Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 10:21:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008764.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_SRR6008764 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008764.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 10:21:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008764.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,457,509
Mapped reads	1,271,969 / 87.27%
Unmapped reads	185,540 / 12.73%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,585 / 0.66%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	88,101 / 6.04%
Duplication rate	5.53%
Clipped reads	604,323 / 41.46%

2.2. ACGT Content

Number/percentage of A's	22,386,563 / 26.78%
Number/percentage of C's	16,111,051 / 19.27%
Number/percentage of T's	25,817,237 / 30.88%
Number/percentage of G's	19,181,951 / 22.94%
Number/percentage of N's	112,428 / 0.13%
GC Percentage	42.21%

2.3. Coverage

Mean	0.027

Standard Deviation	0.2931

2.4. Mapping Quality

Mean Mapping Quality	45.18

2.5. Mismatches and indels

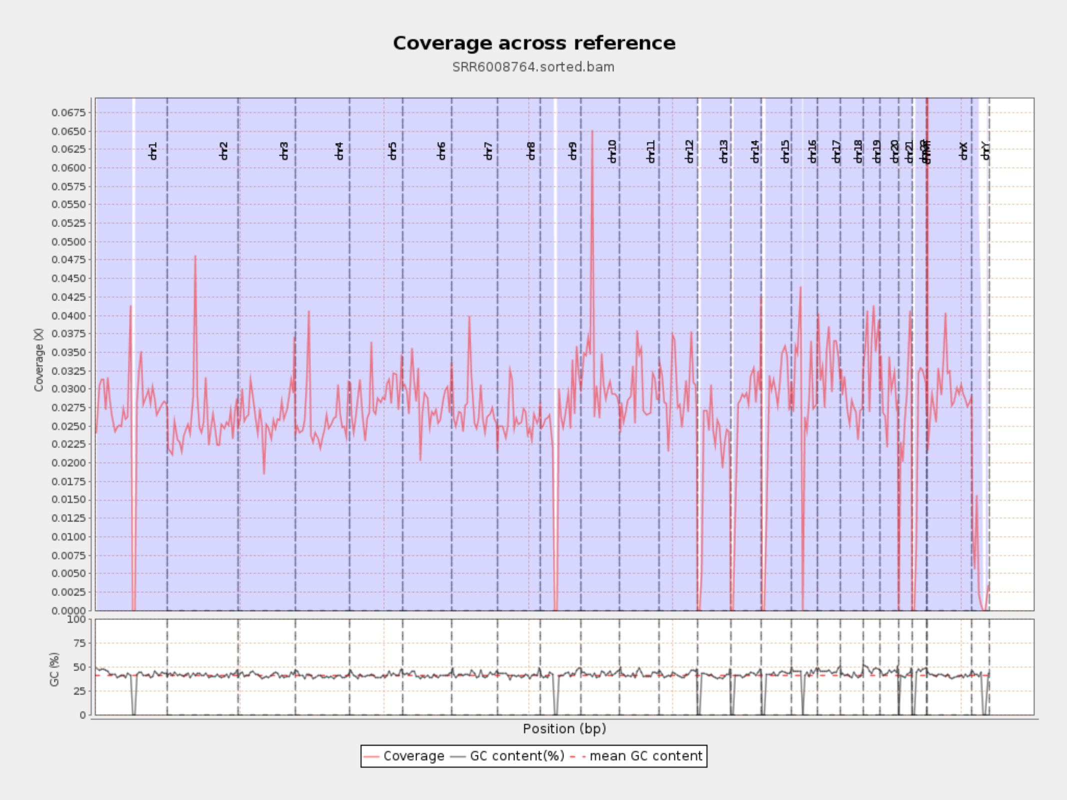
General error rate	0.86%
Mismatches	708,256
Insertions	6,286
Mapped reads with at least one insertion	0.49%
Deletions	22,688
Mapped reads with at least one deletion	1.76%
Homopolymer indels	44.51%

2.6. Chromosome stats

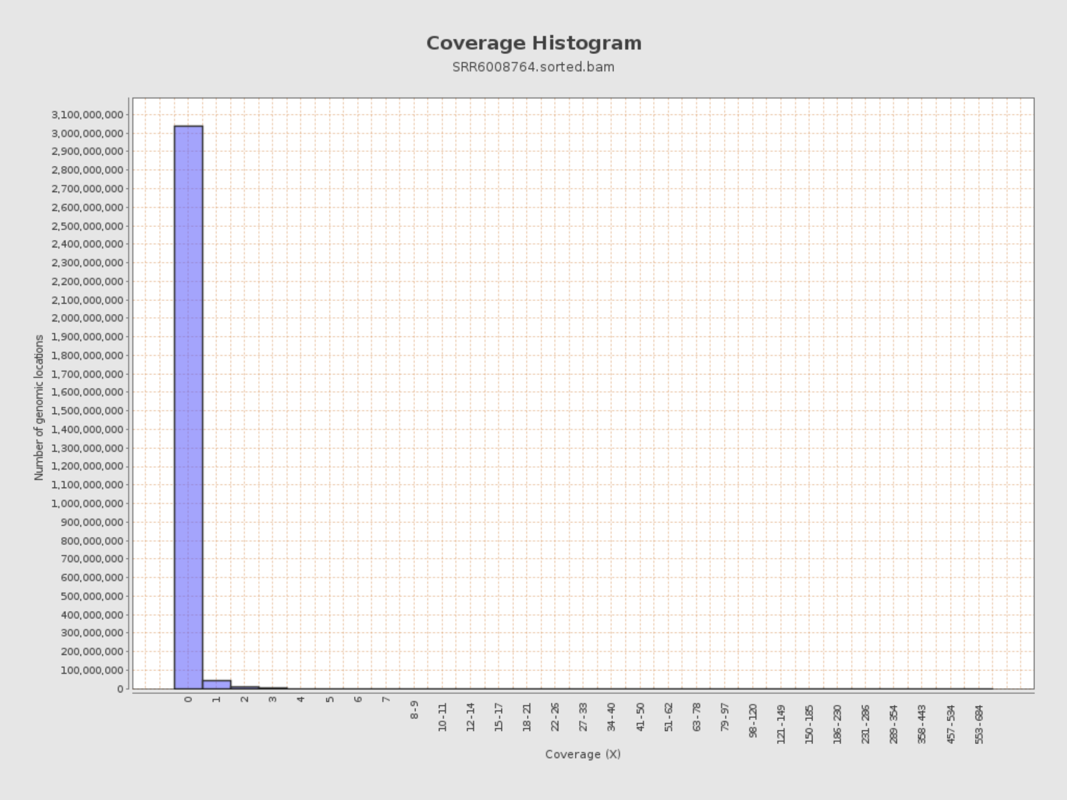
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6691131	0.0268	0.4047
chr2	243199373	6207775	0.0255	0.3886
chr3	198022430	5262508	0.0266	0.2209
chr4	191154276	4961035	0.026	0.2274
chr5	180915260	5189053	0.0287	0.2252
chr6	171115067	4855175	0.0284	0.2426
chr7	159138663	4354652	0.0274	0.295

chr8	146364022	3796590	0.0259	0.4462
chr9	141213431	3467716	0.0246	0.2512
chr10	135534747	4462234	0.0329	0.3755
chr11	135006516	3987719	0.0295	0.2666
chr12	133851895	4007931	0.0299	0.2315
chr13	115169878	2383834	0.0207	0.1904
chr14	107349540	2669408	0.0249	0.2234
chr15	102531392	2598196	0.0253	0.2105
chr16	90354753	2583101	0.0286	0.2597
chr17	81195210	2770706	0.0341	0.2566
chr18	78077248	2155868	0.0276	0.3701
chr19	59128983	2132904	0.0361	0.3545
chr20	63025520	1828623	0.029	0.2328
chr21	48129895	1250852	0.026	0.225
chr22	51304566	1117079	0.0218	0.1955
chrMT	16571	43915	2.6501	2.5314
chrX	155270560	4601410	0.0296	0.2376
chrY	59373566	270601	0.0046	0.1467

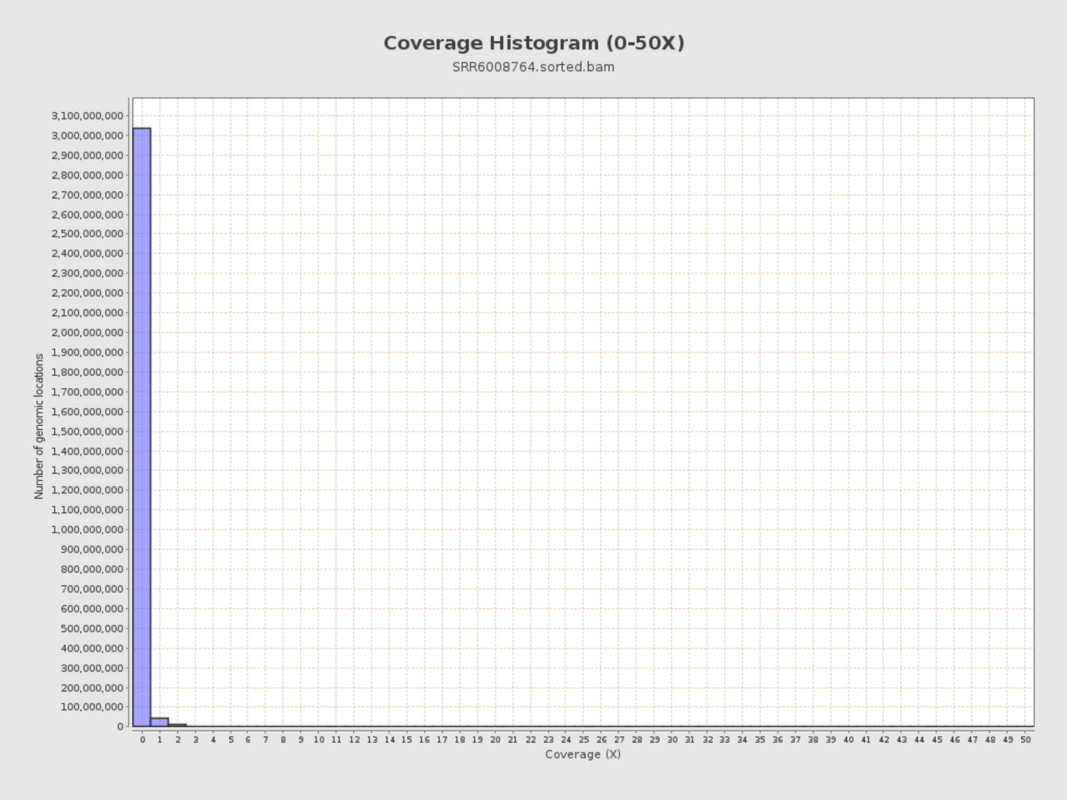
3. Results : Coverage across reference



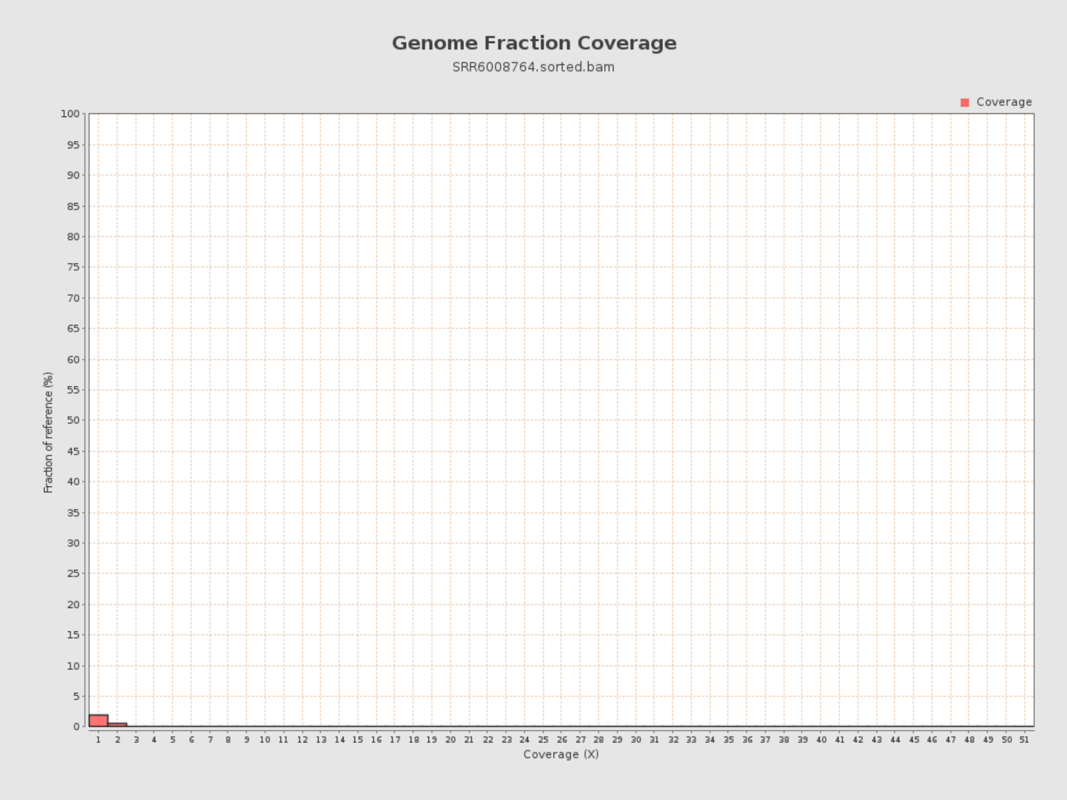
4. Results : Coverage Histogram



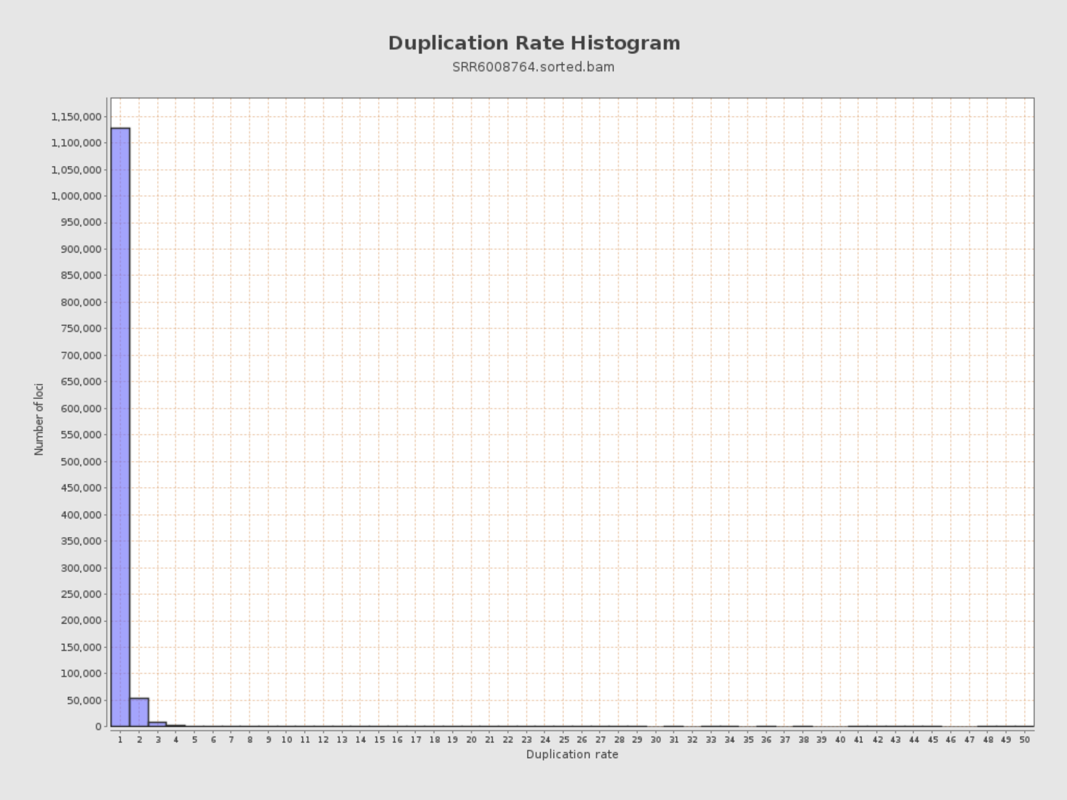
5. Results : Coverage Histogram (0-50X)



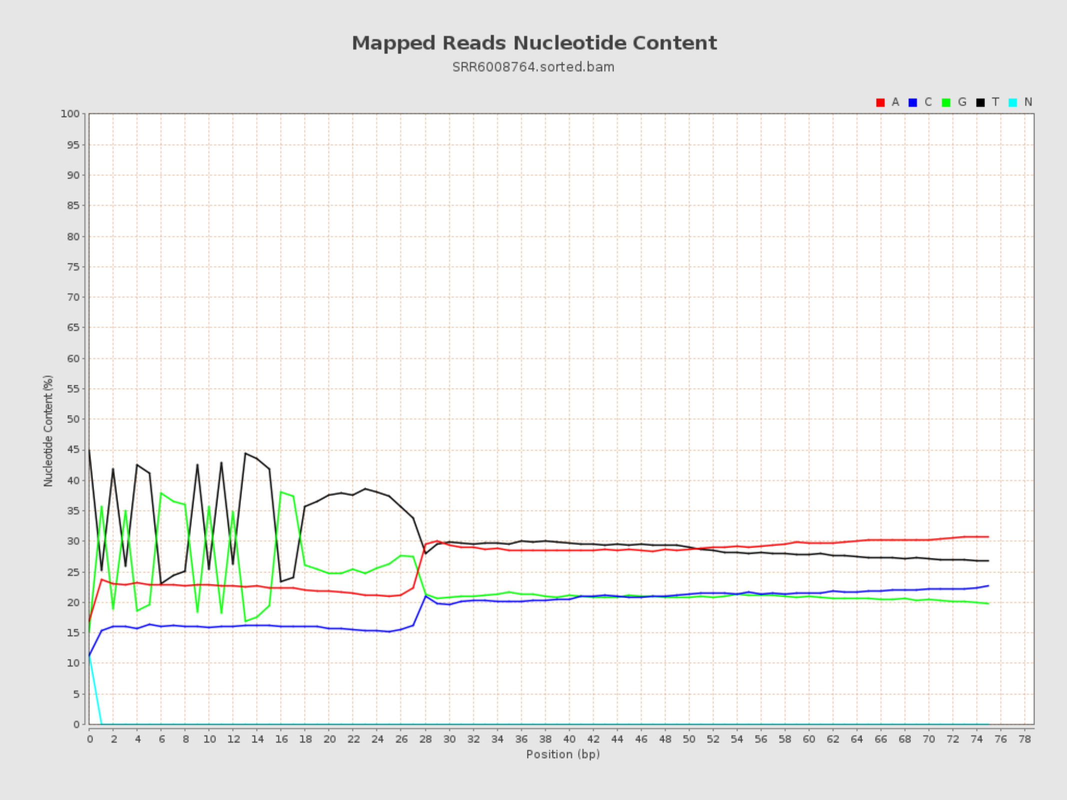
6. Results : Genome Fraction Coverage



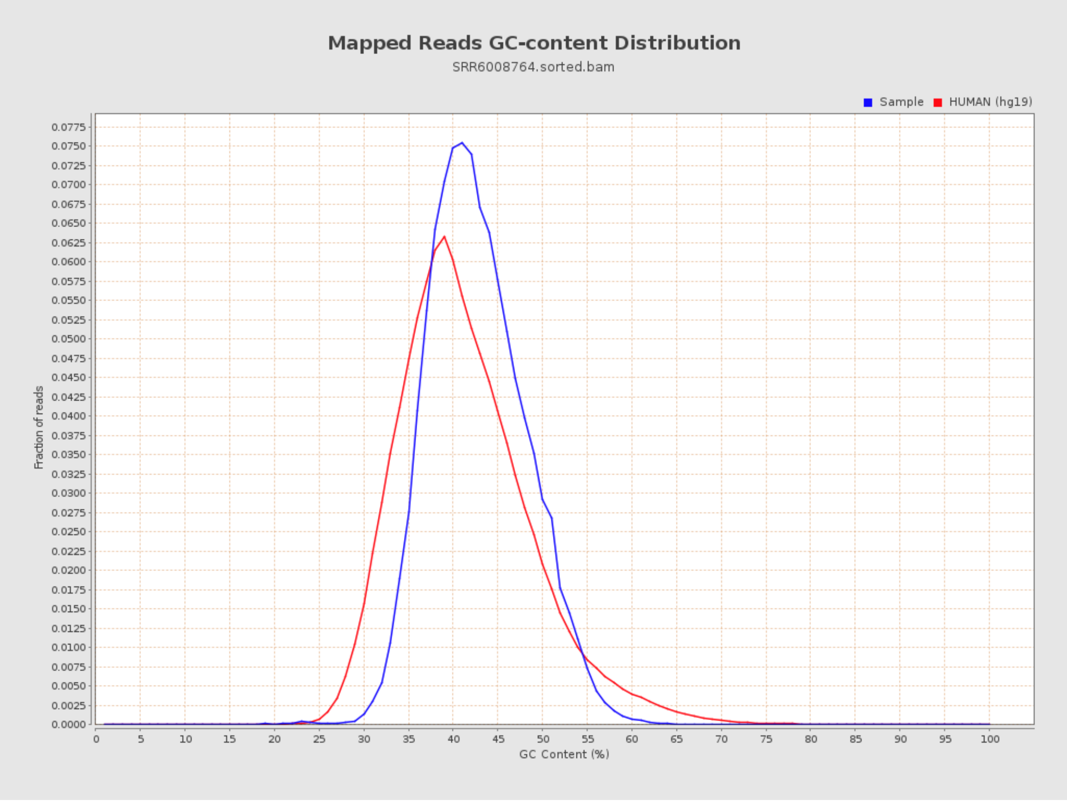
7. Results : Duplication Rate Histogram



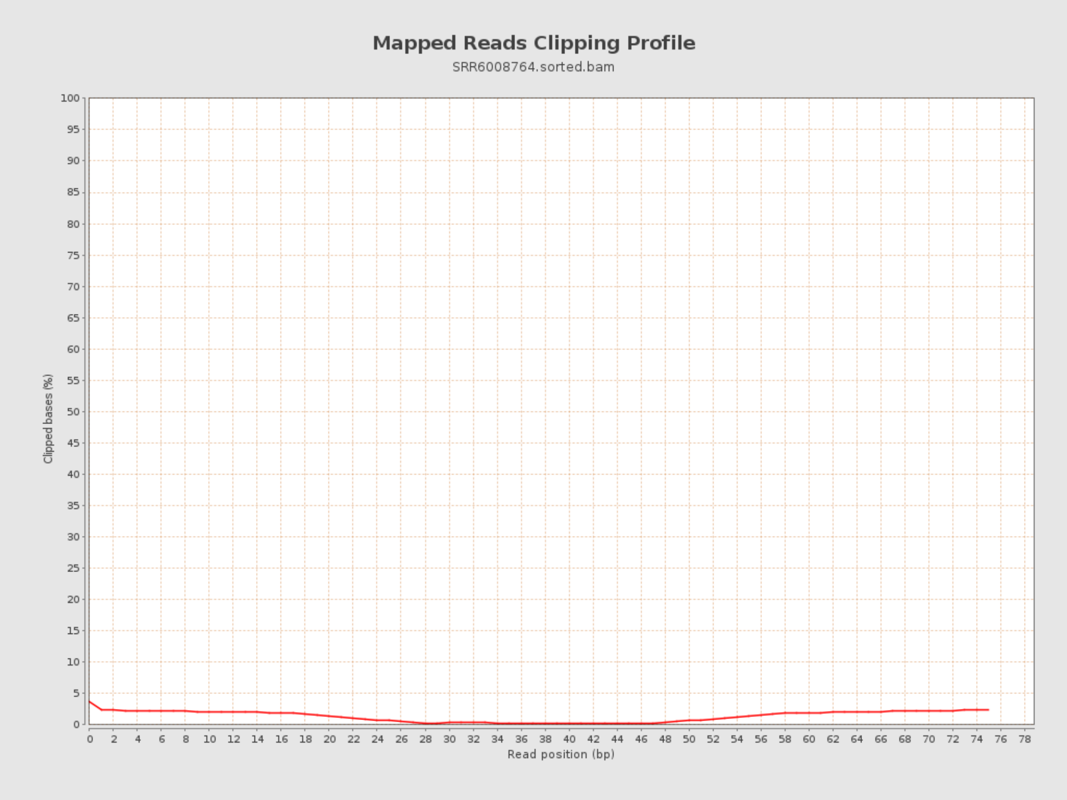
8. Results : Mapped Reads Nucleotide Content



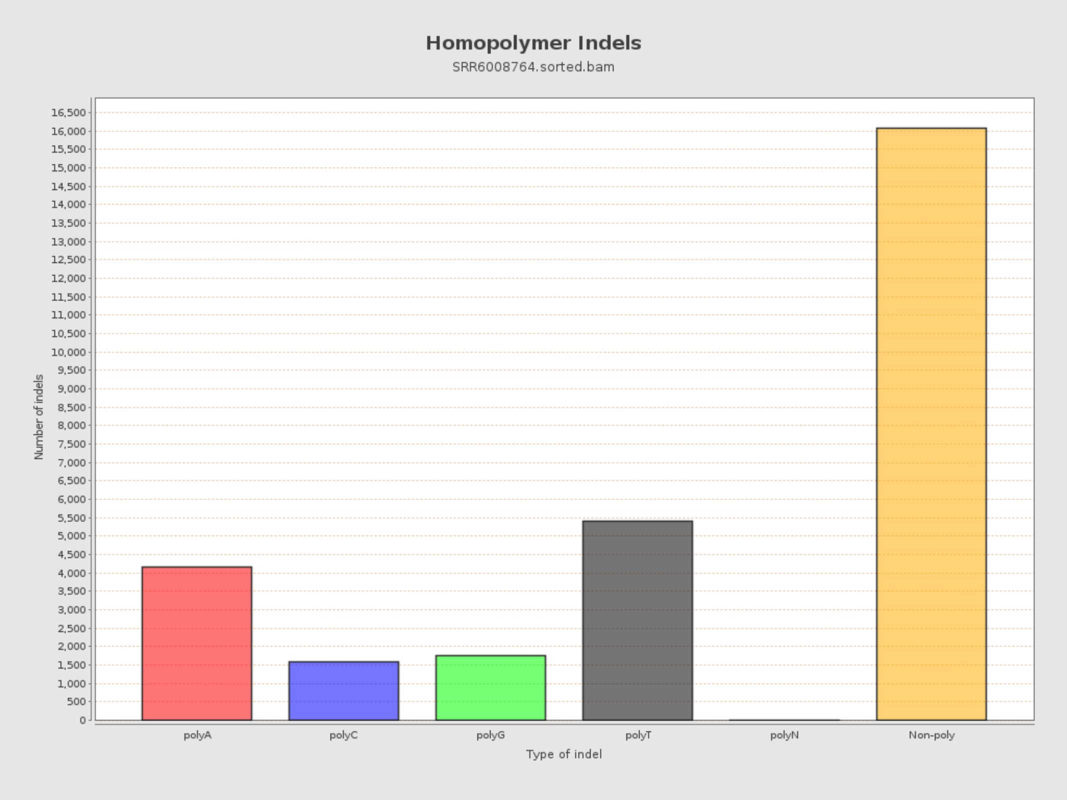
9. Results : Mapped Reads GC-content Distribution



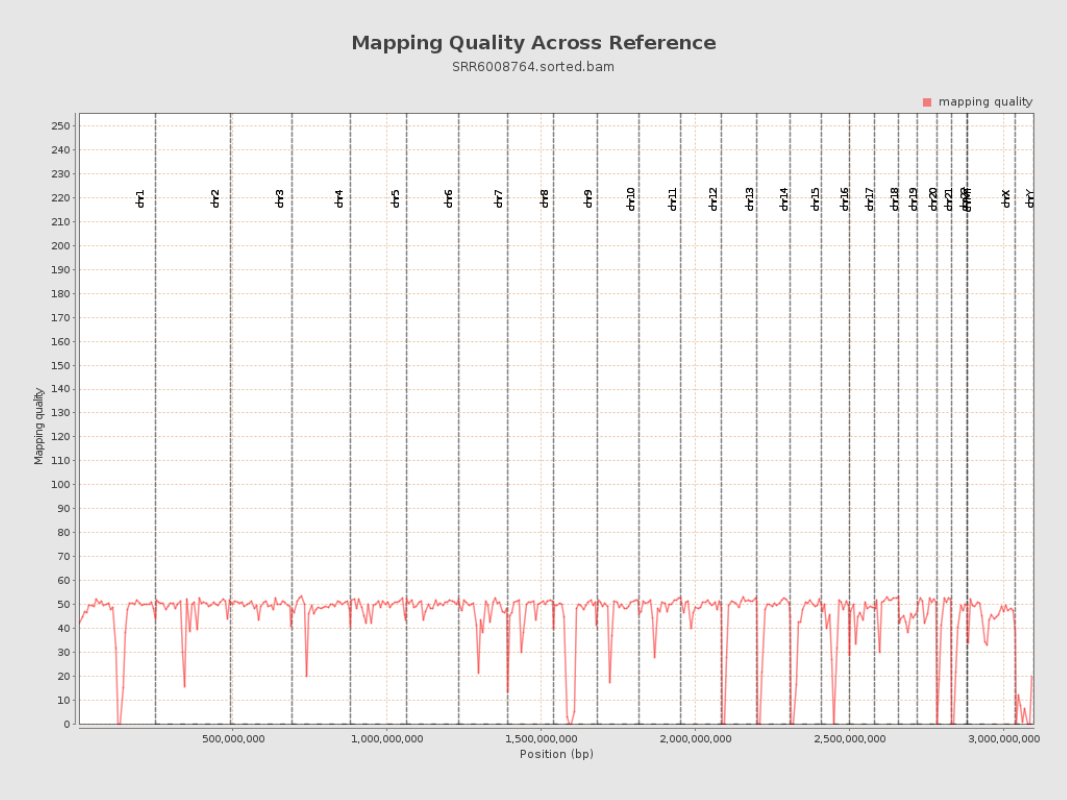
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram