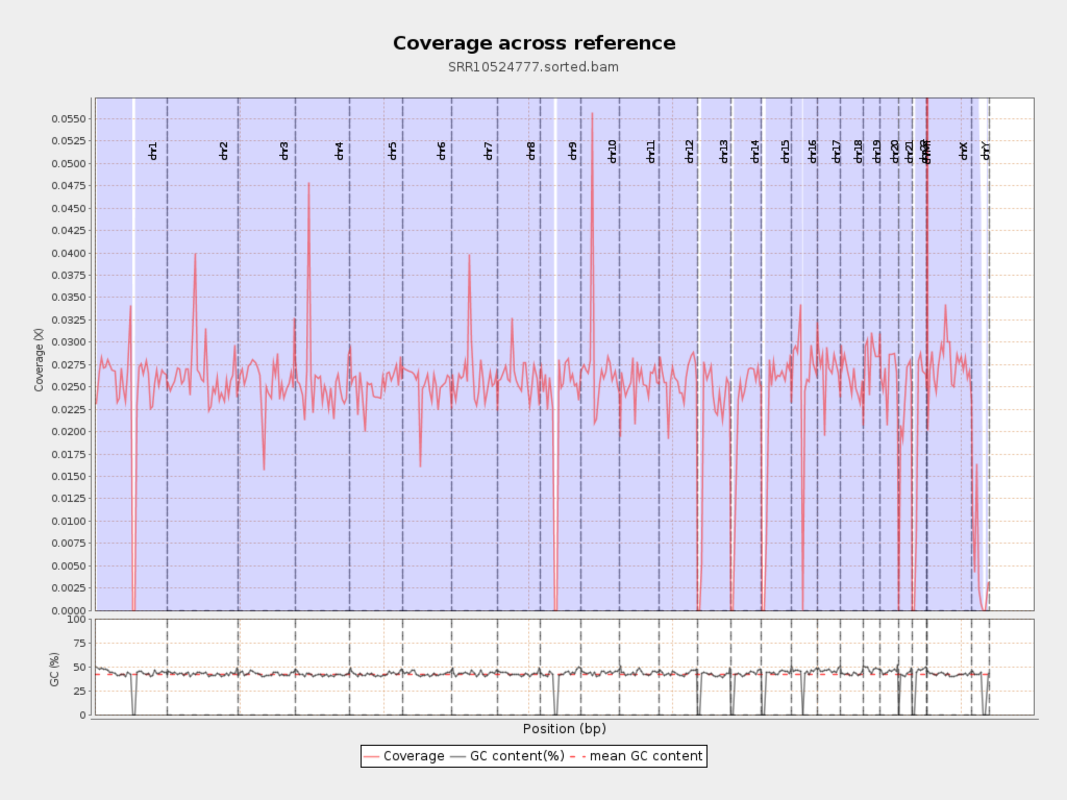
General error rate	0.52%
Mismatches	389,124
Insertions	5,570
Mapped reads with at least one insertion	0.41%
Deletions	15,303
Mapped reads with at least one deletion	1.13%
Homopolymer indels	42.92%

2.6. Chromosome stats

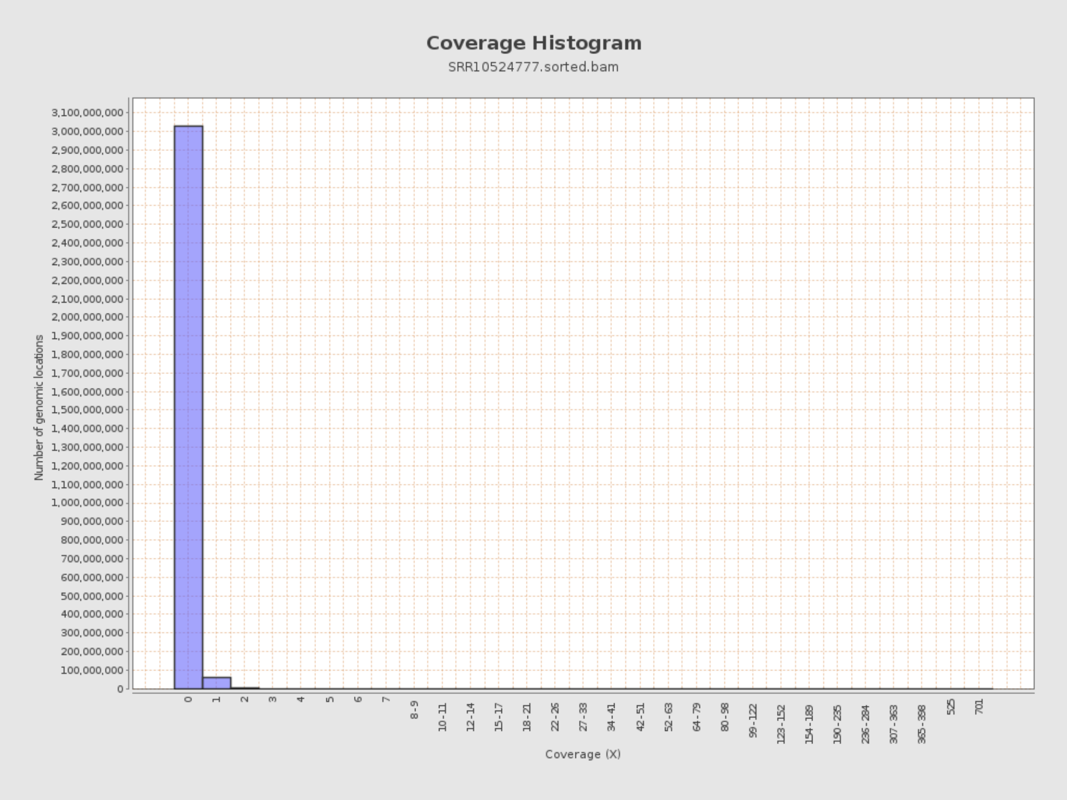
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6127654	0.0246	0.3221
chr2	243199373	6396385	0.0263	0.3562
chr3	198022430	5053735	0.0255	0.1769
chr4	191154276	4911379	0.0257	0.2033
chr5	180915260	4564397	0.0252	0.1731
chr6	171115067	4314648	0.0252	0.1878
chr7	159138663	4192514	0.0263	0.2786

chr8	146364022	3830333	0.0262	0.2161
chr9	141213431	3221860	0.0228	0.2019
chr10	135534747	3750106	0.0277	0.283
chr11	135006516	3446501	0.0255	0.205
chr12	133851895	3464132	0.0259	0.1787
chr13	115169878	2378021	0.0206	0.1578
chr14	107349540	2287814	0.0213	0.1625
chr15	102531392	2207238	0.0215	0.1622
chr16	90354753	2303394	0.0255	0.1947
chr17	81195210	2186820	0.0269	0.1869
chr18	78077248	2023286	0.0259	0.3086
chr19	59128983	1681666	0.0284	0.255
chr20	63025520	1650511	0.0262	0.1841
chr21	48129895	1042906	0.0217	0.1775
chr22	51304566	968357	0.0189	0.1517
chrMT	16571	13922	0.8401	1.1033
chrX	155270560	4266785	0.0275	0.1945
chrY	59373566	265774	0.0045	0.135

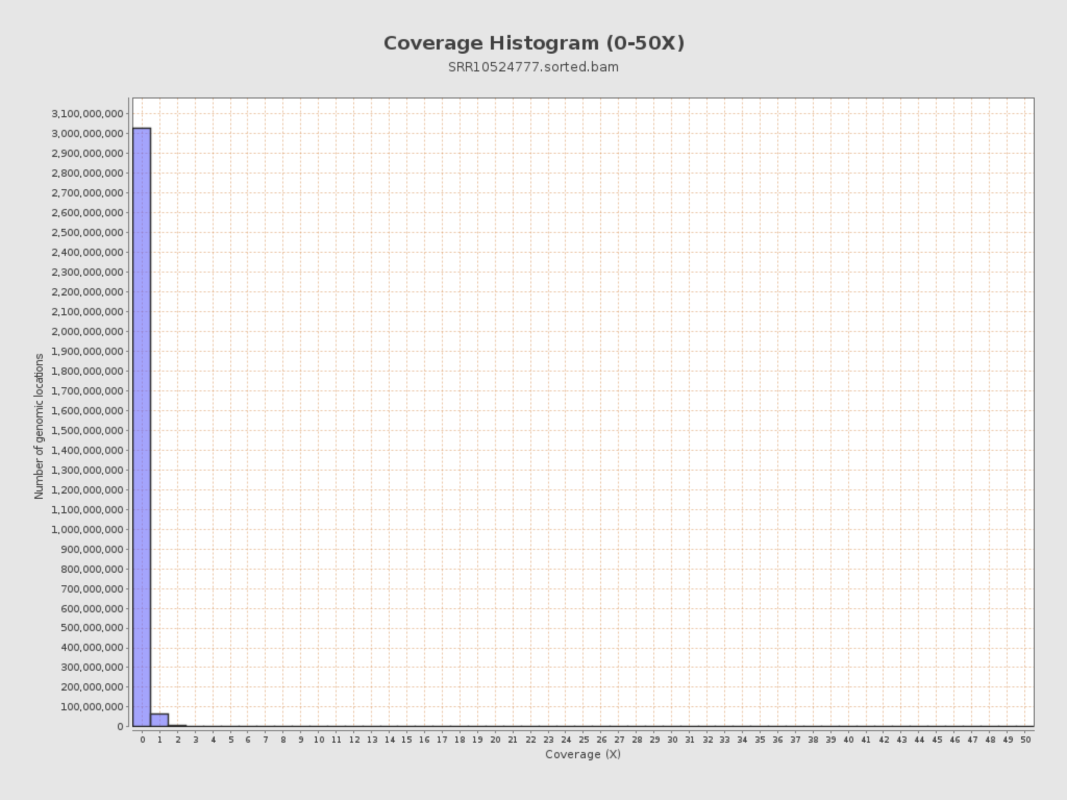
3. Results : Coverage across reference



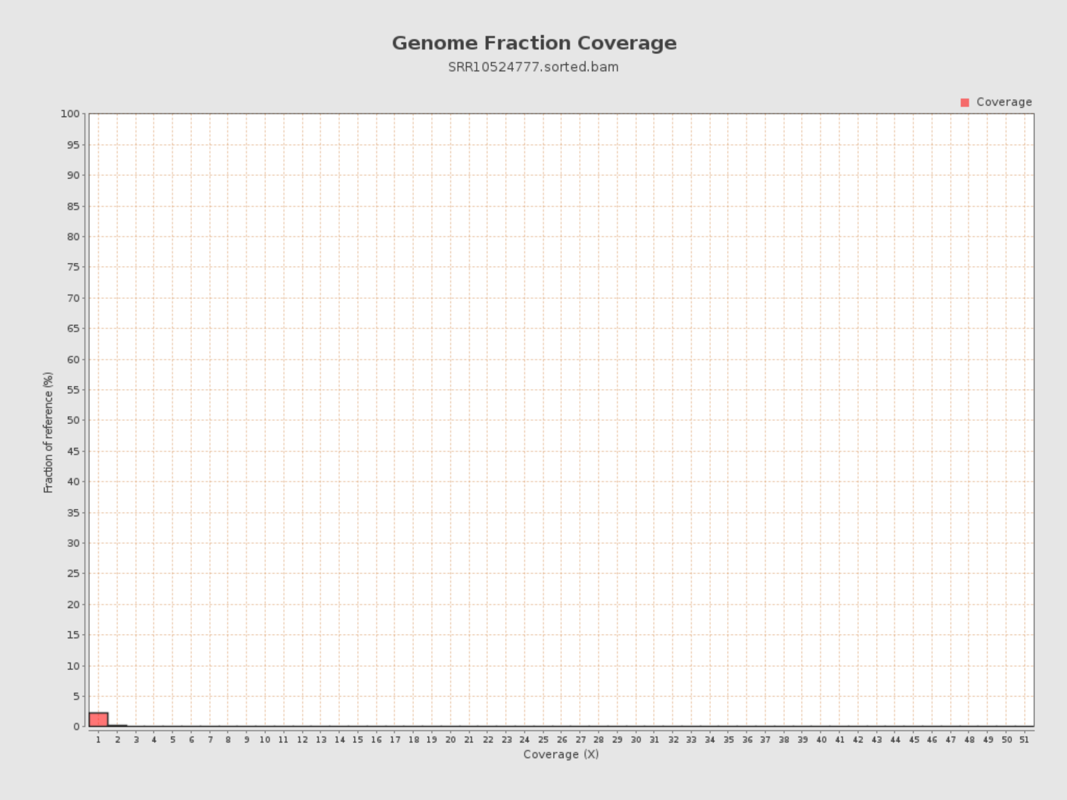
4. Results : Coverage Histogram



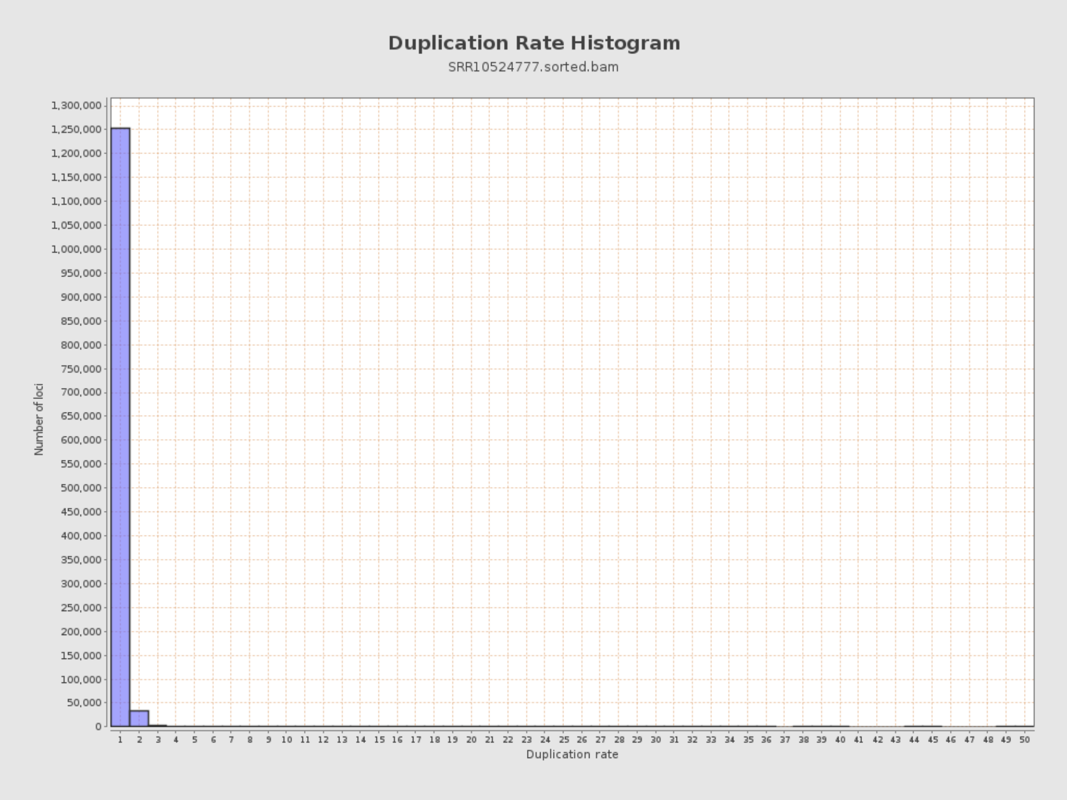
5. Results : Coverage Histogram (0-50X)



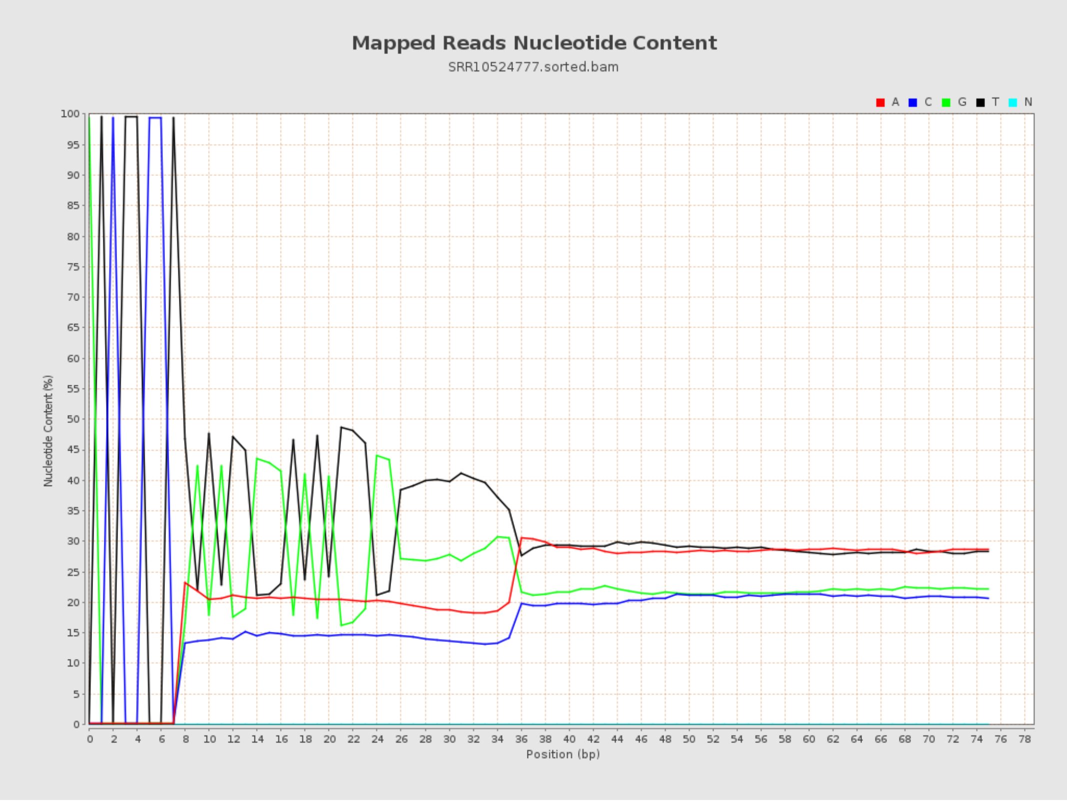
6. Results : Genome Fraction Coverage



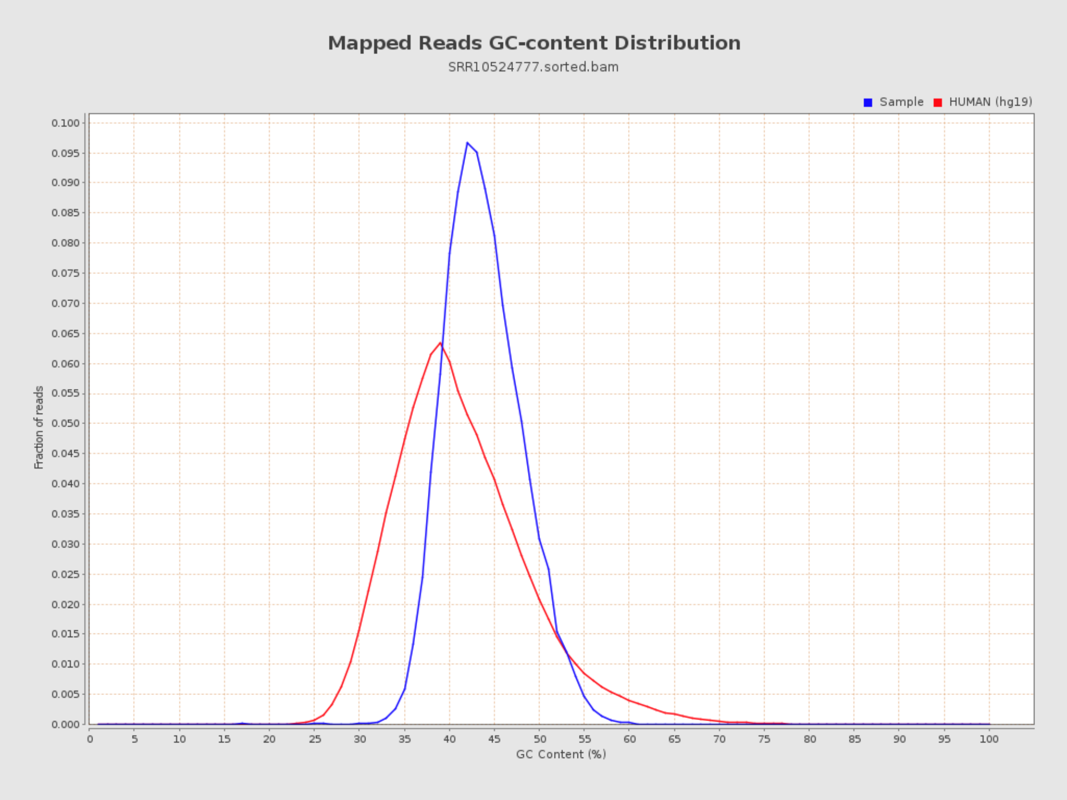
7. Results : Duplication Rate Histogram



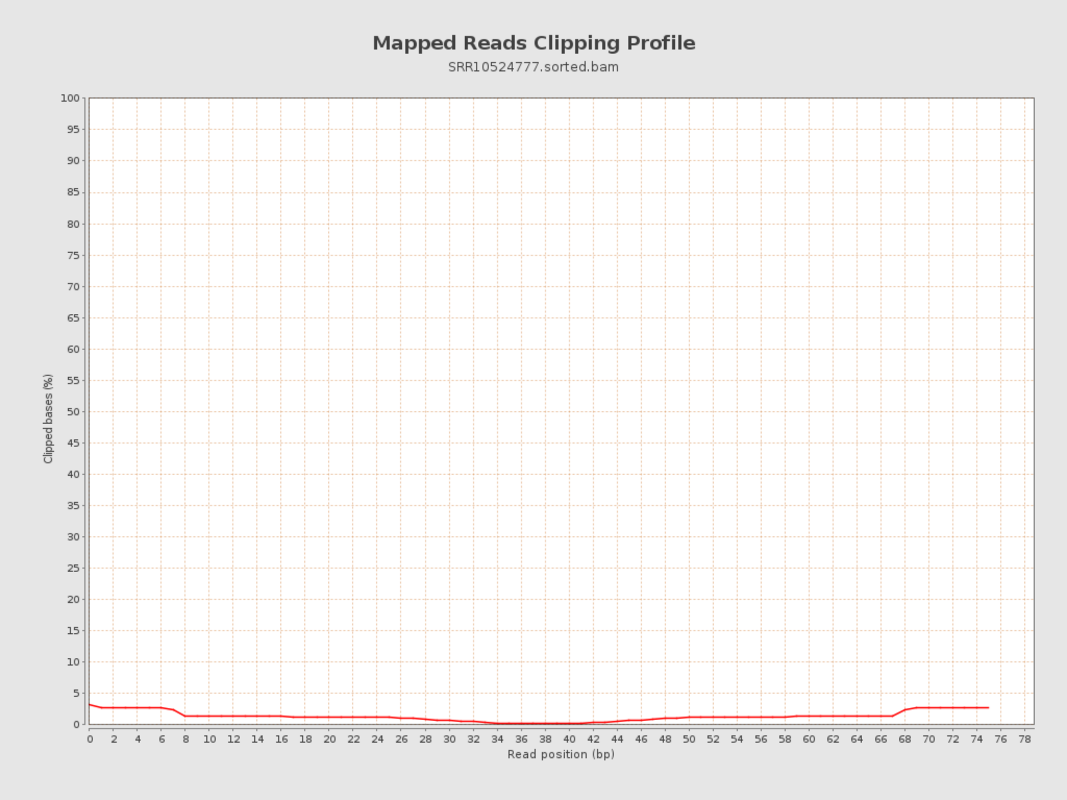
8. Results : Mapped Reads Nucleotide Content



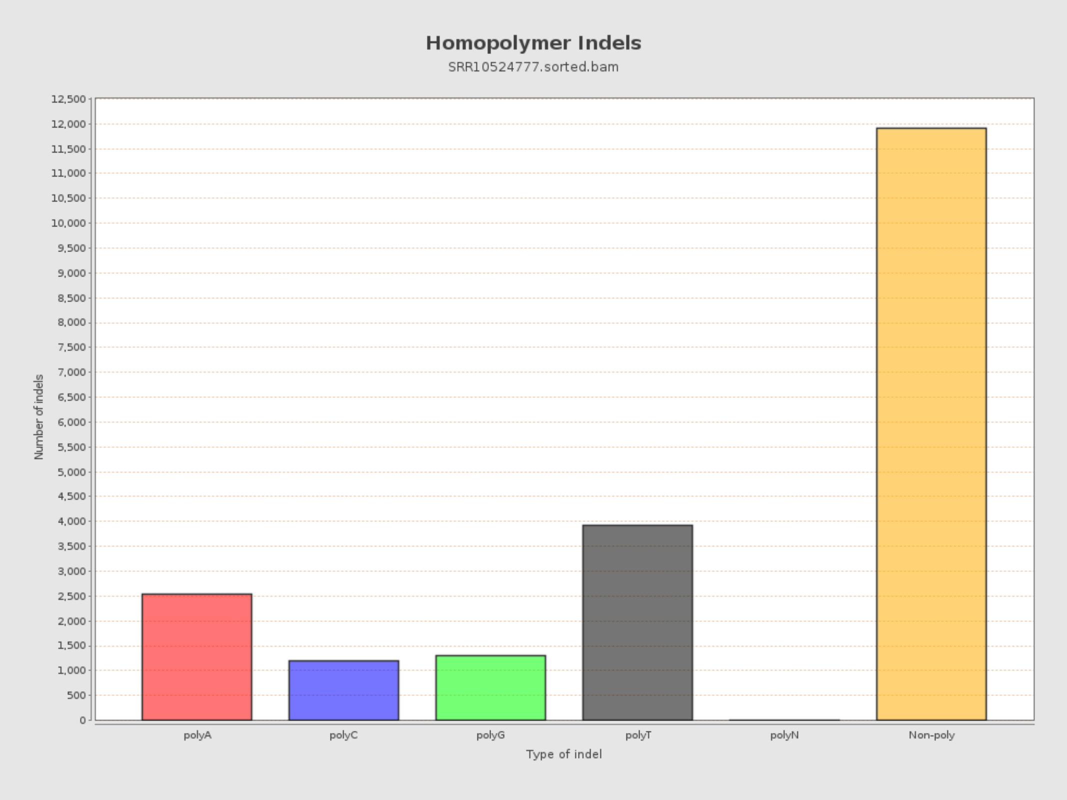
9. Results : Mapped Reads GC-content Distribution



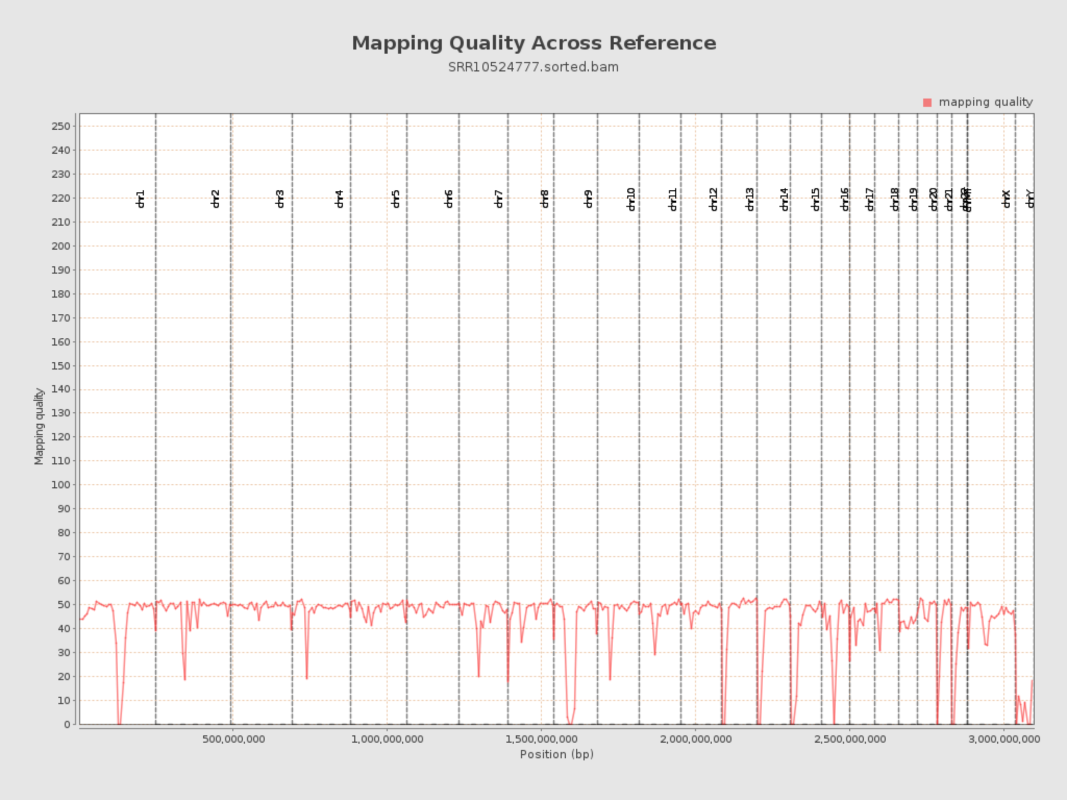
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram