Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 03:27:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3083674.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_SRR3083674 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3083674.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 03:27:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3083674.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,569,872
Mapped reads	2,089,139 / 81.29%
Unmapped reads	480,733 / 18.71%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,537 / 0.6%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	77,145 / 3%
Duplication rate	3.04%
Clipped reads	1,559,257 / 60.67%

2.2. ACGT Content

Number/percentage of A's	36,713,606 / 29.91%
Number/percentage of C's	24,420,870 / 19.89%
Number/percentage of T's	35,466,278 / 28.89%
Number/percentage of G's	26,147,583 / 21.3%
Number/percentage of N's	17,025 / 0.01%
GC Percentage	41.19%

2.3. Coverage

Mean	0.0397

Standard Deviation	0.3292

2.4. Mapping Quality

Mean Mapping Quality	44.48

2.5. Mismatches and indels

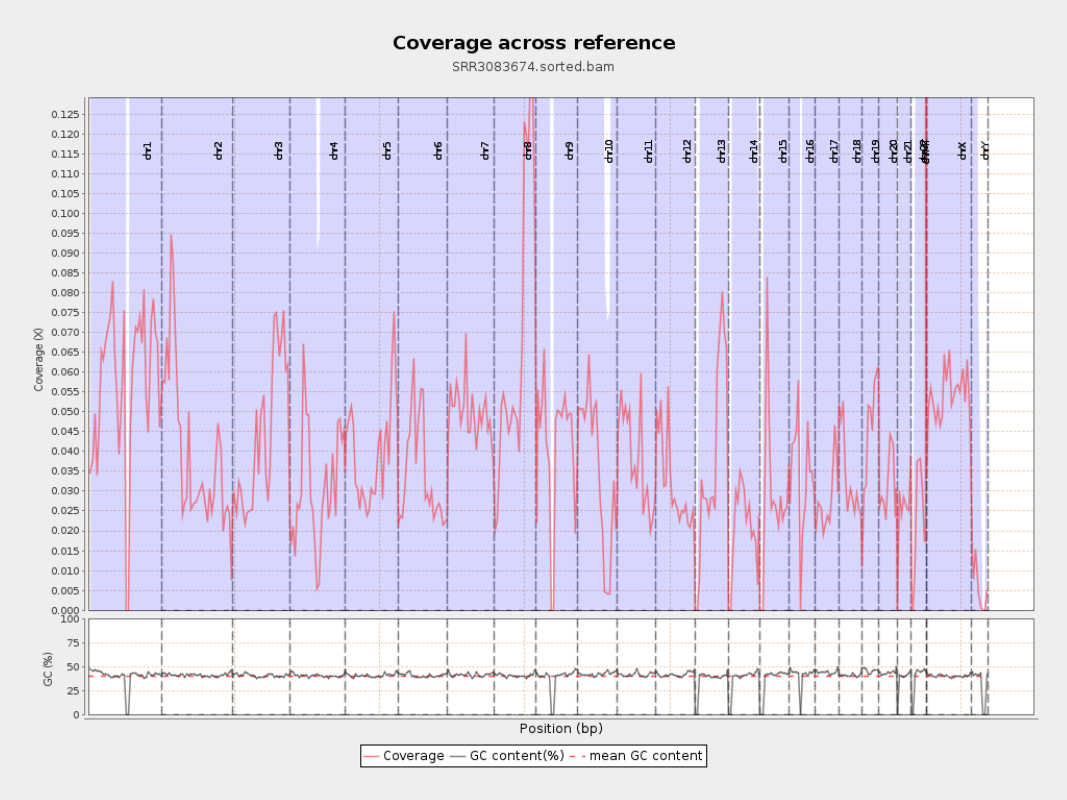
General error rate	0.82%
Mismatches	995,387
Insertions	8,851
Mapped reads with at least one insertion	0.42%
Deletions	23,578
Mapped reads with at least one deletion	1.12%
Homopolymer indels	45.36%

2.6. Chromosome stats

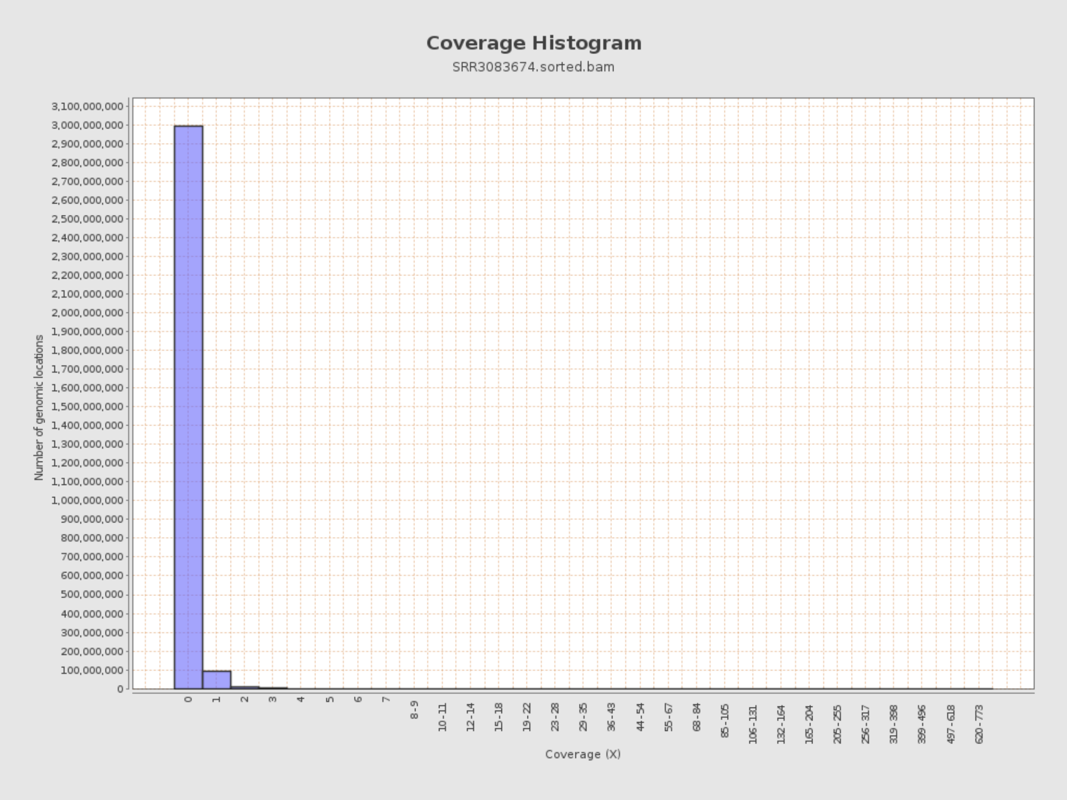
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14205496	0.057	0.6657
chr2	243199373	9565902	0.0393	0.2911
chr3	198022430	8634002	0.0436	0.2363
chr4	191154276	5902279	0.0309	0.2041
chr5	180915260	7211458	0.0399	0.2264
chr6	171115067	5878757	0.0344	0.2445
chr7	159138663	7974788	0.0501	0.4022

chr8	146364022	10071210	0.0688	0.4727
chr9	141213431	5890739	0.0417	0.2944
chr10	135534747	4836035	0.0357	0.2992
chr11	135006516	5139469	0.0381	0.2459
chr12	133851895	4268204	0.0319	0.2046
chr13	115169878	4350662	0.0378	0.2199
chr14	107349540	2203125	0.0205	0.1721
chr15	102531392	2976719	0.029	0.1941
chr16	90354753	3097482	0.0343	0.2282
chr17	81195210	2240367	0.0276	0.1959
chr18	78077248	2608358	0.0334	0.5015
chr19	59128983	2703867	0.0457	0.4079
chr20	63025520	1964826	0.0312	0.2066
chr21	48129895	1229432	0.0255	0.1883
chr22	51304566	1090528	0.0213	0.1631
chrMT	16571	49396	2.9809	2.3026
chrX	155270560	8376214	0.0539	0.2802
chrY	59373566	333481	0.0056	0.115

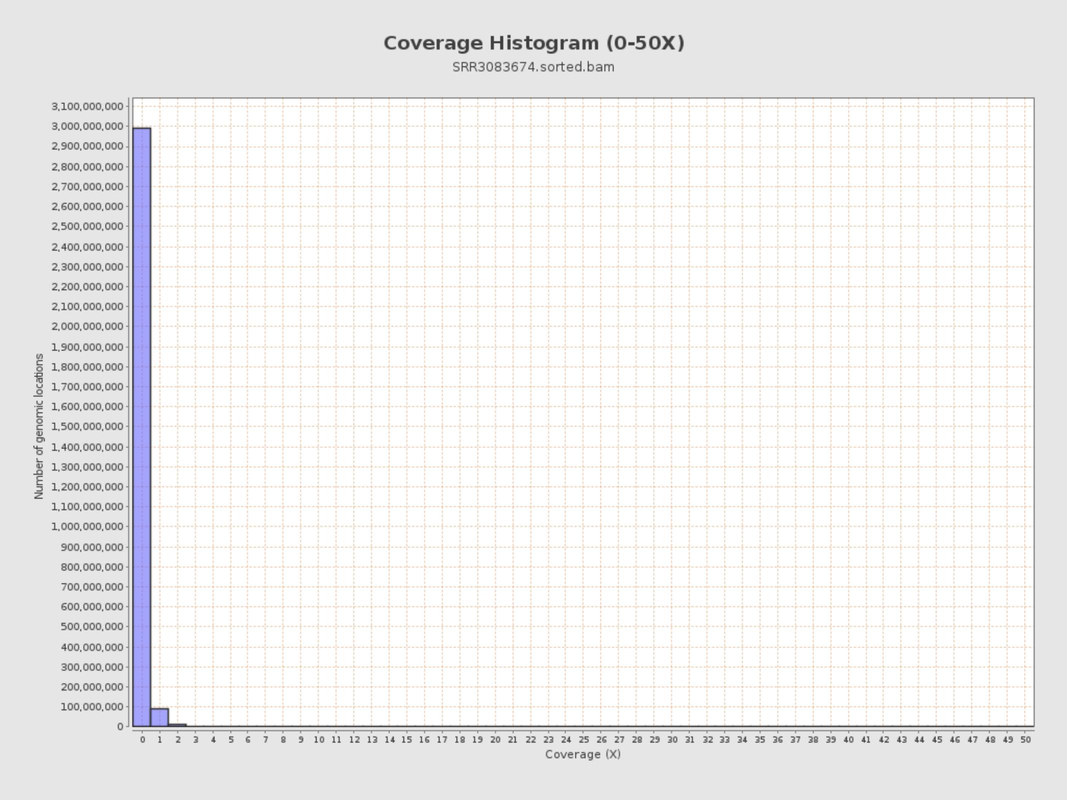
3. Results : Coverage across reference



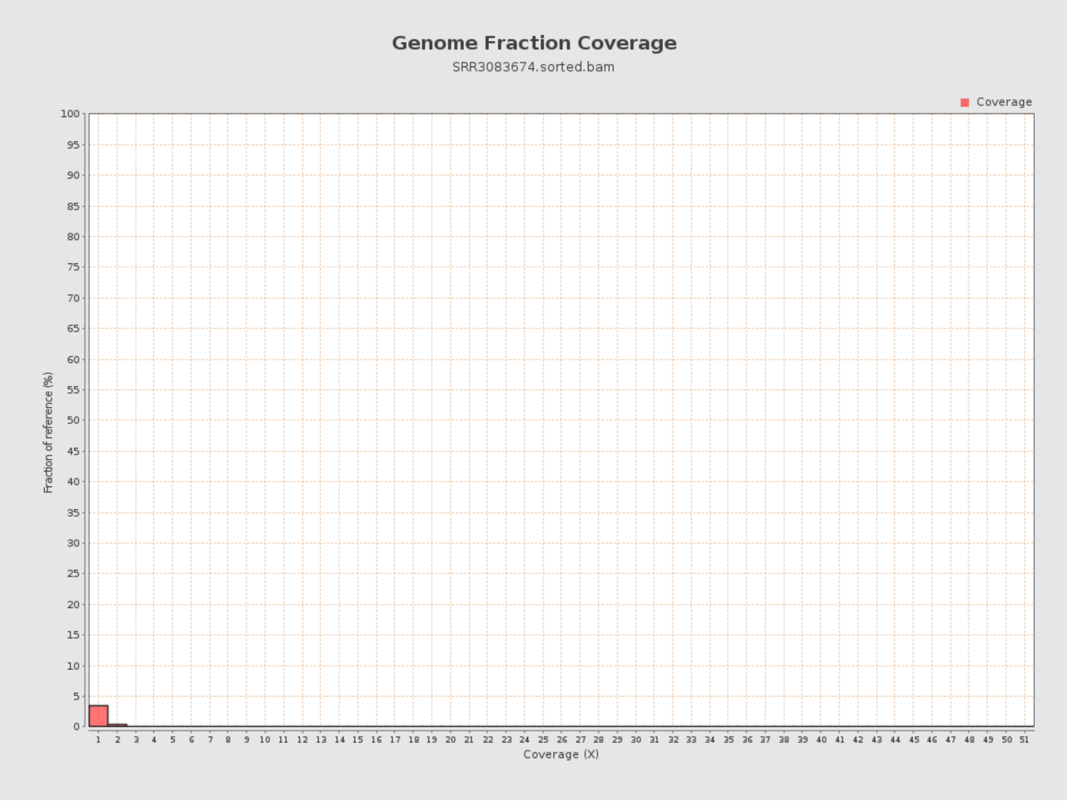
4. Results : Coverage Histogram



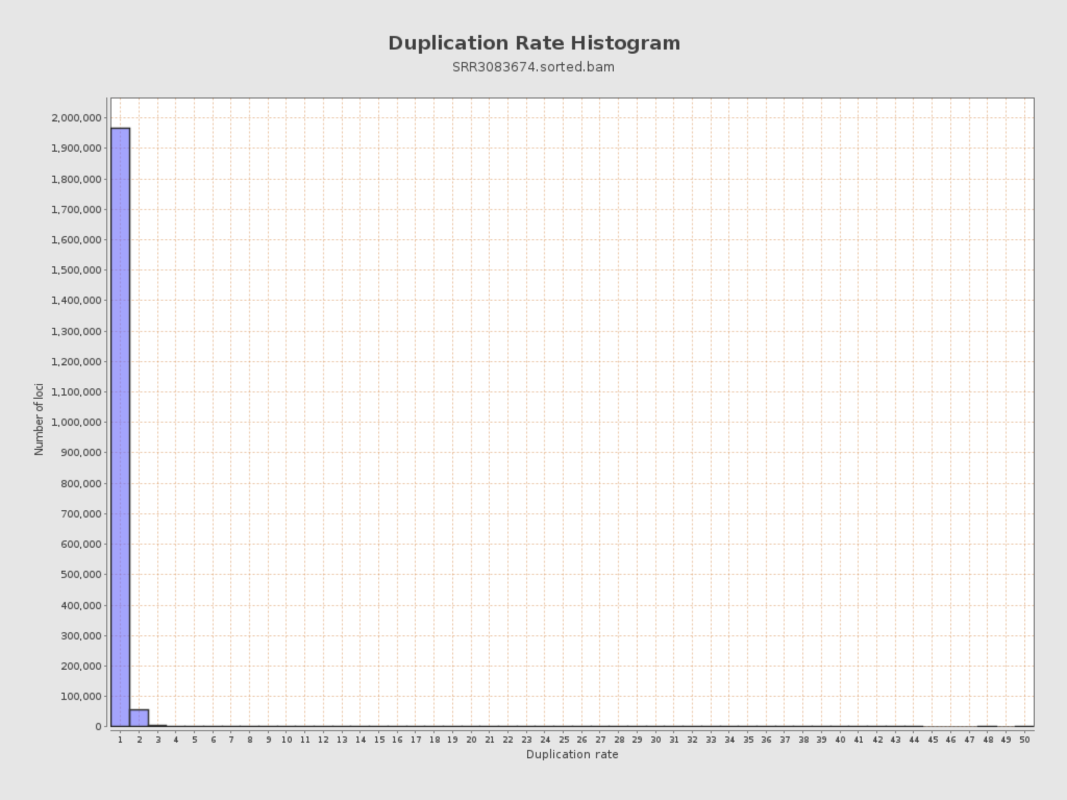
5. Results : Coverage Histogram (0-50X)



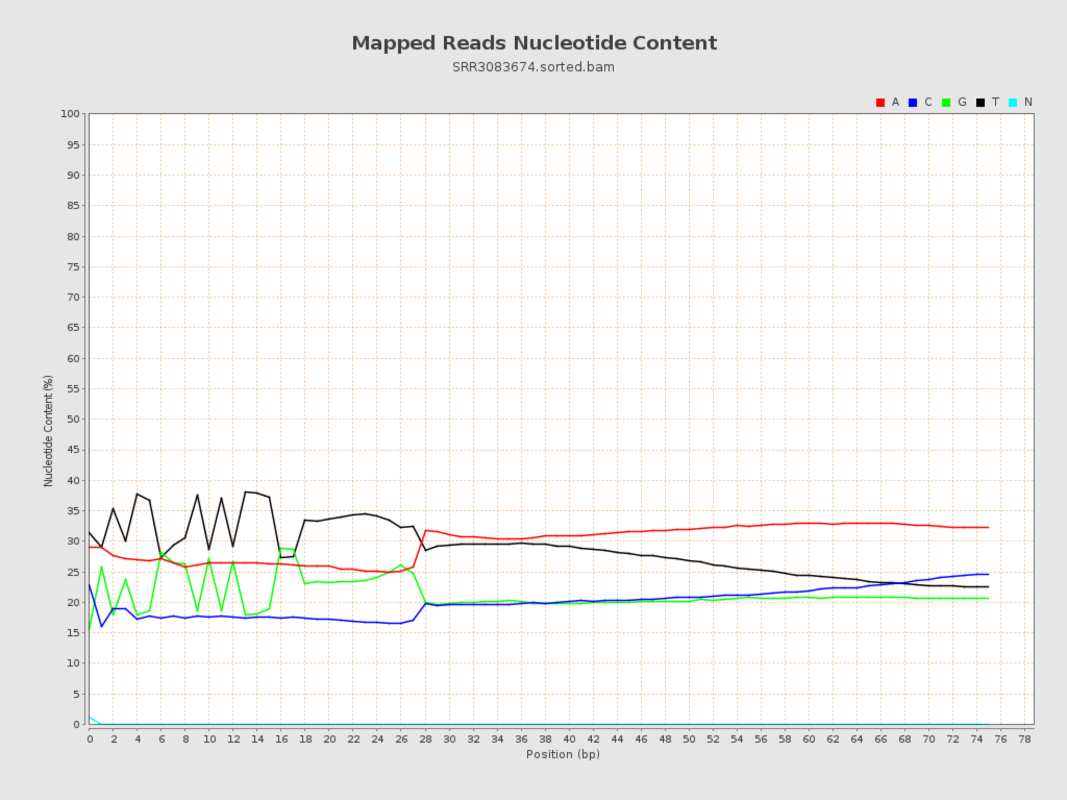
6. Results : Genome Fraction Coverage



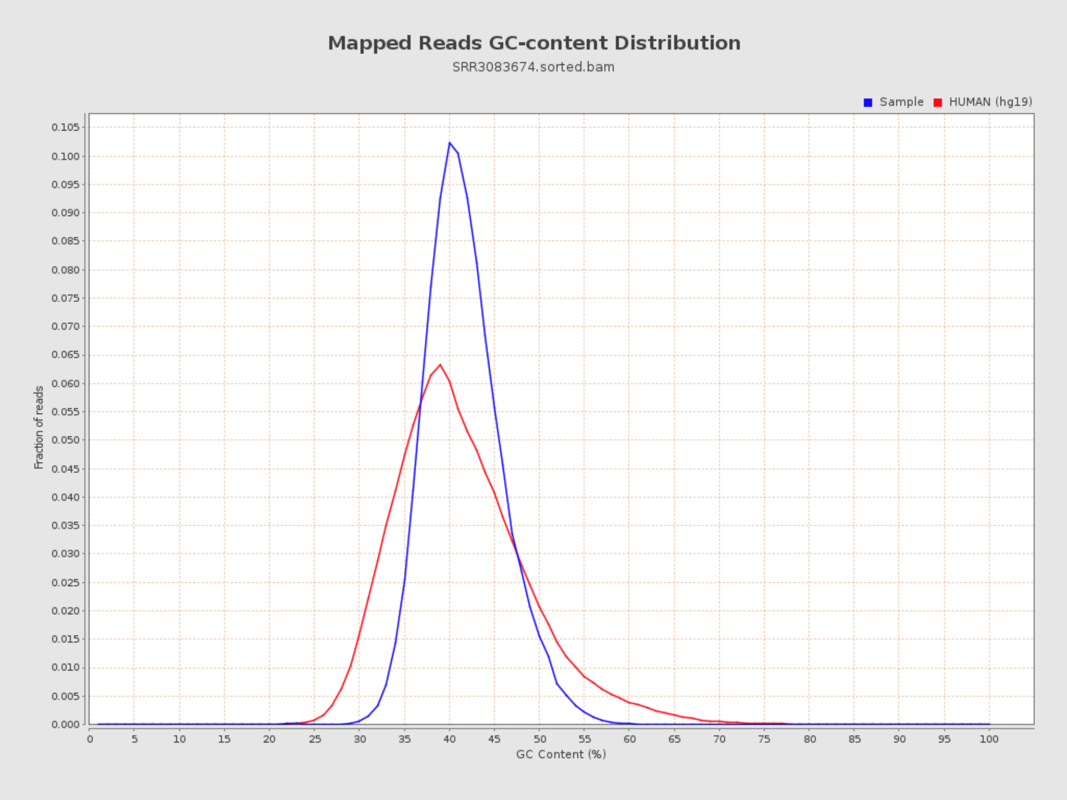
7. Results : Duplication Rate Histogram



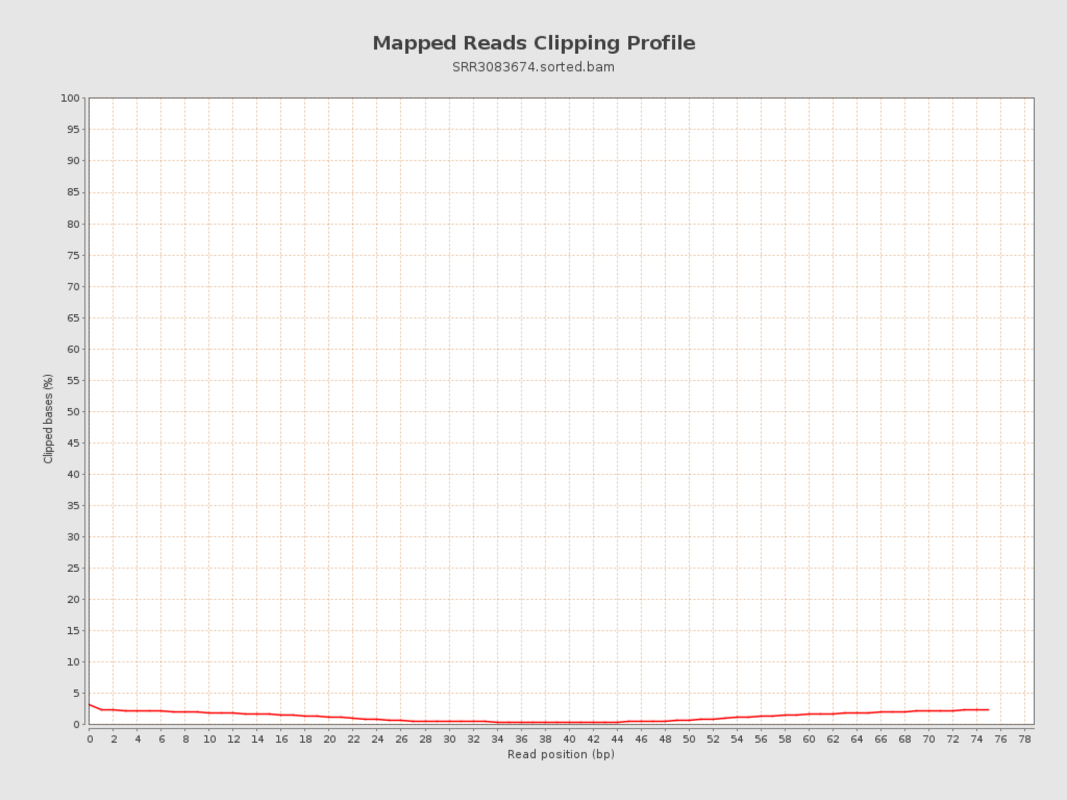
8. Results : Mapped Reads Nucleotide Content



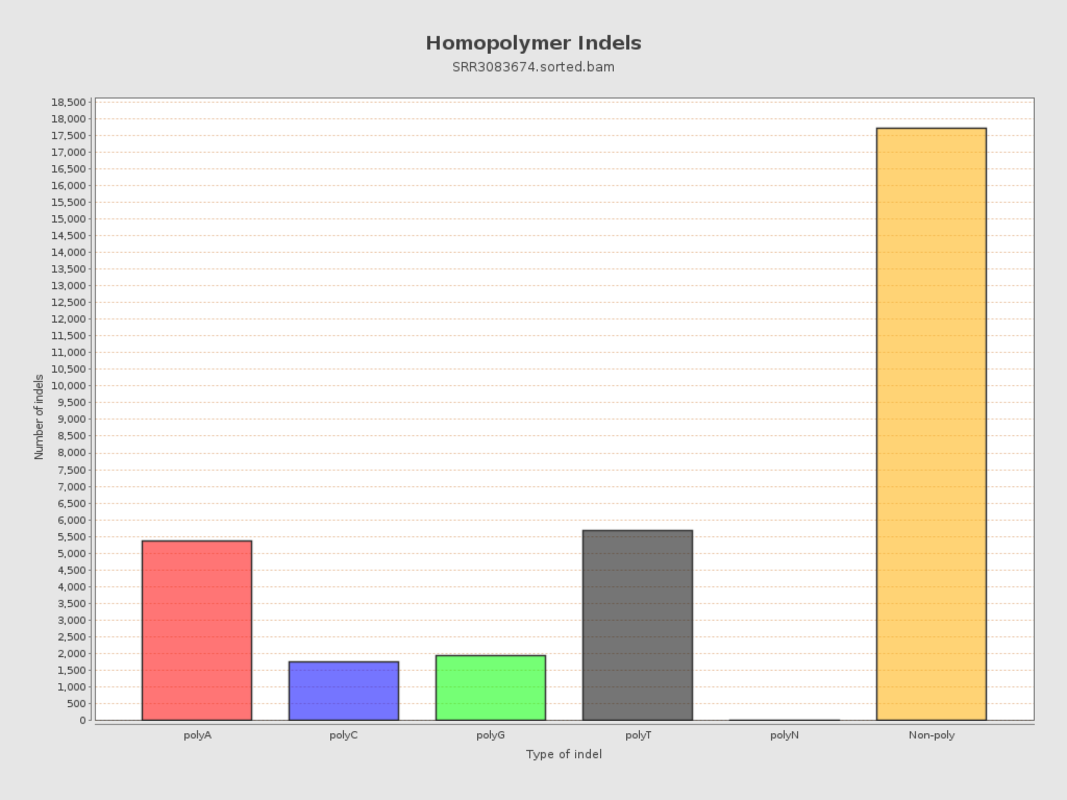
9. Results : Mapped Reads GC-content Distribution



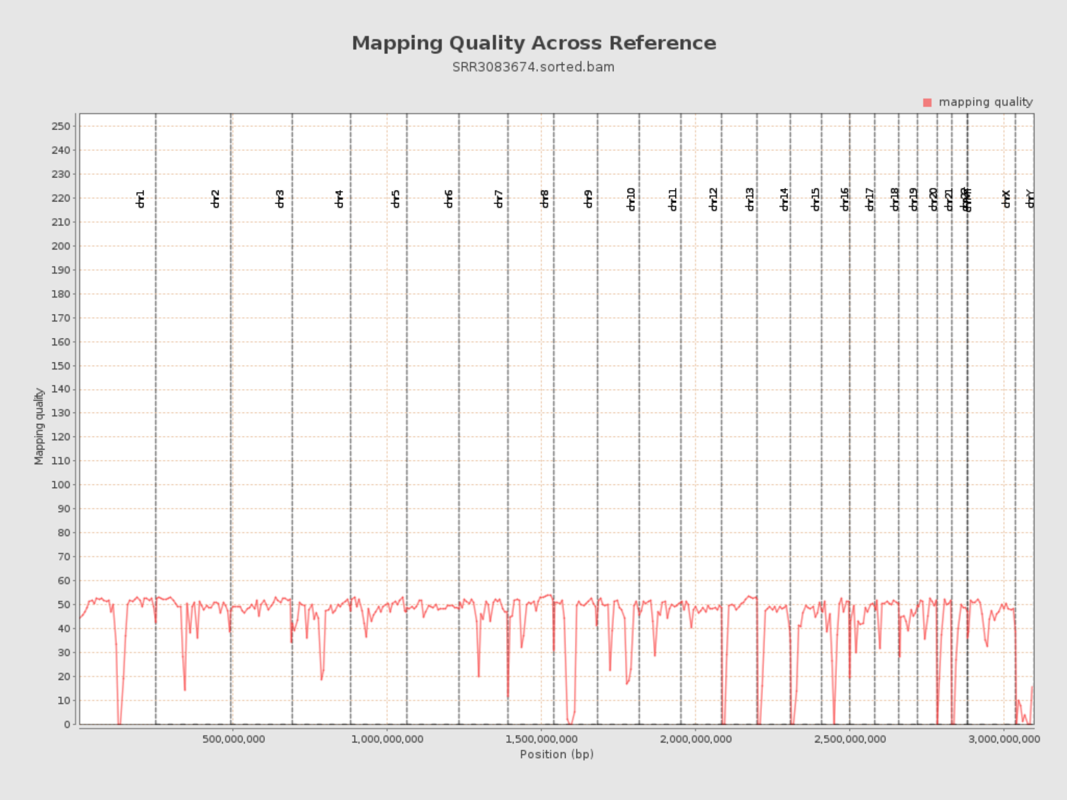
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram