Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 10:43:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524960.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_SRR10524960 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524960.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 10:43:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524960.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,347,769
Mapped reads	1,249,398 / 92.7%
Unmapped reads	98,371 / 7.3%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,469 / 0.26%
Read min/max/mean length	30 / 76 / 76.09
Duplicated reads (estimated)	33,106 / 2.46%
Duplication rate	1.8%
Clipped reads	1,250,228 / 92.76%

2.2. ACGT Content

Number/percentage of A's	18,415,330 / 25.14%
Number/percentage of C's	13,666,330 / 18.65%
Number/percentage of T's	23,212,378 / 31.68%
Number/percentage of G's	17,967,384 / 24.52%
Number/percentage of N's	831 / 0%
GC Percentage	43.18%

2.3. Coverage

Mean	0.0237

Standard Deviation	0.233

2.4. Mapping Quality

Mean Mapping Quality	44.17

2.5. Mismatches and indels

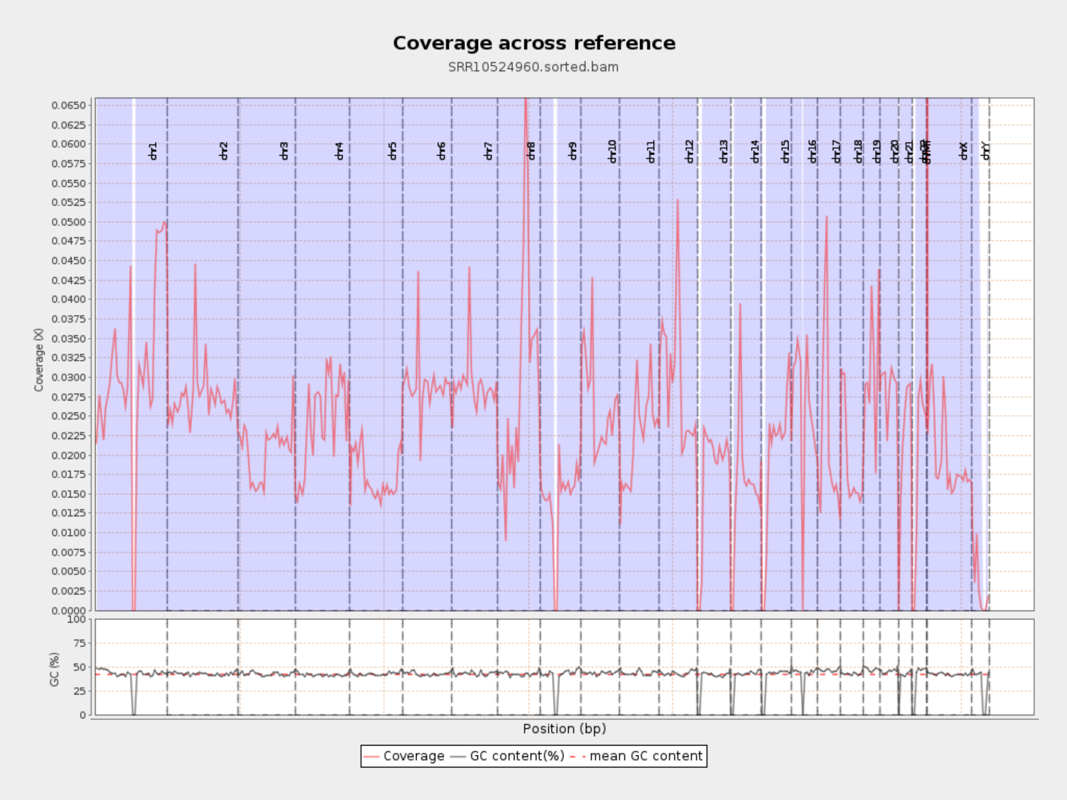
General error rate	0.5%
Mismatches	358,676
Insertions	4,648
Mapped reads with at least one insertion	0.37%
Deletions	14,202
Mapped reads with at least one deletion	1.13%
Homopolymer indels	43.9%

2.6. Chromosome stats

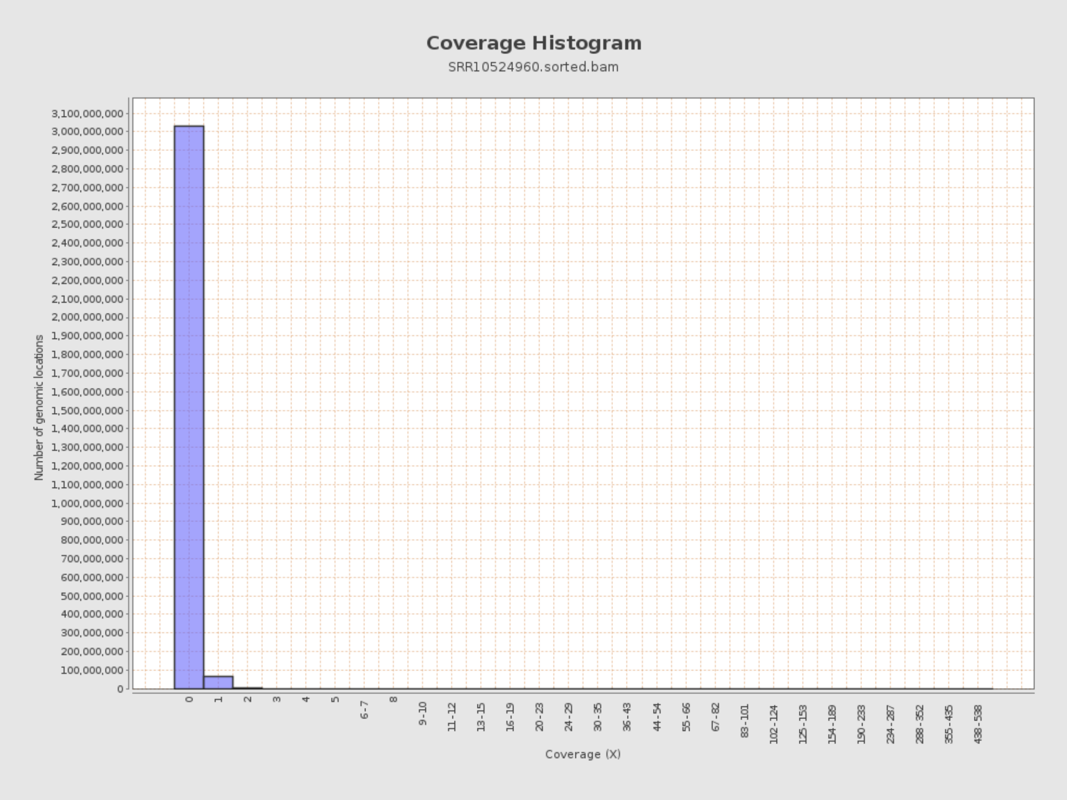
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7688659	0.0308	0.433
chr2	243199373	6729153	0.0277	0.2711
chr3	198022430	4098065	0.0207	0.1537
chr4	191154276	4703650	0.0246	0.1754
chr5	180915260	3146956	0.0174	0.143
chr6	171115067	4959012	0.029	0.2418
chr7	159138663	4642460	0.0292	0.3094

chr8	146364022	4308945	0.0294	0.2316
chr9	141213431	1991786	0.0141	0.1837
chr10	135534747	3620815	0.0267	0.2207
chr11	135006516	3069744	0.0227	0.2066
chr12	133851895	3954711	0.0295	0.1842
chr13	115169878	2009751	0.0175	0.1416
chr14	107349540	1707567	0.0159	0.1395
chr15	102531392	2035496	0.0199	0.1596
chr16	90354753	2337558	0.0259	0.1785
chr17	81195210	1841656	0.0227	0.2095
chr18	78077248	1480398	0.019	0.2958
chr19	59128983	1835221	0.031	0.2754
chr20	63025520	1795301	0.0285	0.183
chr21	48129895	1042218	0.0217	0.1619
chr22	51304566	956295	0.0186	0.1443
chrMT	16571	19059	1.1501	1.3095
chrX	155270560	3118148	0.0201	0.1728
chrY	59373566	194342	0.0033	0.0812

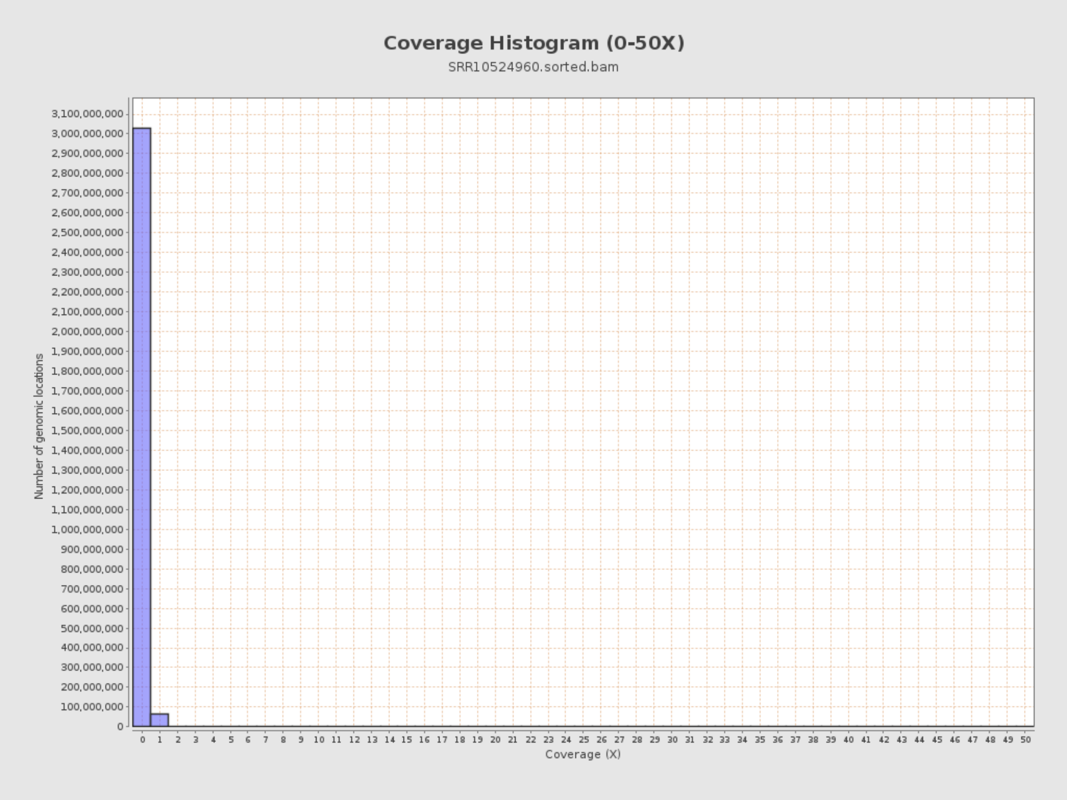
3. Results : Coverage across reference



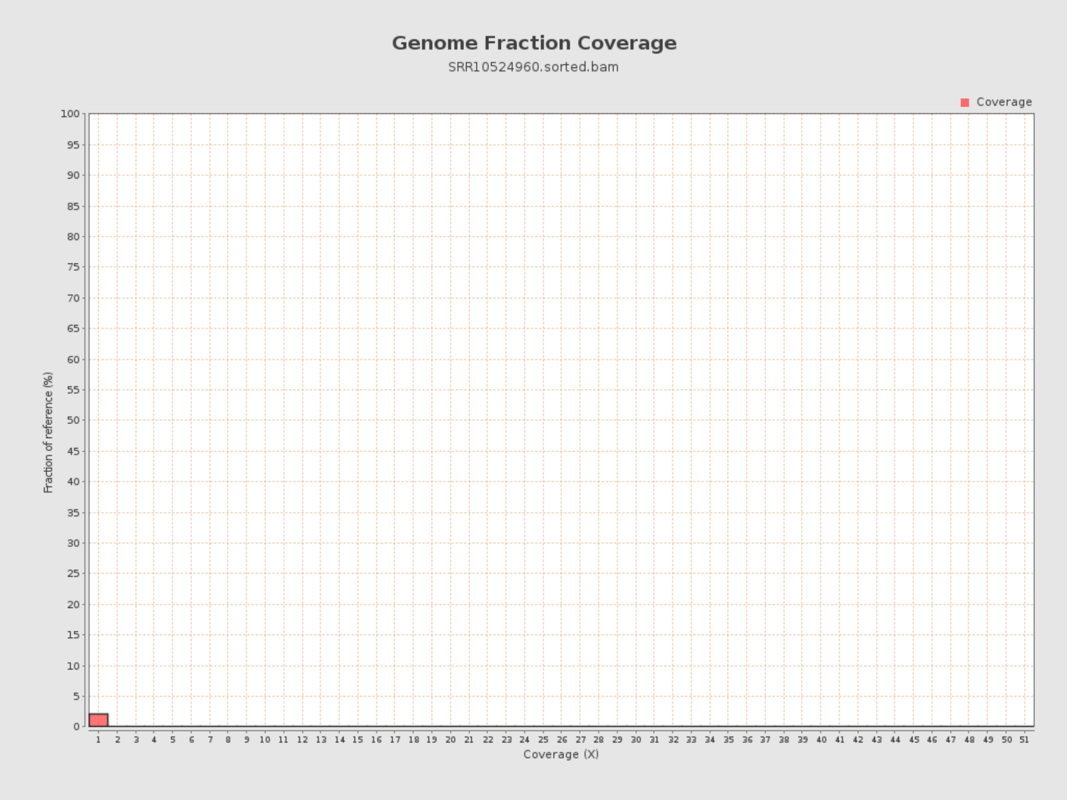
4. Results : Coverage Histogram



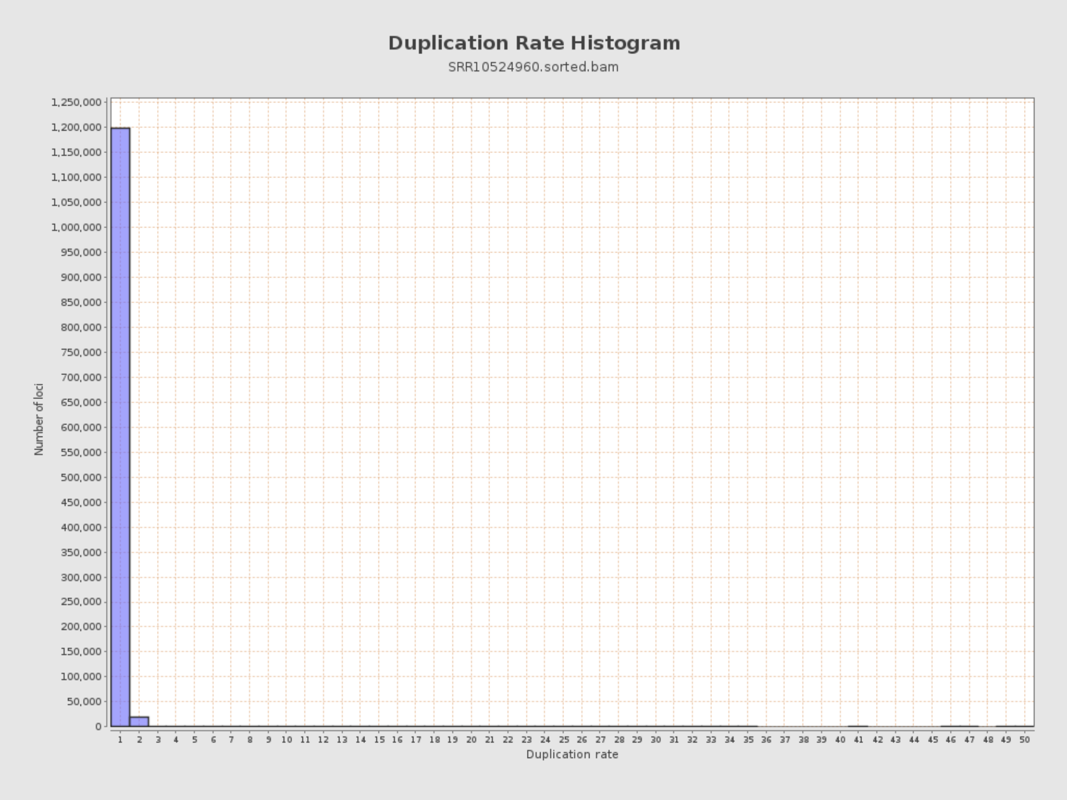
5. Results : Coverage Histogram (0-50X)



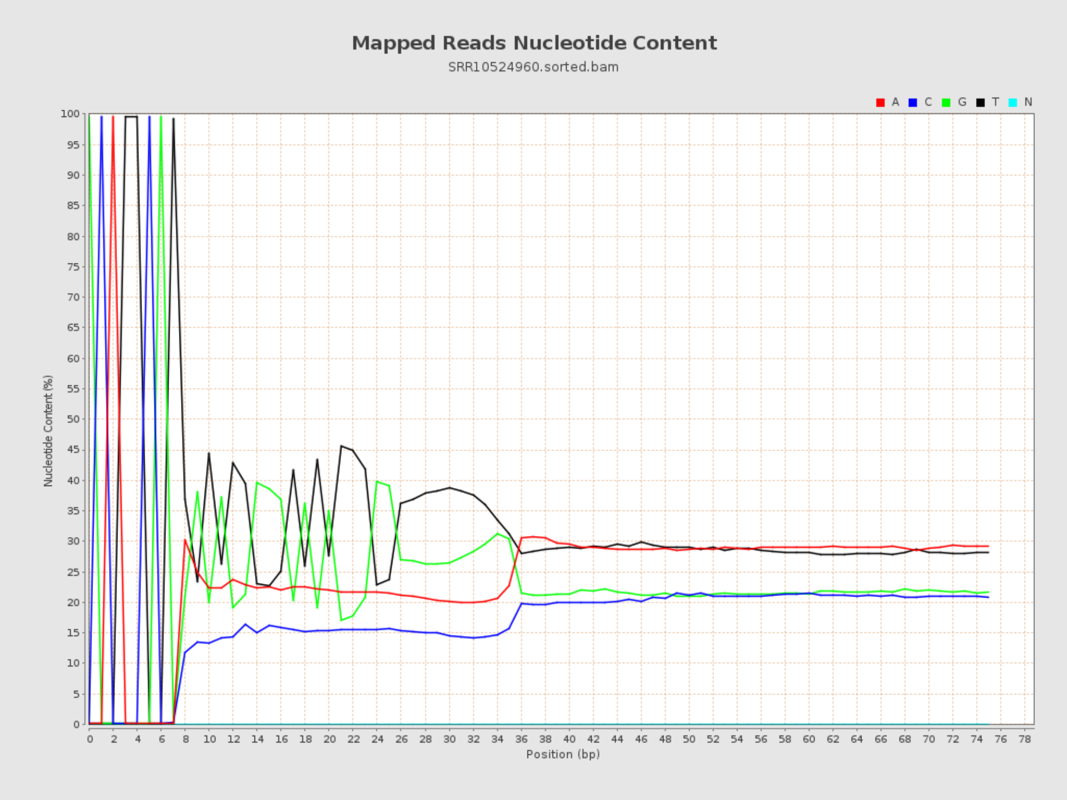
6. Results : Genome Fraction Coverage



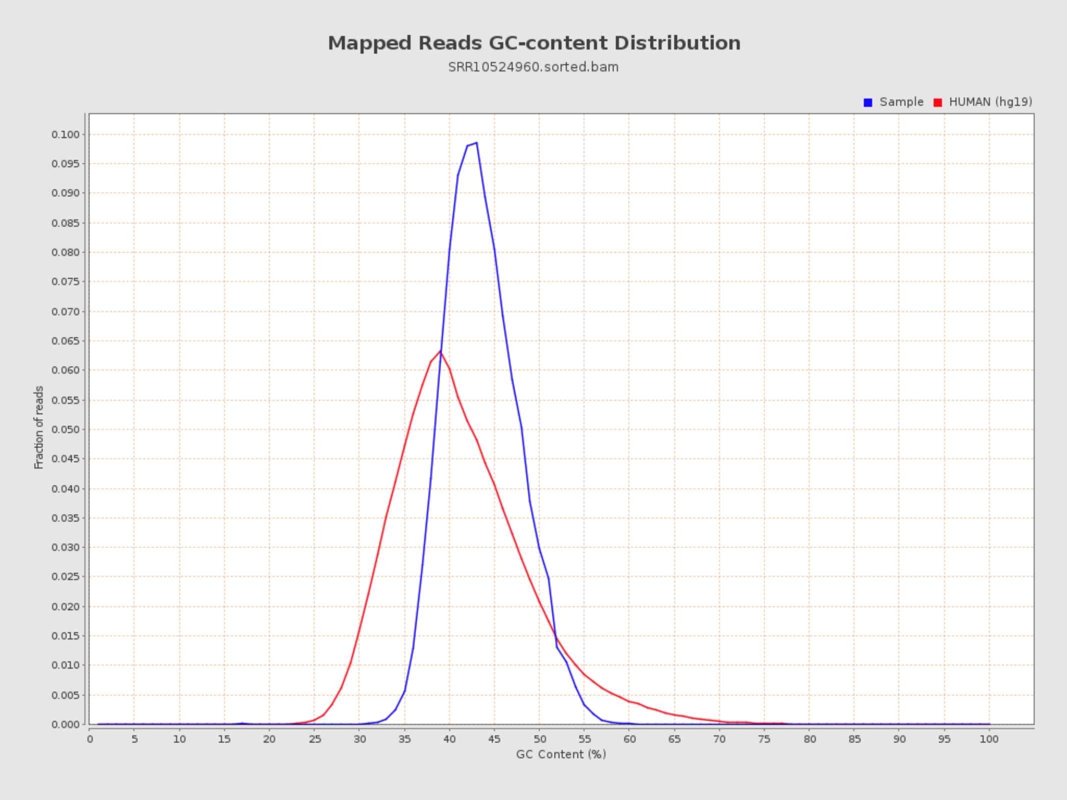
7. Results : Duplication Rate Histogram



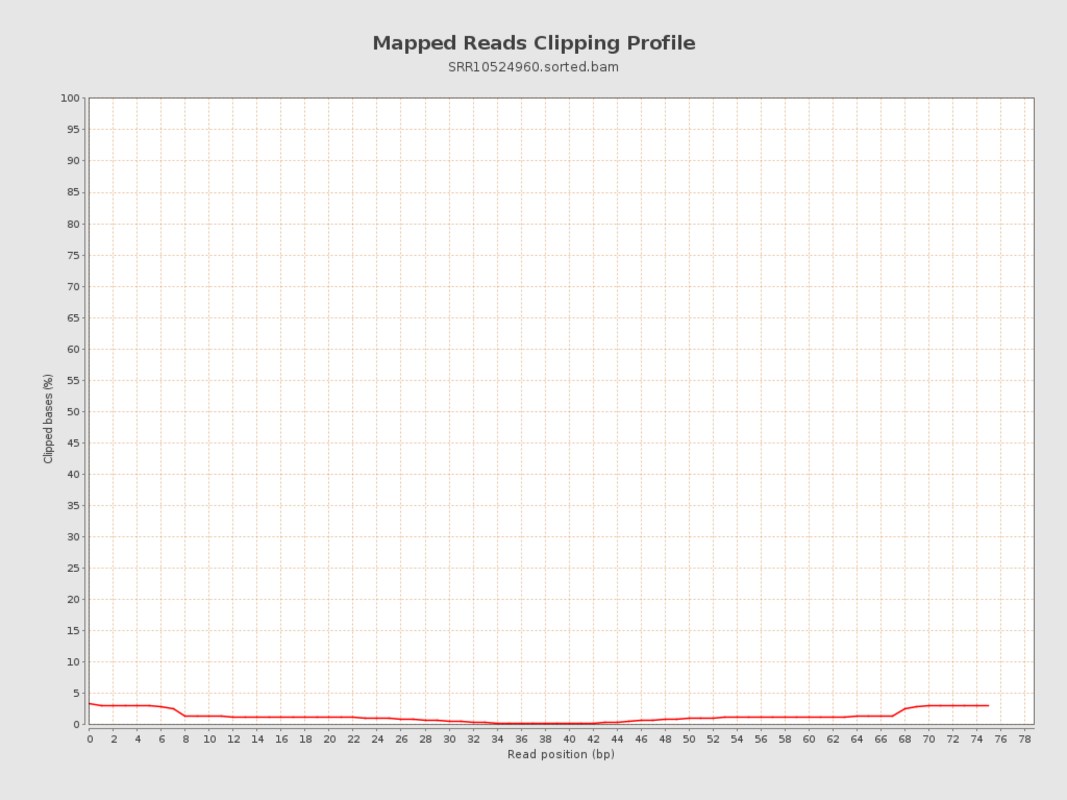
8. Results : Mapped Reads Nucleotide Content



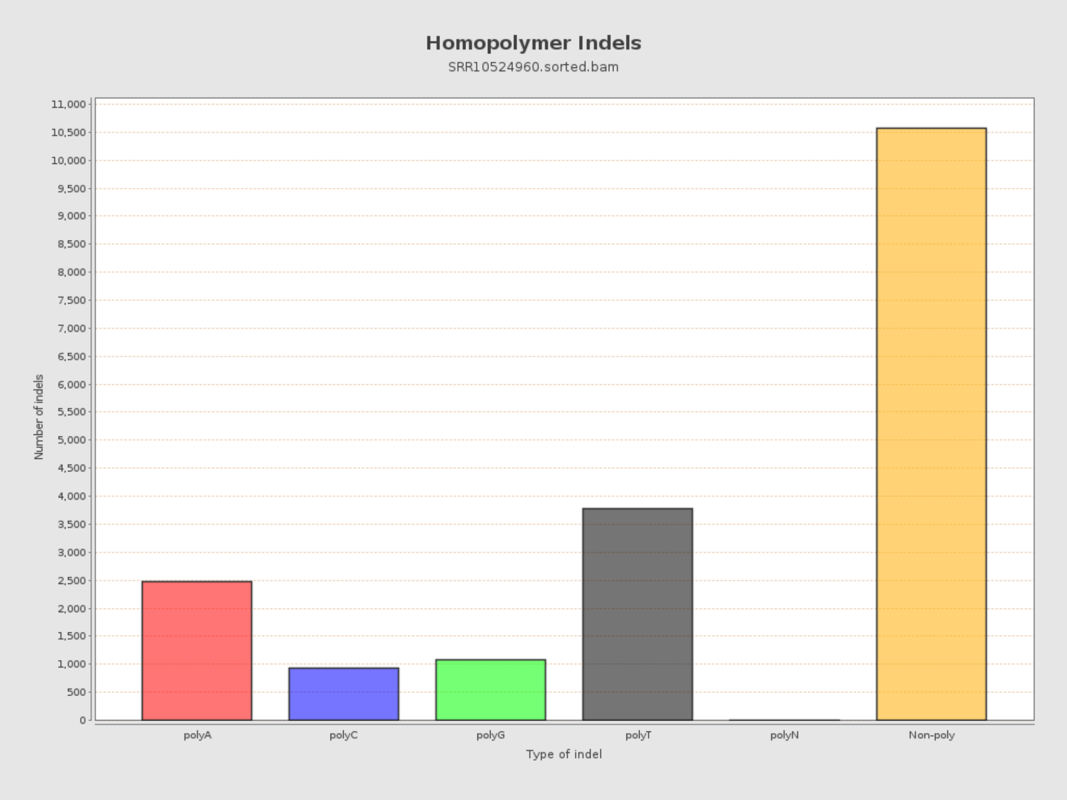
9. Results : Mapped Reads GC-content Distribution



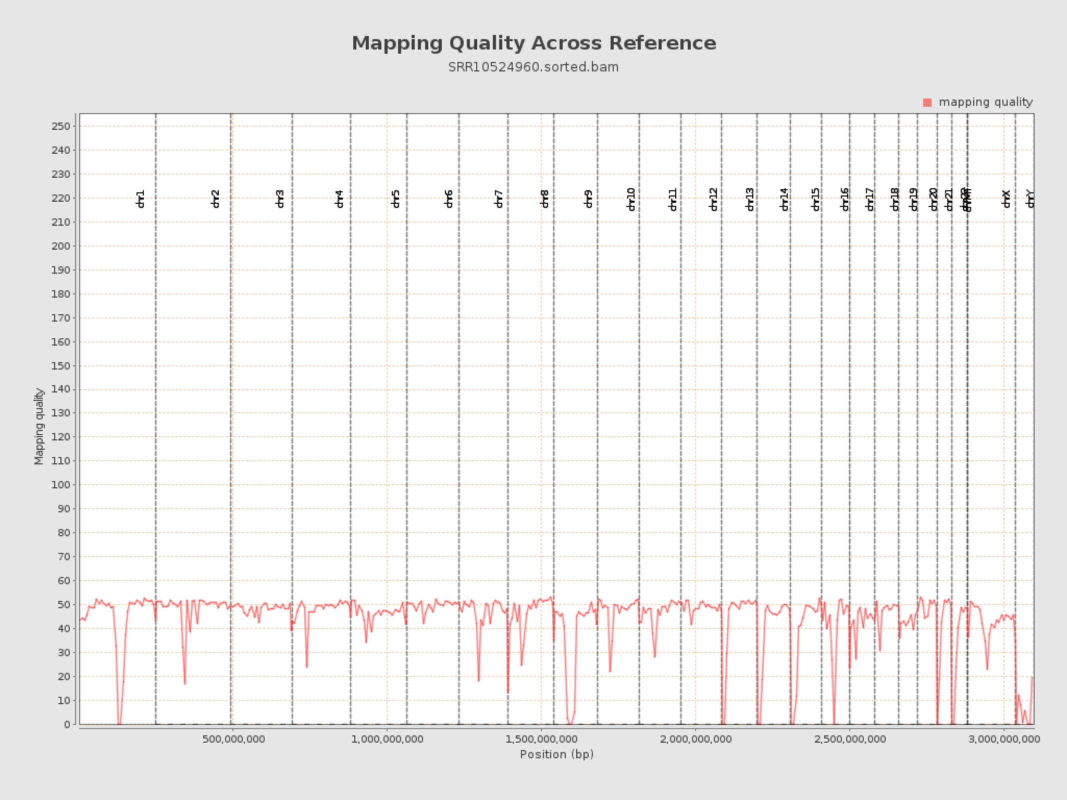
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram