Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 09:29:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008744.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_SRR6008744 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008744.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 09:29:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008744.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,805,521
Mapped reads	1,235,516 / 68.43%
Unmapped reads	570,005 / 31.57%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,082 / 0.28%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	41,153 / 2.28%
Duplication rate	2.46%
Clipped reads	691,692 / 38.31%

2.2. ACGT Content

Number/percentage of A's	22,705,348 / 28.84%
Number/percentage of C's	13,507,271 / 17.16%
Number/percentage of T's	23,769,283 / 30.19%
Number/percentage of G's	18,741,807 / 23.81%
Number/percentage of N's	3,814 / 0%
GC Percentage	40.96%

2.3. Coverage

Mean	0.0254

Standard Deviation	0.2257

2.4. Mapping Quality

Mean Mapping Quality	45.44

2.5. Mismatches and indels

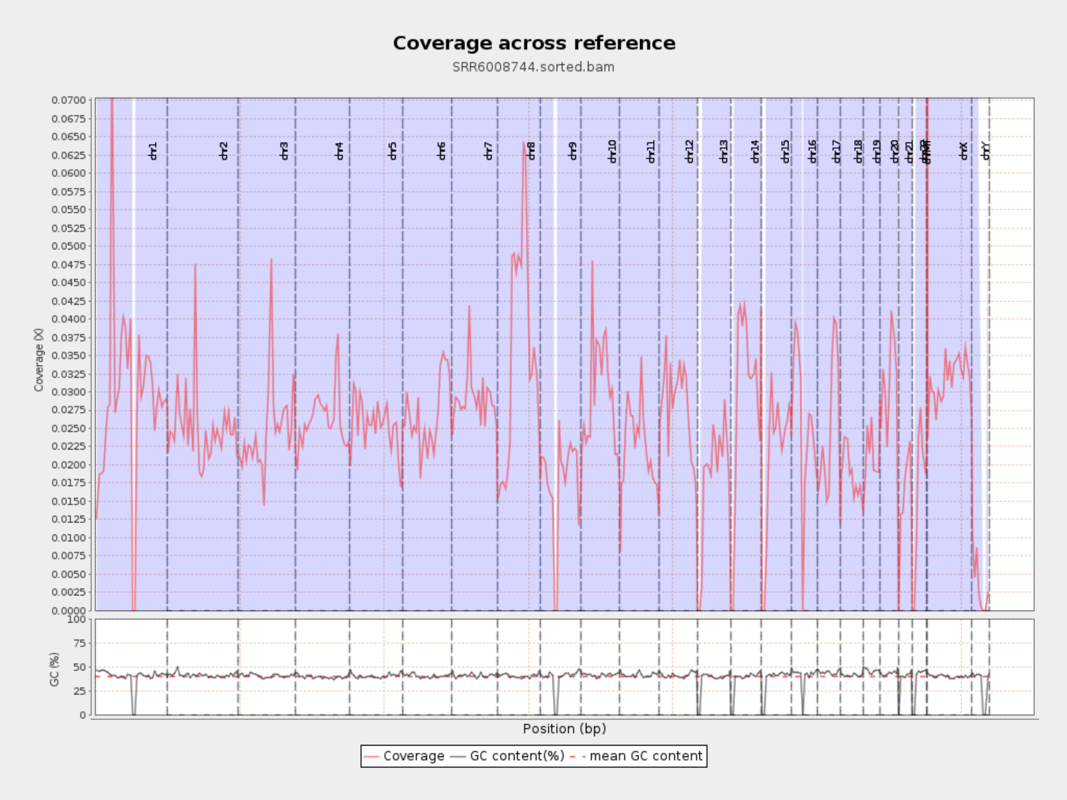
General error rate	0.97%
Mismatches	754,374
Insertions	6,548
Mapped reads with at least one insertion	0.53%
Deletions	29,217
Mapped reads with at least one deletion	2.33%
Homopolymer indels	47.05%

2.6. Chromosome stats

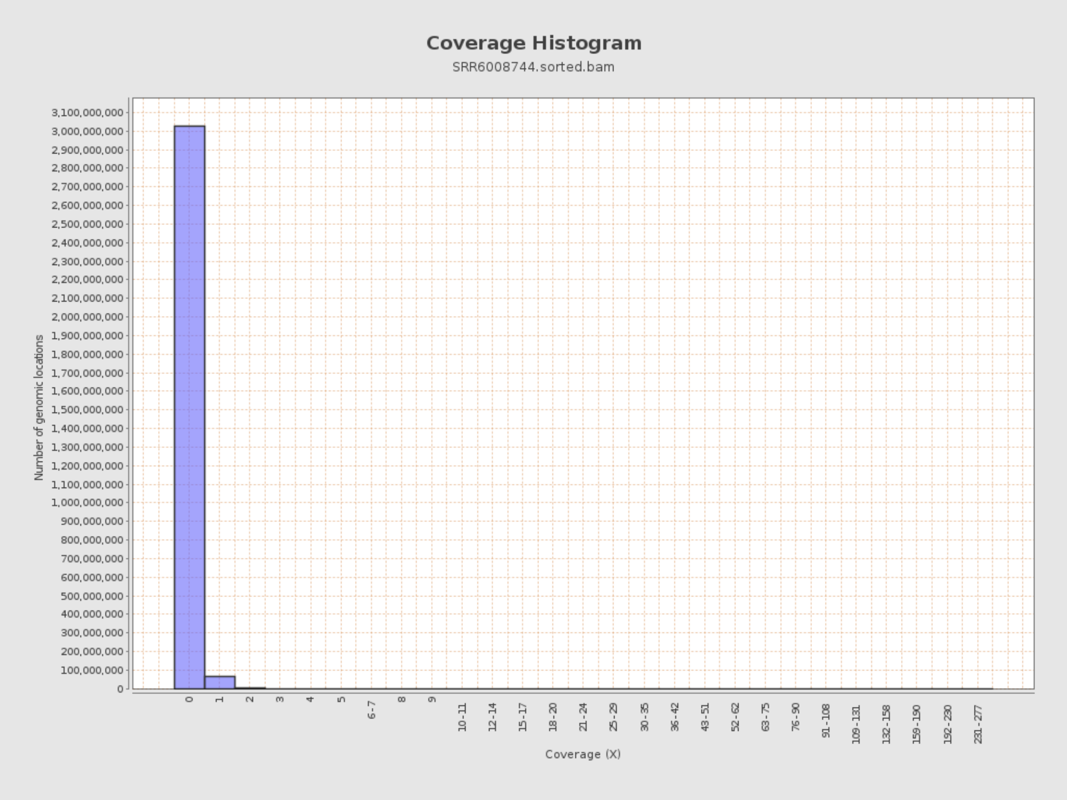
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7255907	0.0291	0.3021
chr2	243199373	6096323	0.0251	0.3172
chr3	198022430	4879025	0.0246	0.1776
chr4	191154276	5017404	0.0262	0.179
chr5	180915260	4607634	0.0255	0.1744
chr6	171115067	4578913	0.0268	0.1957
chr7	159138663	4634431	0.0291	0.3083

chr8	146364022	5238108	0.0358	0.2755
chr9	141213431	2491401	0.0176	0.1967
chr10	135534747	4034349	0.0298	0.2552
chr11	135006516	3059861	0.0227	0.2043
chr12	133851895	3775275	0.0282	0.1889
chr13	115169878	2079469	0.0181	0.1523
chr14	107349540	3130157	0.0292	0.1929
chr15	102531392	2165030	0.0211	0.1619
chr16	90354753	2291421	0.0254	0.184
chr17	81195210	2027855	0.025	0.1866
chr18	78077248	1459597	0.0187	0.2704
chr19	59128983	1256207	0.0212	0.2084
chr20	63025520	1951695	0.031	0.1937
chr21	48129895	766422	0.0159	0.1424
chr22	51304566	826849	0.0161	0.14
chrMT	16571	26753	1.6144	1.6551
chrX	155270560	4927020	0.0317	0.2078
chrY	59373566	196691	0.0033	0.0722

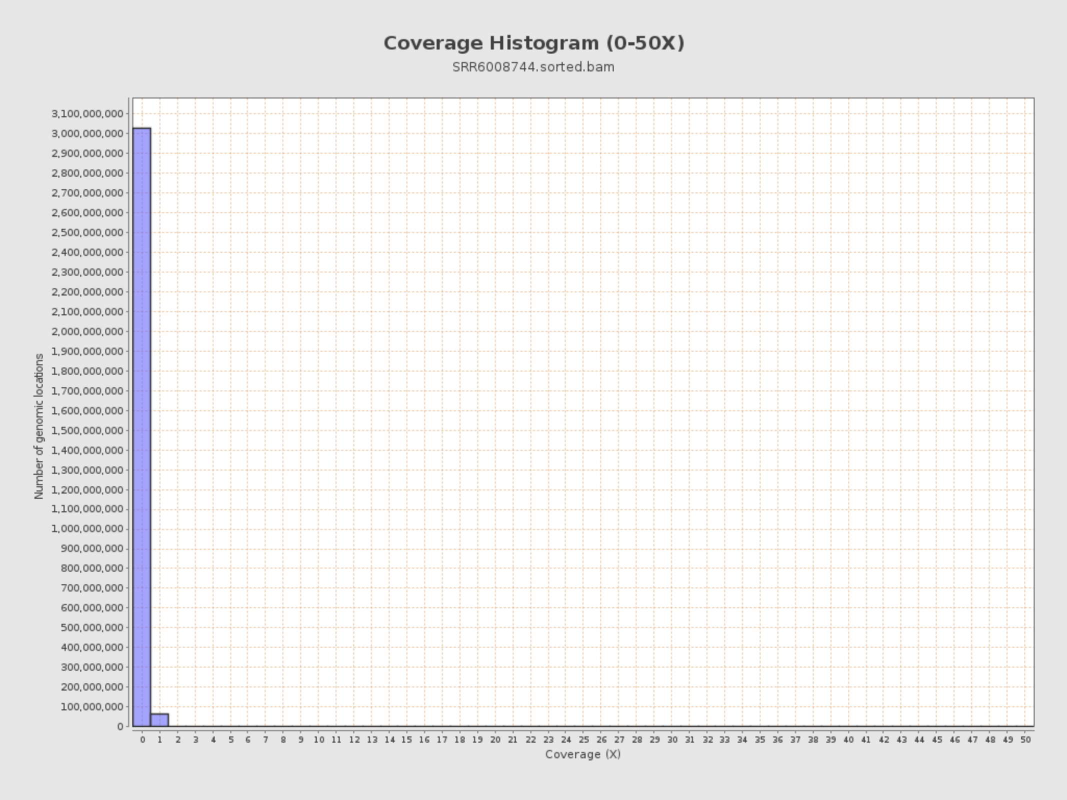
3. Results : Coverage across reference



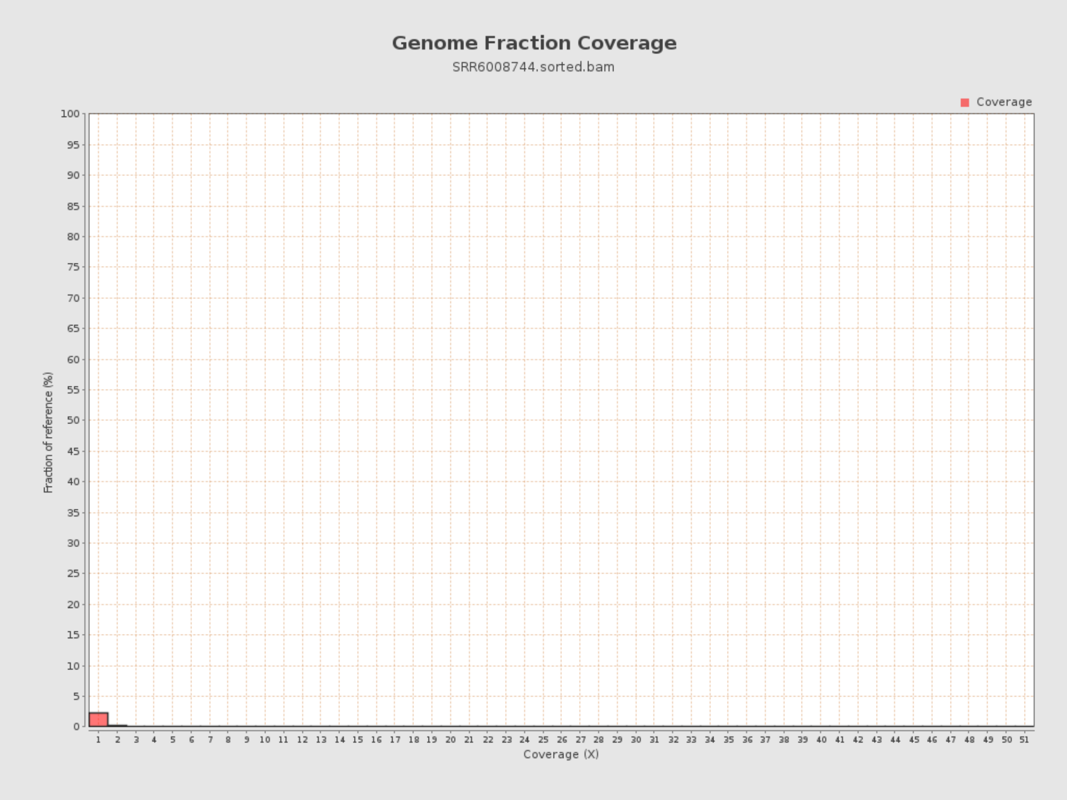
4. Results : Coverage Histogram



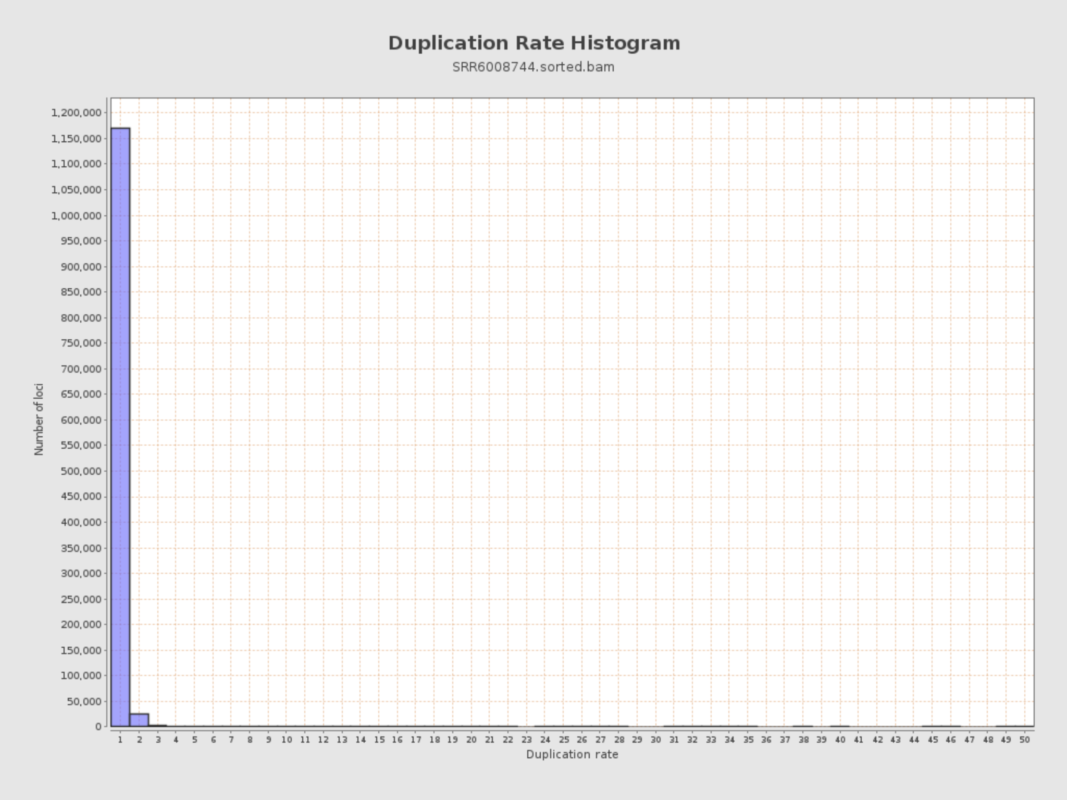
5. Results : Coverage Histogram (0-50X)



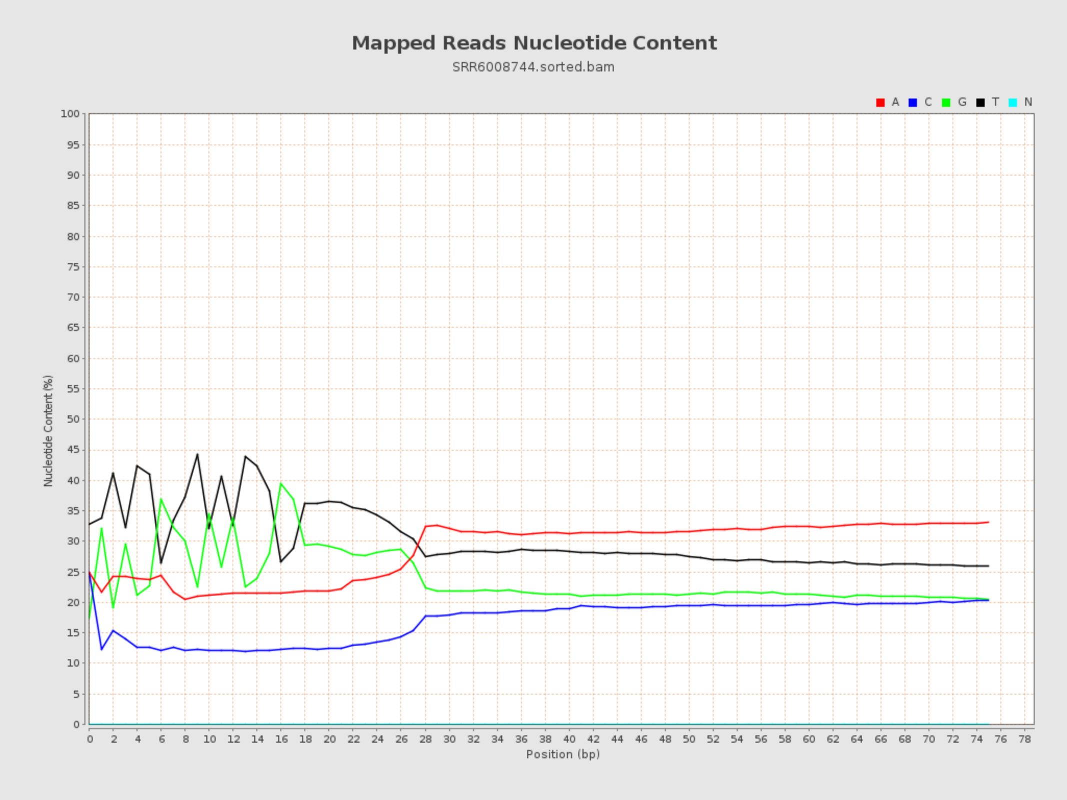
6. Results : Genome Fraction Coverage



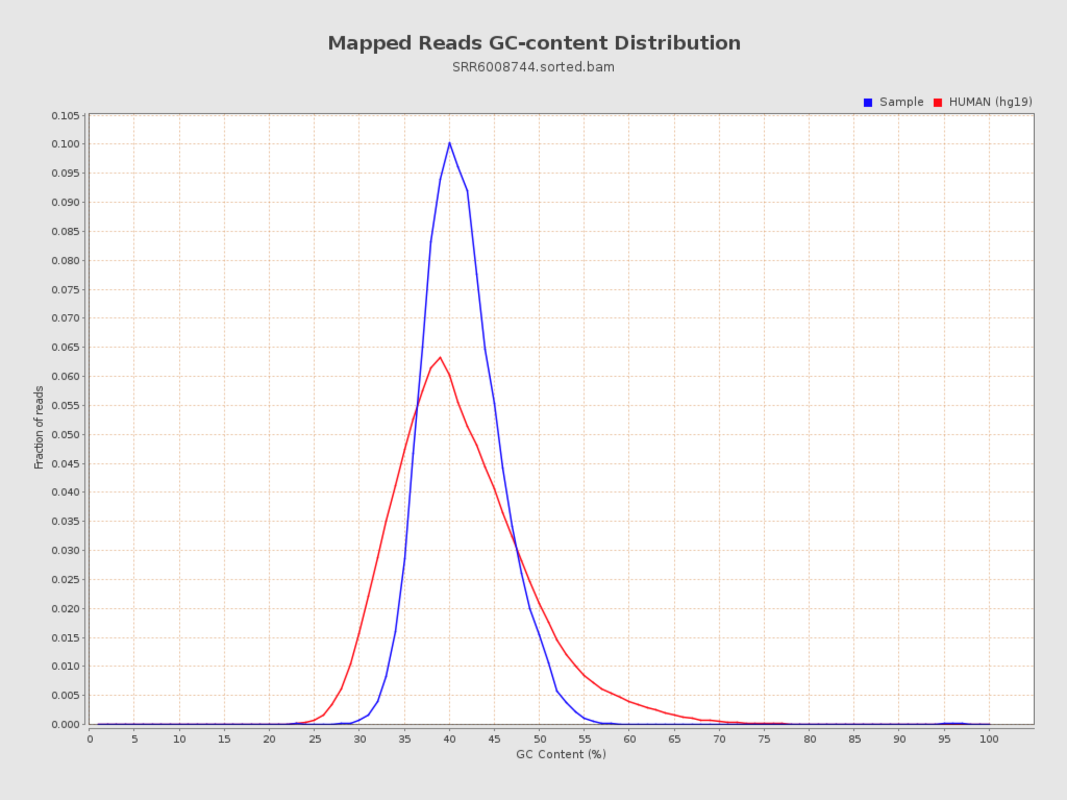
7. Results : Duplication Rate Histogram



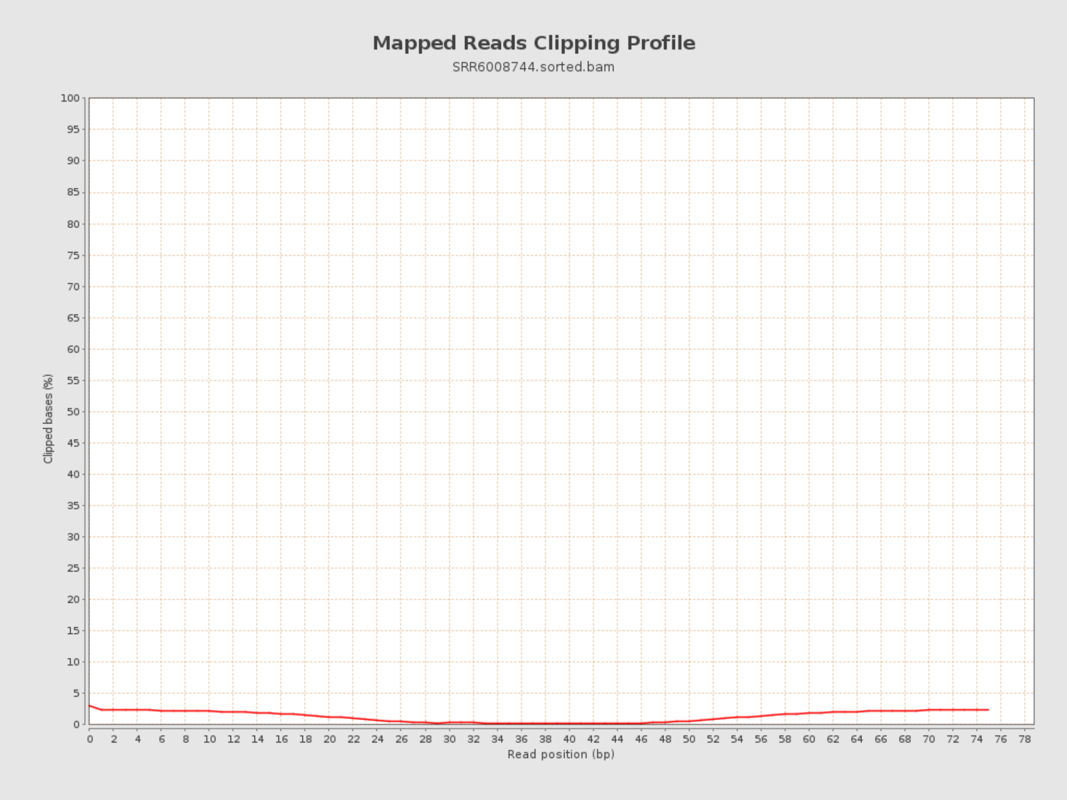
8. Results : Mapped Reads Nucleotide Content



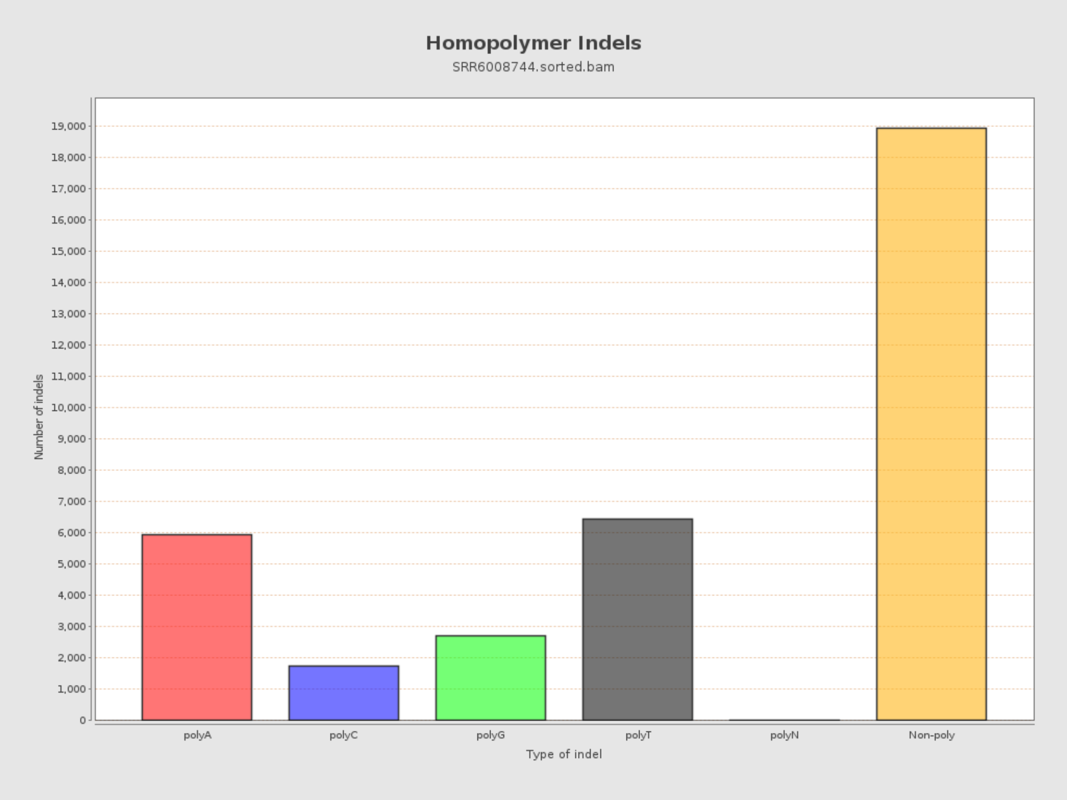
9. Results : Mapped Reads GC-content Distribution



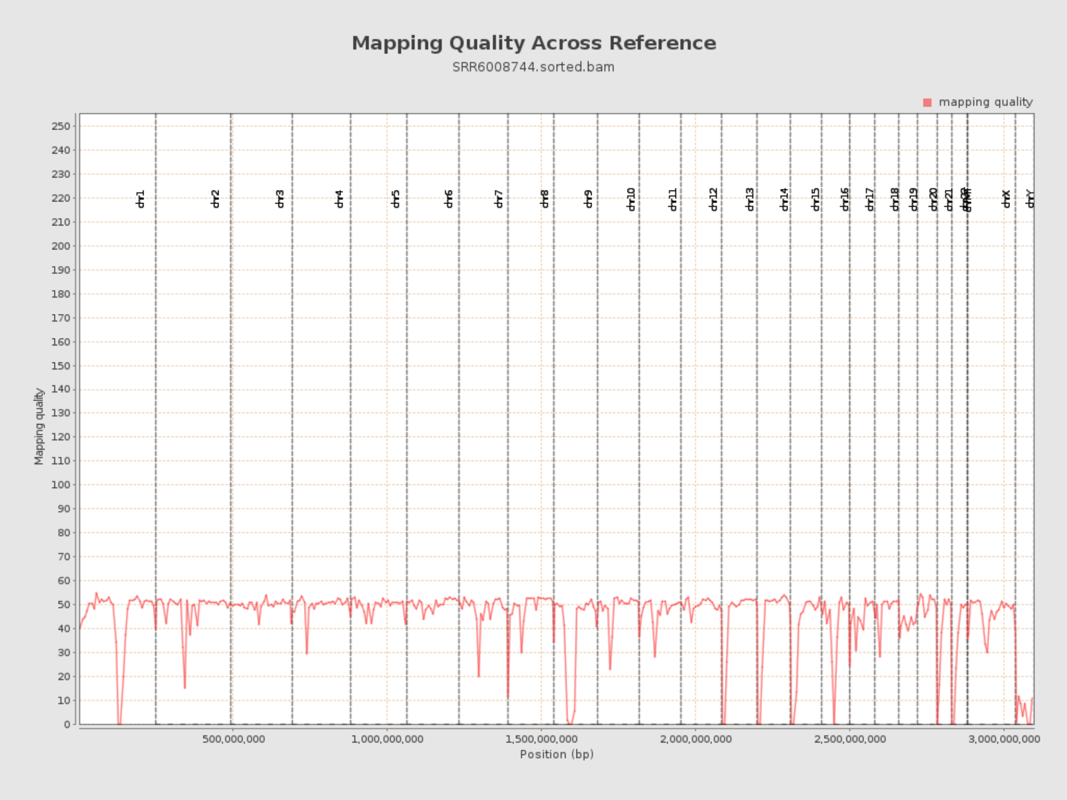
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram