Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 17:02:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9867864.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_SRR9867864 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9867864.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 17:02:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9867864.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,867,628
Mapped reads	1,715,740 / 91.87%
Unmapped reads	151,888 / 8.13%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,536 / 0.4%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	77,434 / 4.15%
Duplication rate	3.38%
Clipped reads	1,719,429 / 92.06%

2.2. ACGT Content

Number/percentage of A's	25,857,393 / 25.71%
Number/percentage of C's	18,695,798 / 18.59%
Number/percentage of T's	32,340,344 / 32.15%
Number/percentage of G's	23,675,425 / 23.54%
Number/percentage of N's	13,409 / 0.01%
GC Percentage	42.13%

2.3. Coverage

Mean	0.0325

Standard Deviation	0.3064

2.4. Mapping Quality

Mean Mapping Quality	45.58

2.5. Mismatches and indels

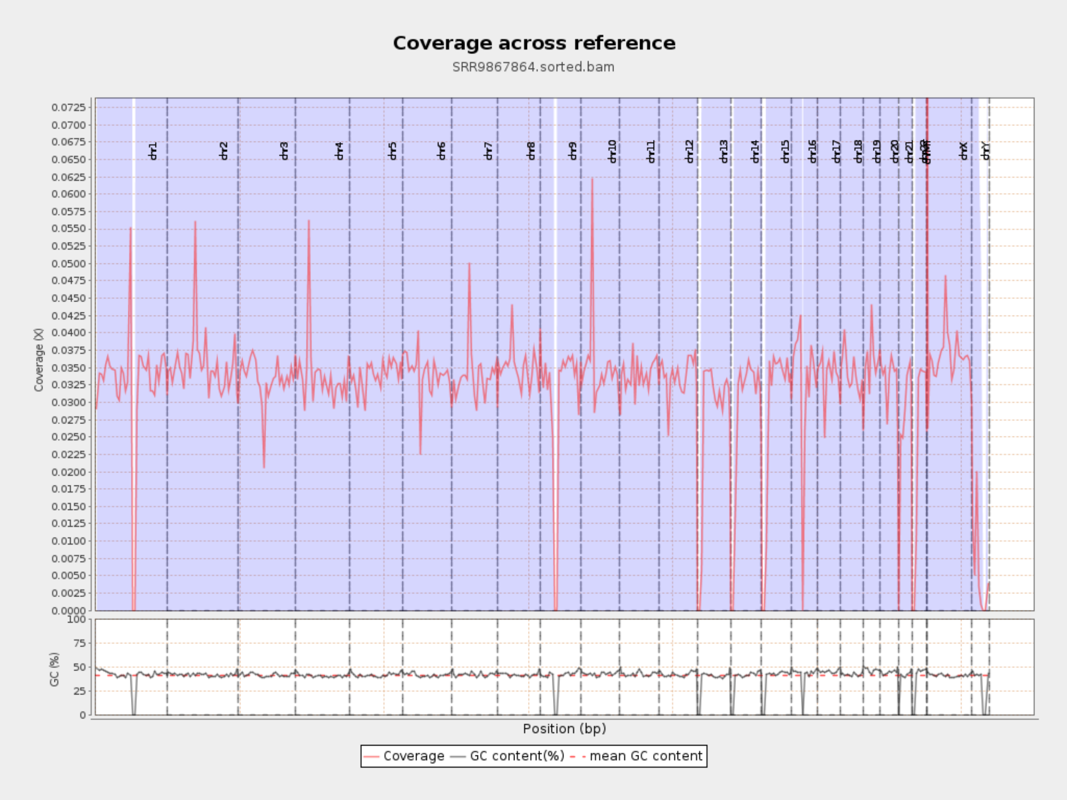
General error rate	0.52%
Mismatches	507,781
Insertions	7,681
Mapped reads with at least one insertion	0.45%
Deletions	18,631
Mapped reads with at least one deletion	1.08%
Homopolymer indels	41.9%

2.6. Chromosome stats

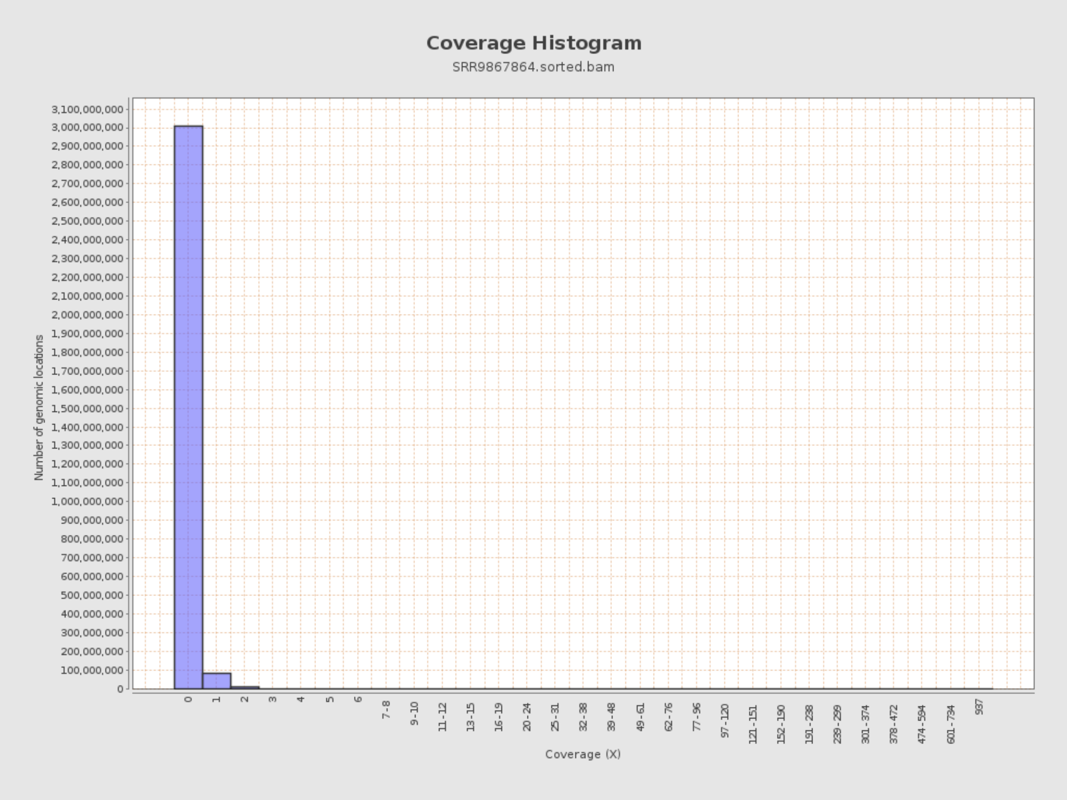
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8083112	0.0324	0.5445
chr2	243199373	8644095	0.0355	0.4528
chr3	198022430	6587240	0.0333	0.2003
chr4	191154276	6495264	0.034	0.232
chr5	180915260	6138512	0.0339	0.2041
chr6	171115067	5843858	0.0342	0.2345
chr7	159138663	5413051	0.034	0.3442

chr8	146364022	5131964	0.0351	0.3079
chr9	141213431	4265701	0.0302	0.2557
chr10	135534747	4799414	0.0354	0.3095
chr11	135006516	4603787	0.0341	0.2612
chr12	133851895	4530903	0.0339	0.2066
chr13	115169878	3107498	0.027	0.1834
chr14	107349540	2981464	0.0278	0.1931
chr15	102531392	2879689	0.0281	0.1894
chr16	90354753	2910578	0.0322	0.2128
chr17	81195210	2760121	0.034	0.2153
chr18	78077248	2671992	0.0342	0.4575
chr19	59128983	2127938	0.036	0.3966
chr20	63025520	2110152	0.0335	0.2055
chr21	48129895	1312858	0.0273	0.2132
chr22	51304566	1197247	0.0233	0.1676
chrMT	16571	9766	0.5893	0.8407
chrX	155270560	5682503	0.0366	0.2328
chrY	59373566	323597	0.0055	0.1848

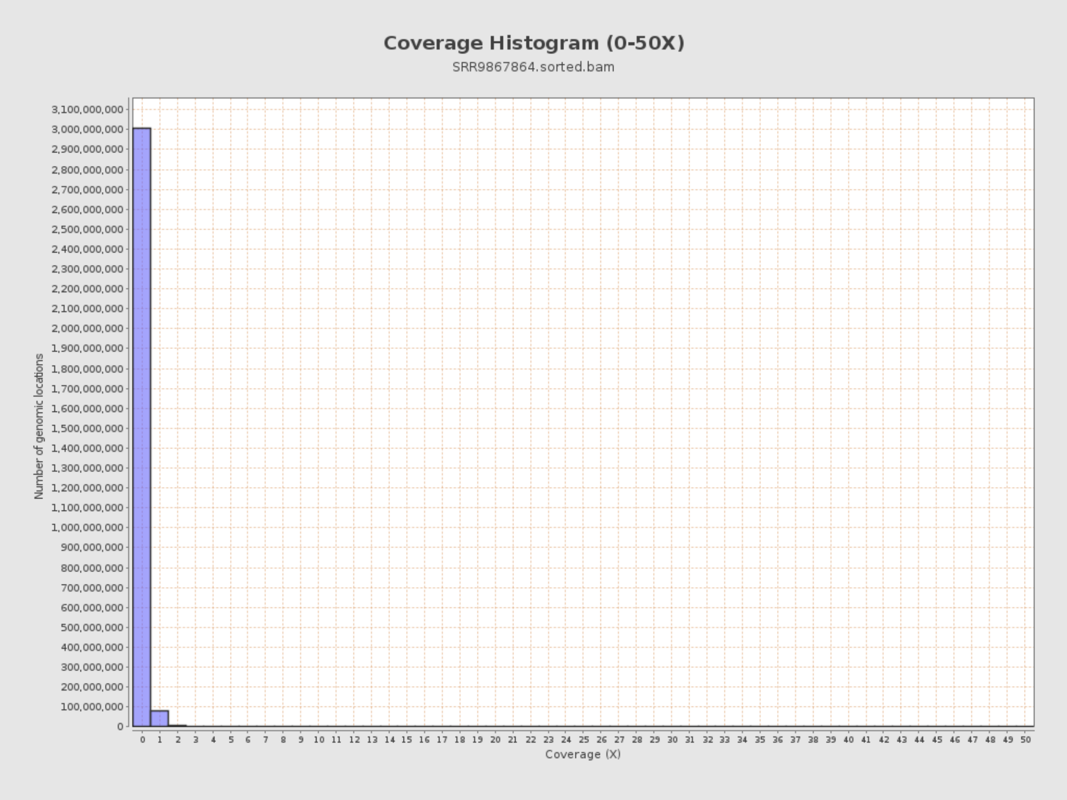
3. Results : Coverage across reference



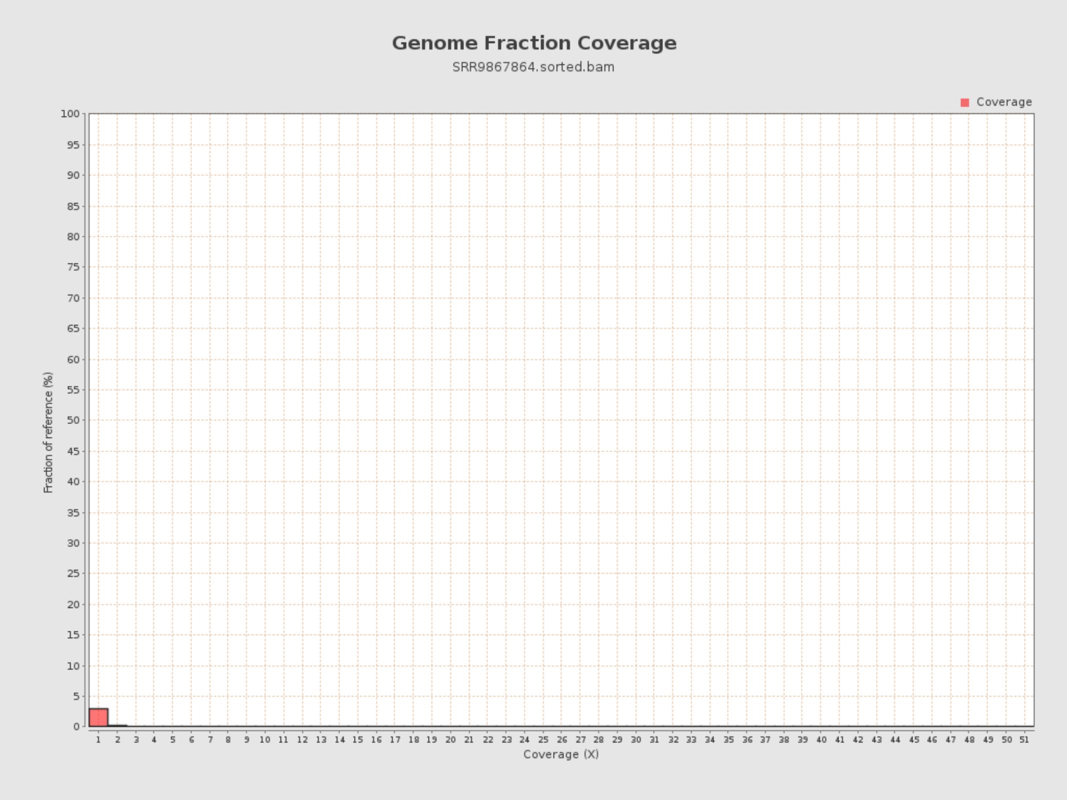
4. Results : Coverage Histogram



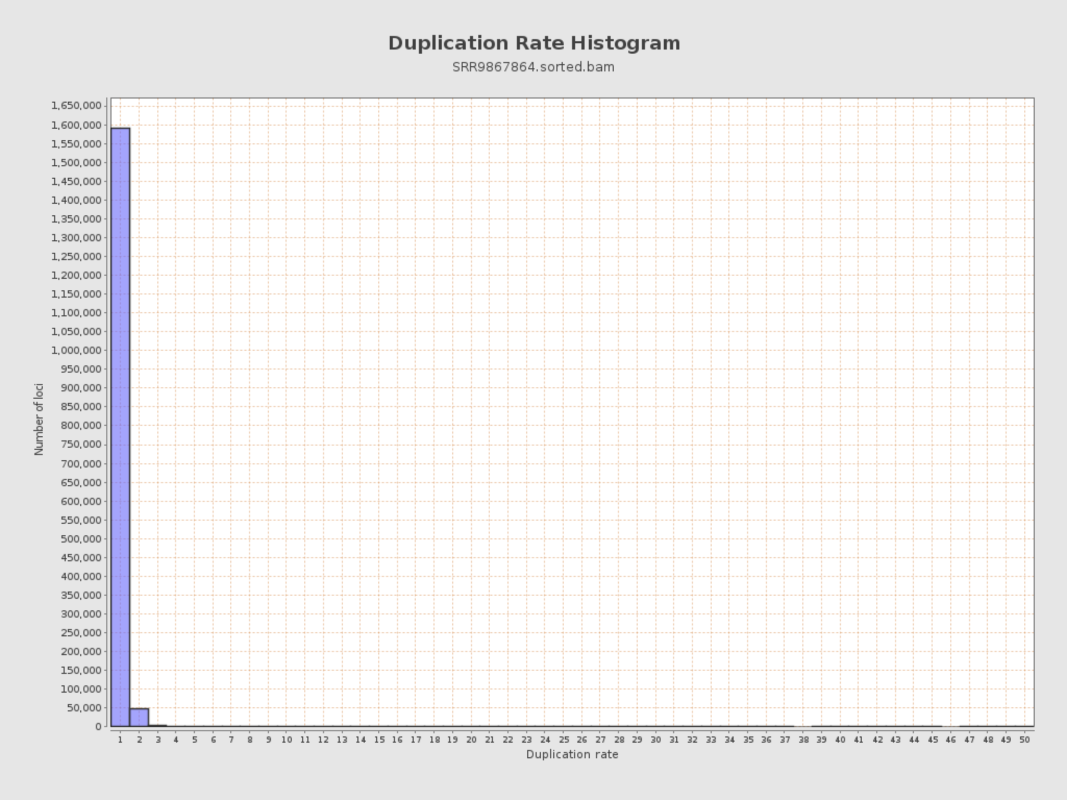
5. Results : Coverage Histogram (0-50X)



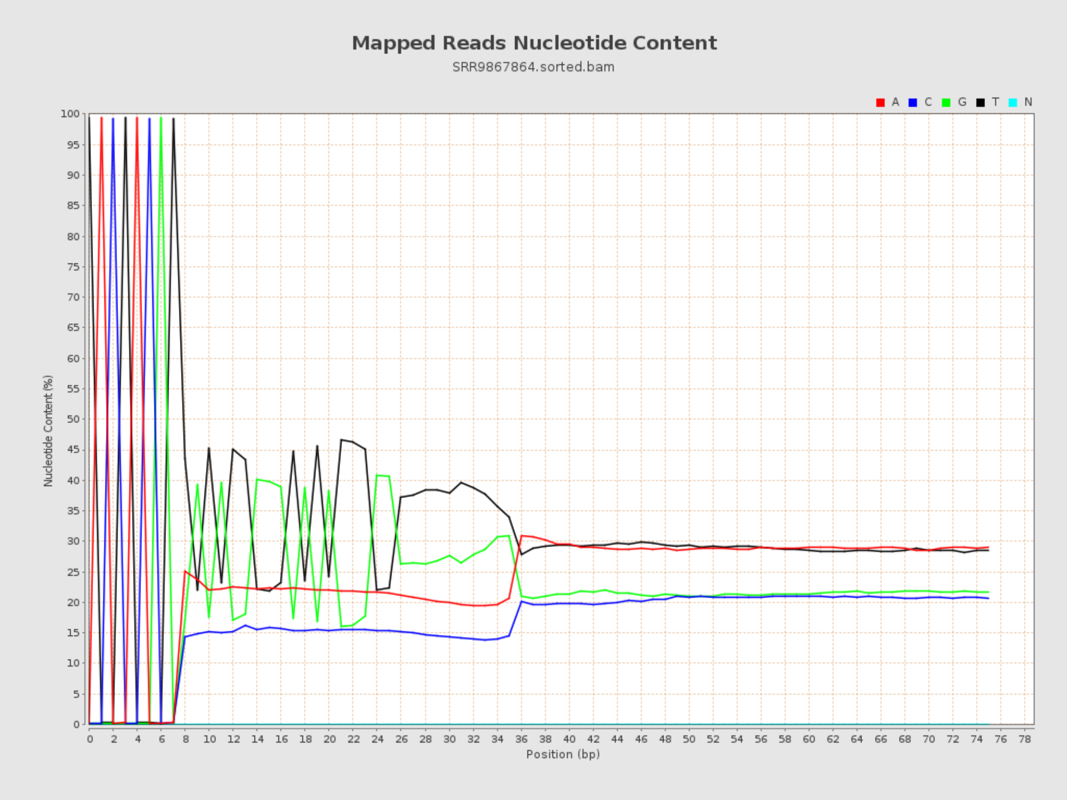
6. Results : Genome Fraction Coverage



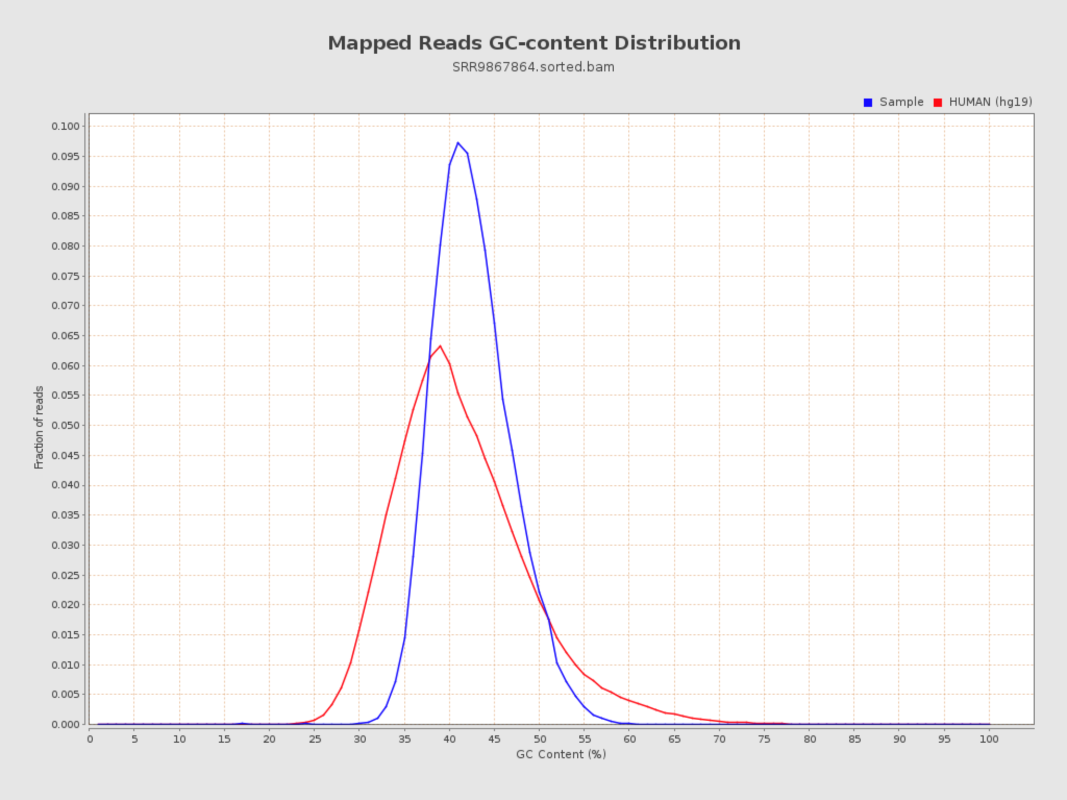
7. Results : Duplication Rate Histogram



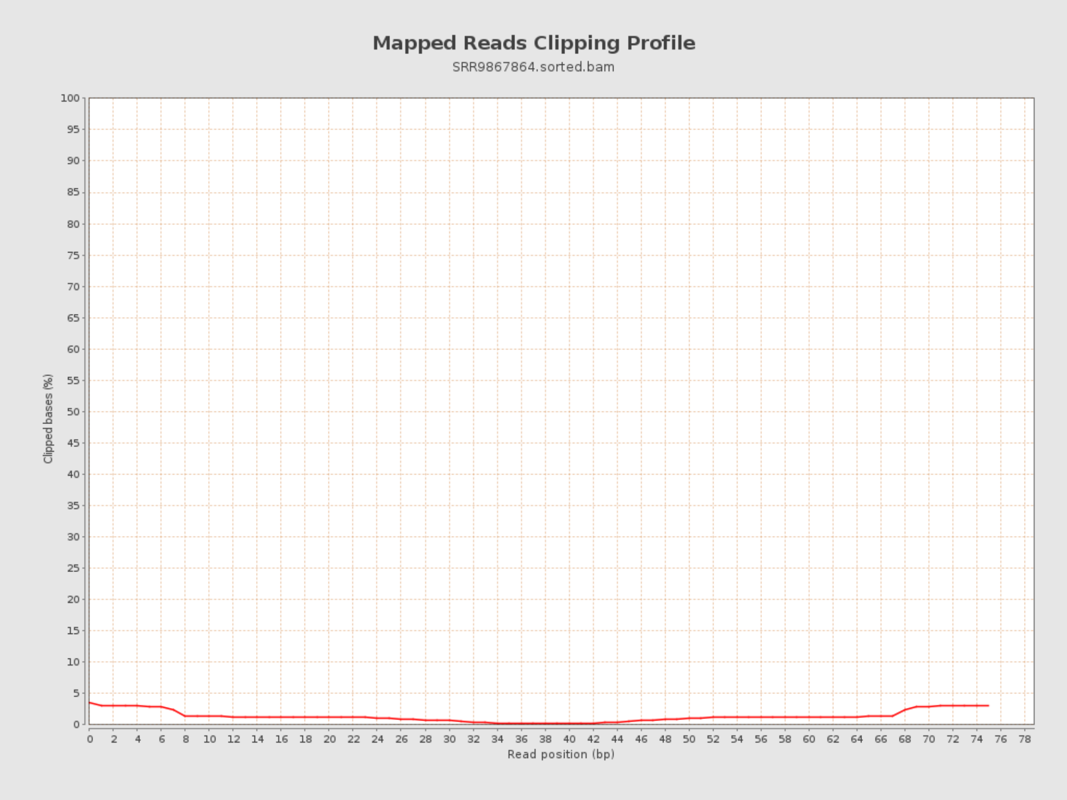
8. Results : Mapped Reads Nucleotide Content



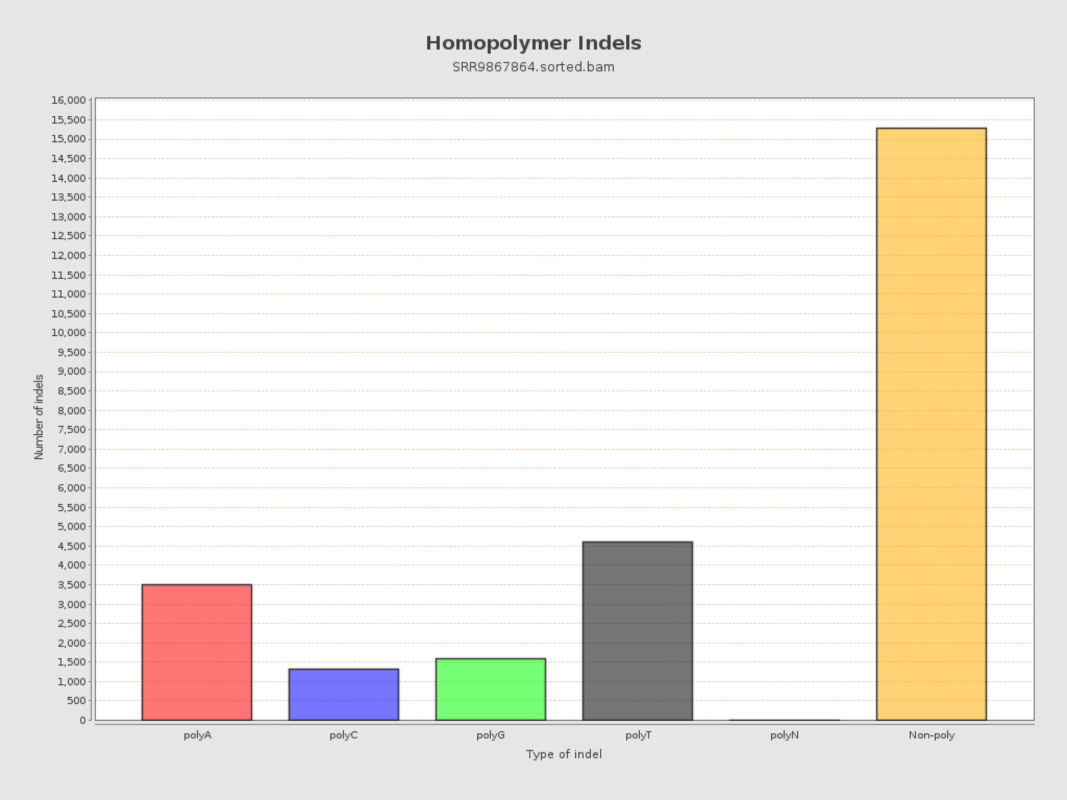
9. Results : Mapped Reads GC-content Distribution



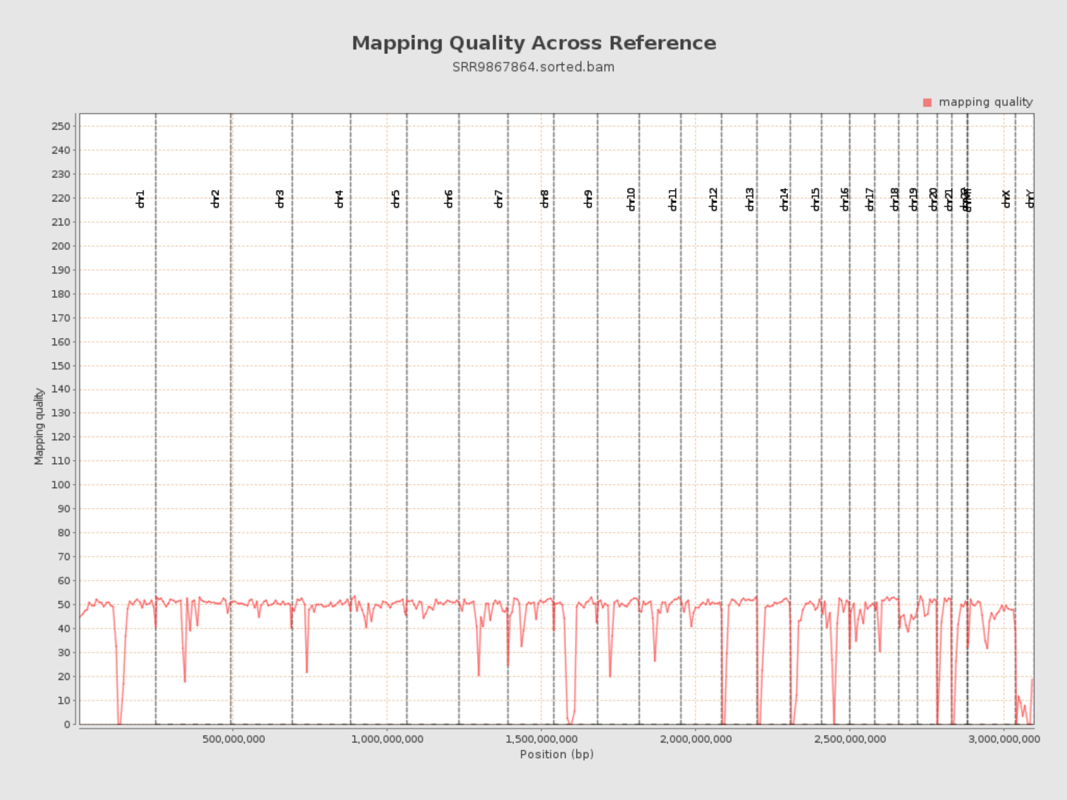
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram