Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 23:59:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716603.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_SRR9716603 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716603.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 23:59:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716603.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,636,334
Mapped reads	1,463,771 / 89.45%
Unmapped reads	172,563 / 10.55%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	40,474 / 2.47%
Read min/max/mean length	30 / 101 / 101.9
Duplicated reads (estimated)	40,435 / 2.47%
Duplication rate	1.78%
Clipped reads	1,500,893 / 91.72%

2.2. ACGT Content

Number/percentage of A's	29,297,530 / 26.36%
Number/percentage of C's	22,686,106 / 20.41%
Number/percentage of T's	33,642,733 / 30.27%
Number/percentage of G's	25,494,614 / 22.94%
Number/percentage of N's	14,041 / 0.01%
GC Percentage	43.35%

2.3. Coverage

Mean	0.0359

Standard Deviation	0.3243

2.4. Mapping Quality

Mean Mapping Quality	45.76

2.5. Mismatches and indels

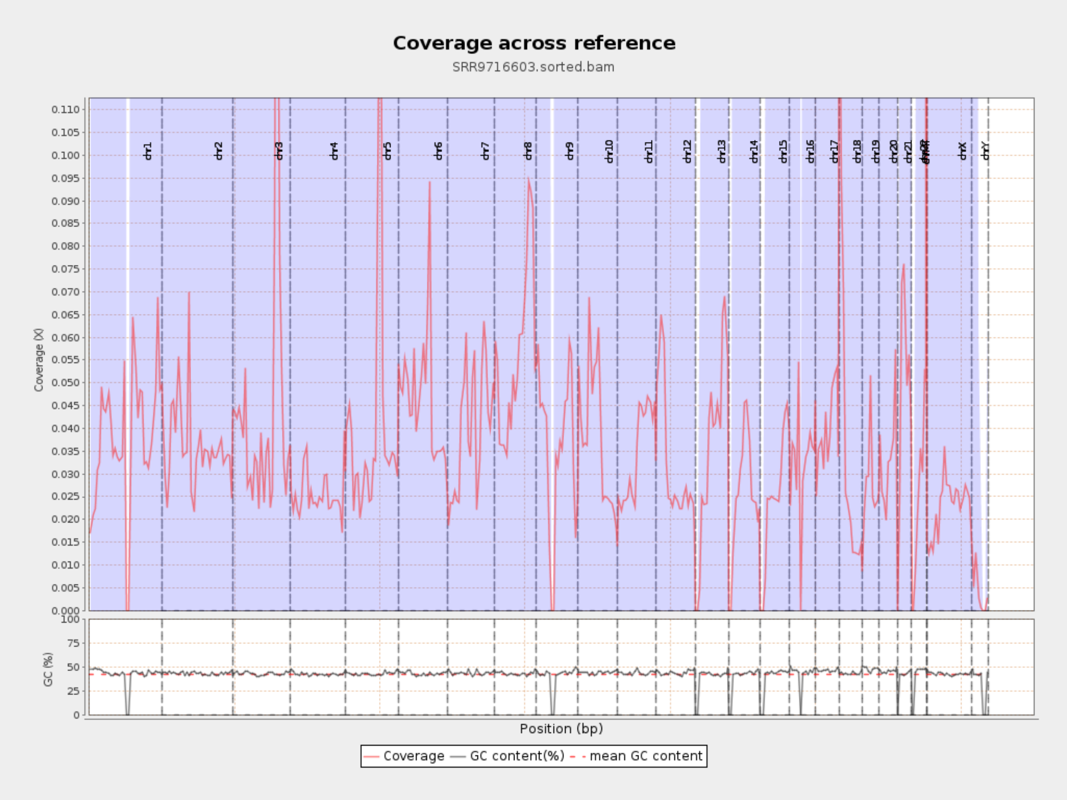
General error rate	0.76%
Mismatches	821,011
Insertions	10,021
Mapped reads with at least one insertion	0.68%
Deletions	24,323
Mapped reads with at least one deletion	1.64%
Homopolymer indels	40.71%

2.6. Chromosome stats

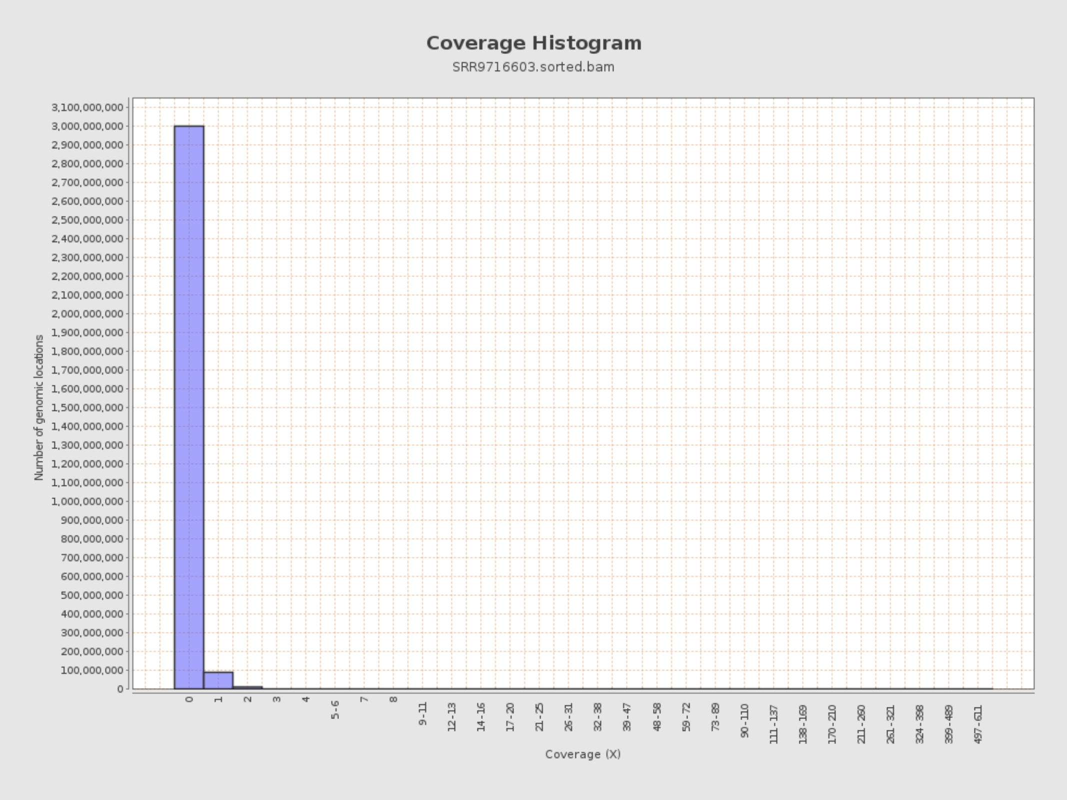
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9393851	0.0377	0.4808
chr2	243199373	8793274	0.0362	0.4756
chr3	198022430	8905221	0.045	0.2385
chr4	191154276	4842220	0.0253	0.1826
chr5	180915260	7393674	0.0409	0.2247
chr6	171115067	8061807	0.0471	0.2696
chr7	159138663	6412128	0.0403	0.4388

chr8	146364022	8364521	0.0571	0.4192
chr9	141213431	5044177	0.0357	0.3033
chr10	135534747	5279754	0.039	0.3478
chr11	135006516	4636539	0.0343	0.2563
chr12	133851895	4300404	0.0321	0.1983
chr13	115169878	4199060	0.0365	0.2091
chr14	107349540	2718202	0.0253	0.192
chr15	102531392	2534191	0.0247	0.1712
chr16	90354753	2924052	0.0324	0.2237
chr17	81195210	3211303	0.0396	0.2436
chr18	78077248	2857777	0.0366	0.5925
chr19	59128983	1659174	0.0281	0.3763
chr20	63025520	2101576	0.0333	0.2176
chr21	48129895	2355058	0.0489	0.2516
chr22	51304566	1247429	0.0243	0.1714
chrMT	16571	125784	7.5906	5.4096
chrX	155270560	3575981	0.023	0.2046
chrY	59373566	239744	0.004	0.1241

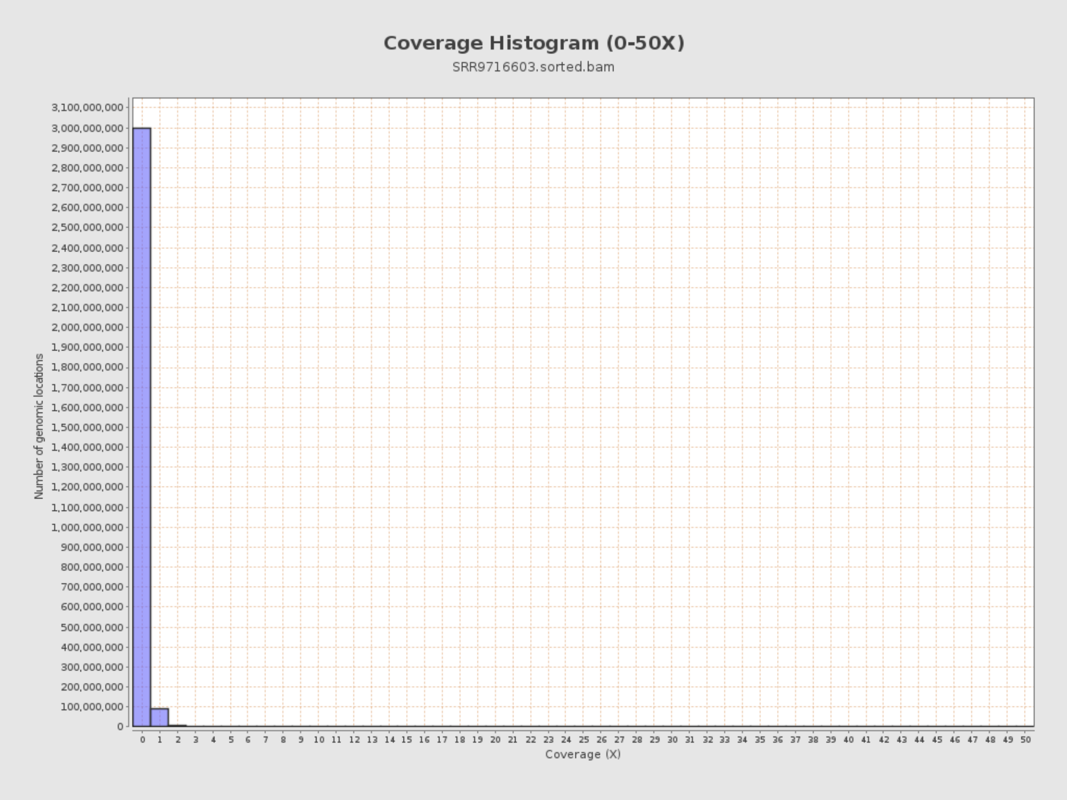
3. Results : Coverage across reference



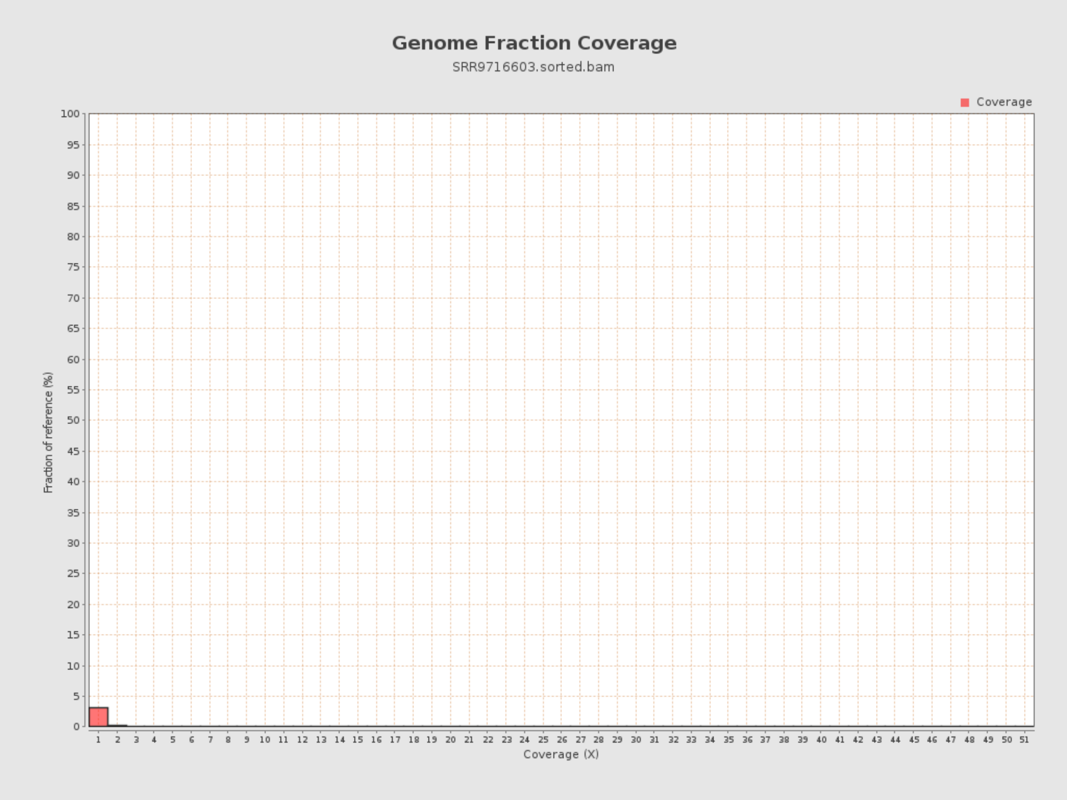
4. Results : Coverage Histogram



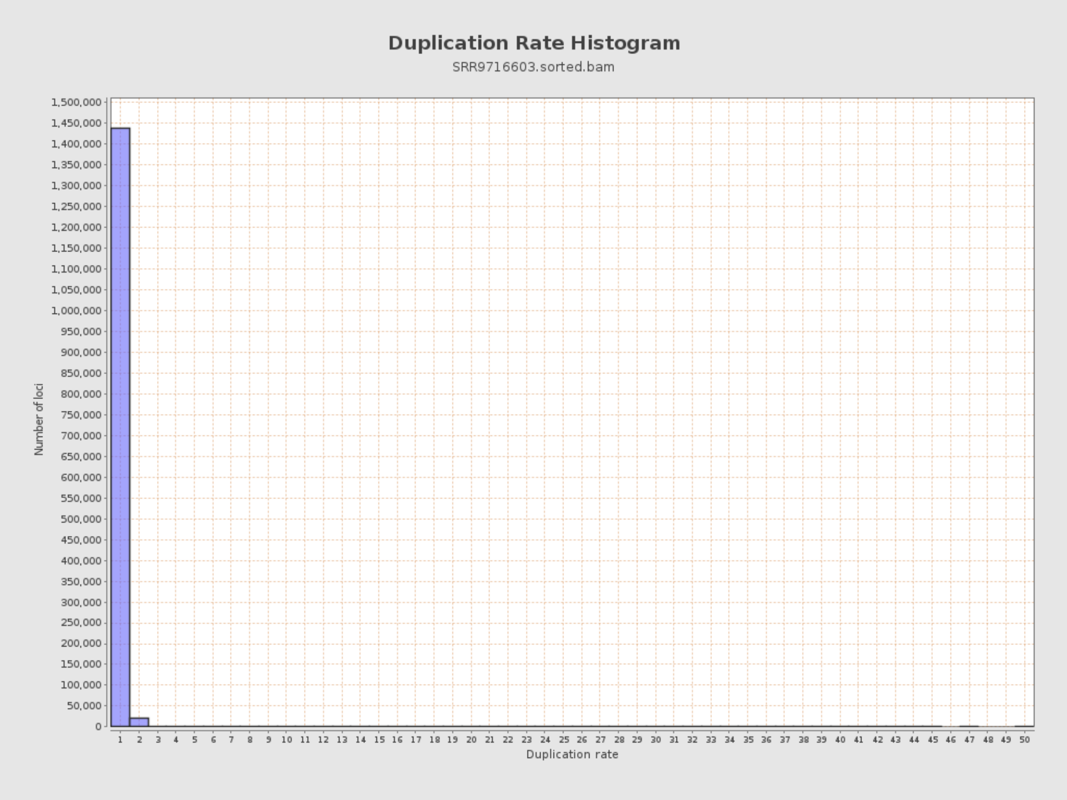
5. Results : Coverage Histogram (0-50X)



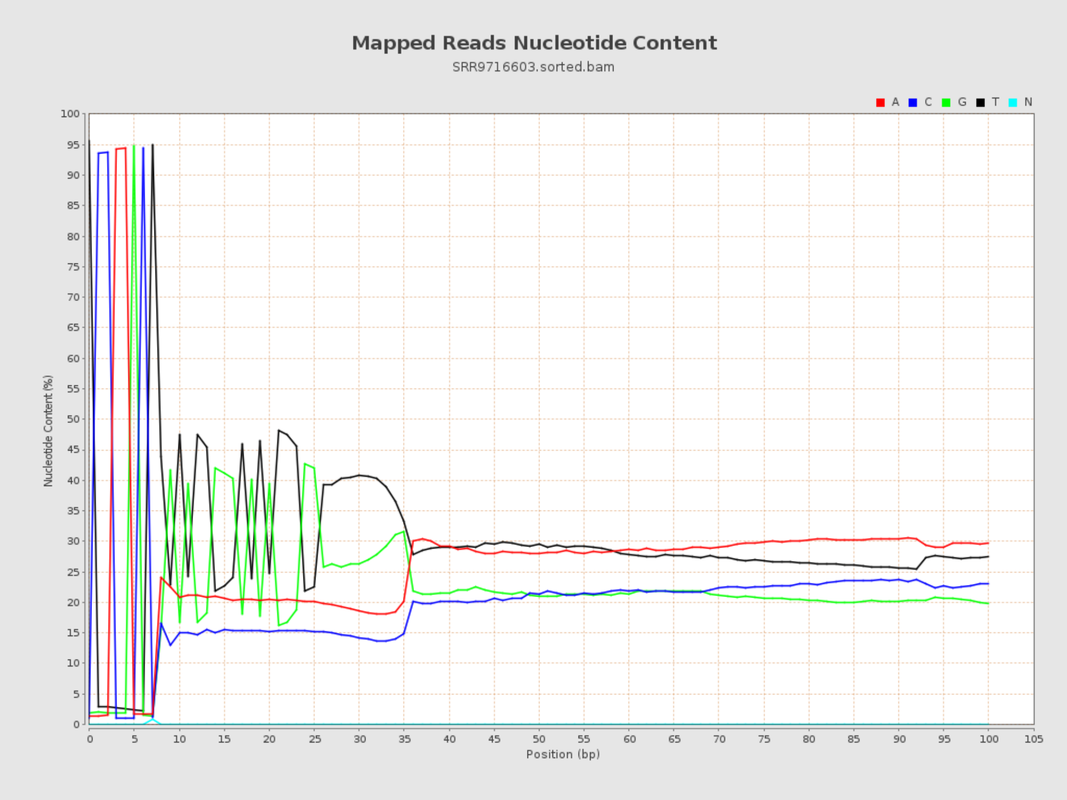
6. Results : Genome Fraction Coverage



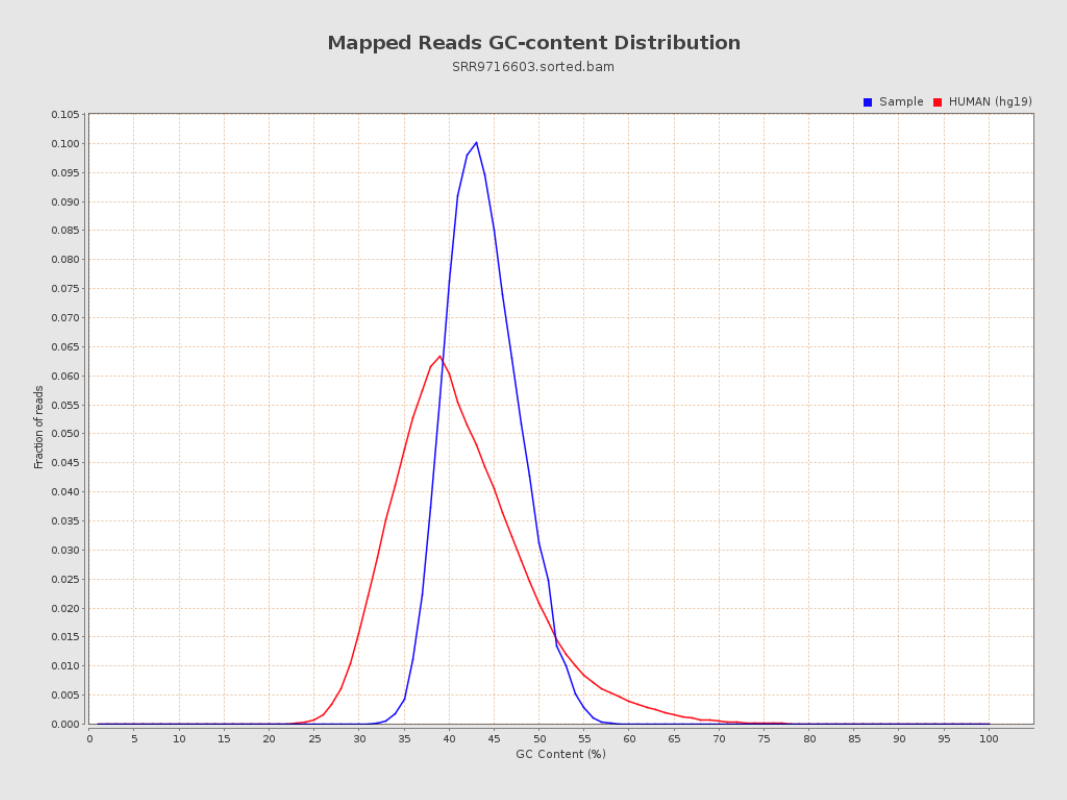
7. Results : Duplication Rate Histogram



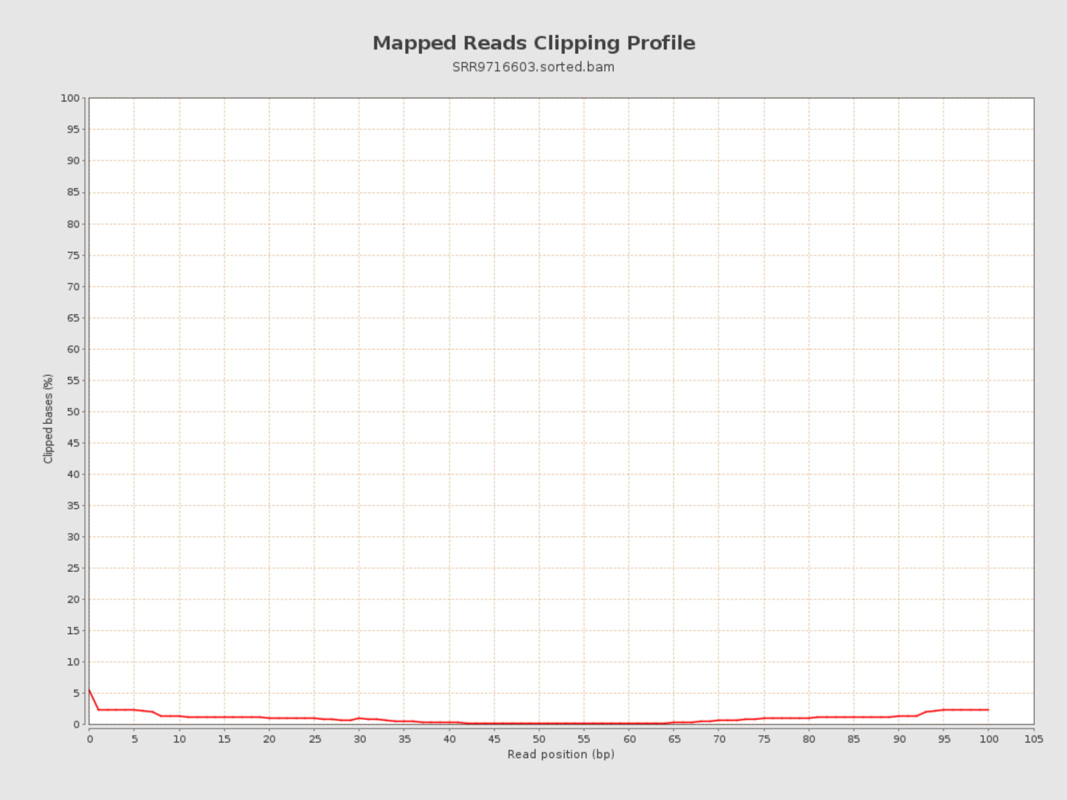
8. Results : Mapped Reads Nucleotide Content



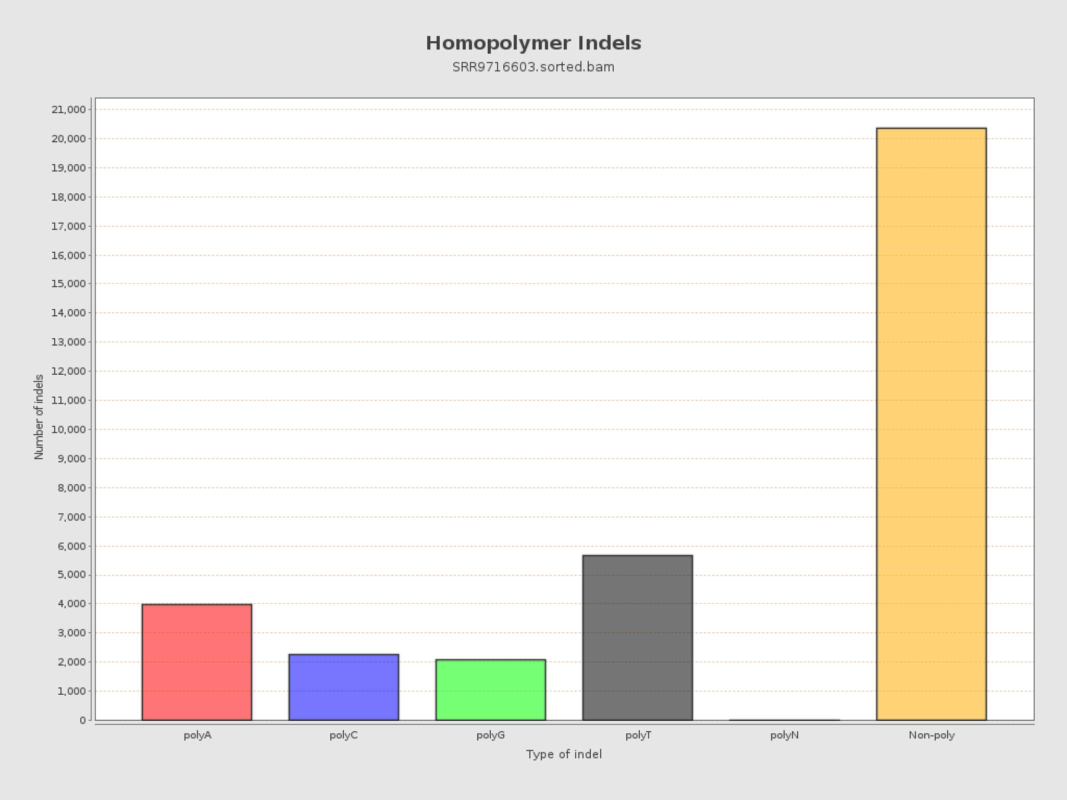
9. Results : Mapped Reads GC-content Distribution



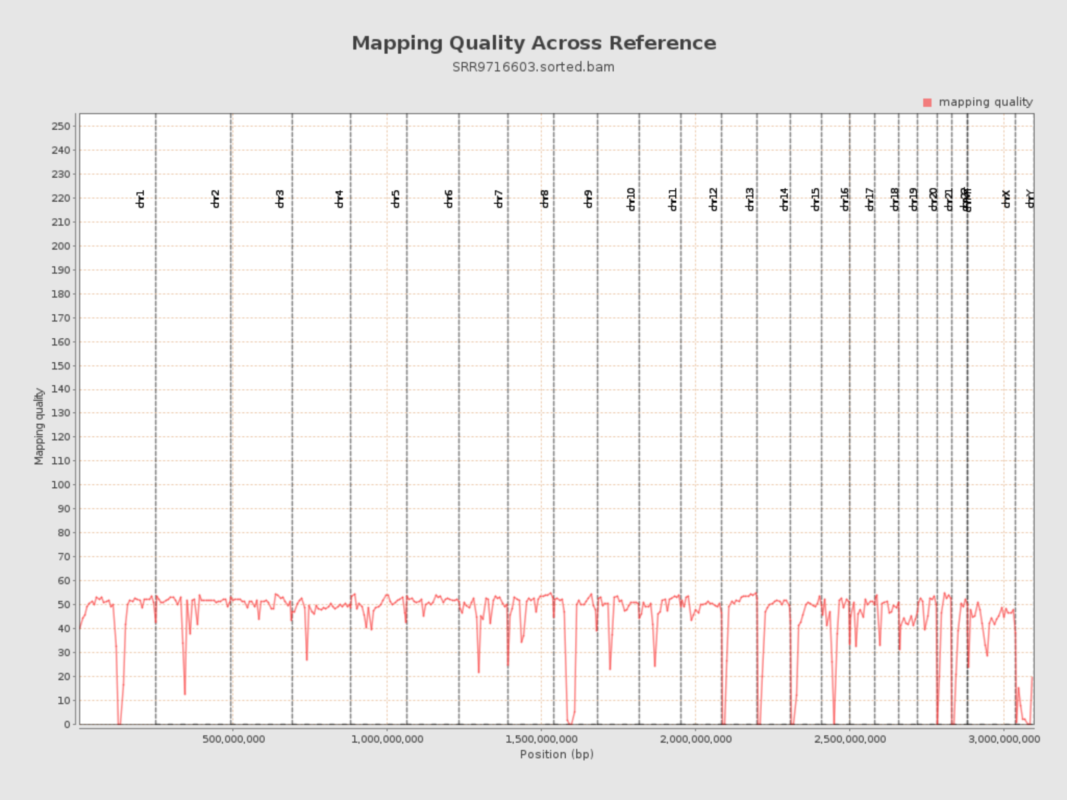
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram