Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 10:01:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9867845.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_SRR9867845 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9867845.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 10:01:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9867845.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,616,665
Mapped reads	2,409,374 / 92.08%
Unmapped reads	207,291 / 7.92%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,040 / 0.38%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	134,284 / 5.13%
Duplication rate	4.15%
Clipped reads	2,414,336 / 92.27%

2.2. ACGT Content

Number/percentage of A's	34,339,859 / 24.17%
Number/percentage of C's	26,715,897 / 18.8%
Number/percentage of T's	45,440,747 / 31.98%
Number/percentage of G's	35,562,744 / 25.03%
Number/percentage of N's	18,537 / 0.01%
GC Percentage	43.83%

2.3. Coverage

Mean	0.0459

Standard Deviation	0.4094

2.4. Mapping Quality

Mean Mapping Quality	45.84

2.5. Mismatches and indels

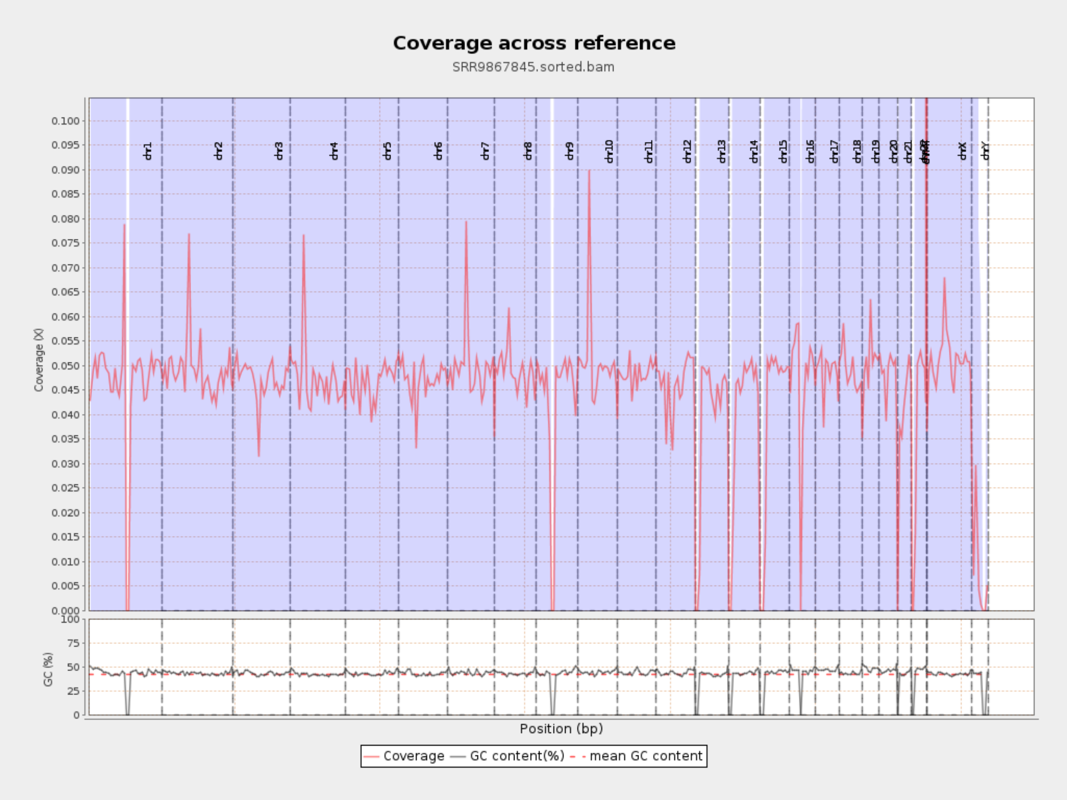
General error rate	0.52%
Mismatches	716,422
Insertions	9,661
Mapped reads with at least one insertion	0.4%
Deletions	26,331
Mapped reads with at least one deletion	1.08%
Homopolymer indels	44.61%

2.6. Chromosome stats

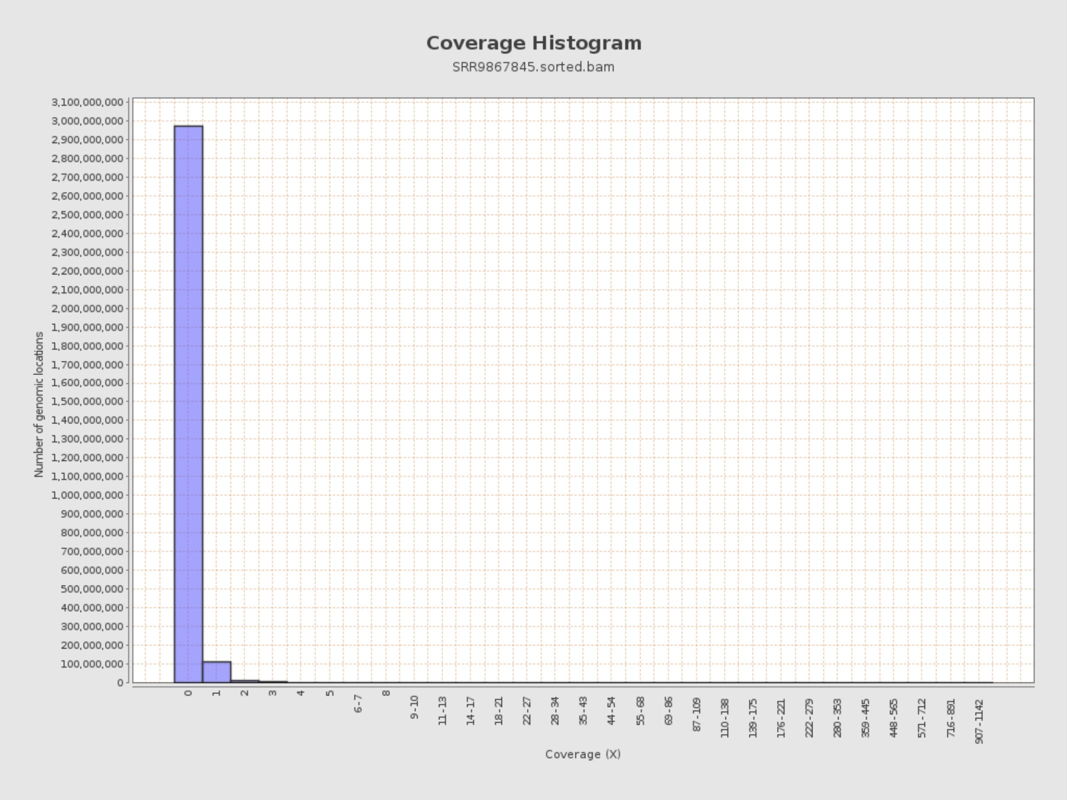
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11563610	0.0464	0.758
chr2	243199373	11993168	0.0493	0.5619
chr3	198022430	9341524	0.0472	0.2453
chr4	191154276	9047257	0.0473	0.2937
chr5	180915260	8474189	0.0468	0.247
chr6	171115067	8073819	0.0472	0.2935
chr7	159138663	7972589	0.0501	0.5188

chr8	146364022	7167432	0.049	0.416
chr9	141213431	5943665	0.0421	0.3383
chr10	135534747	6919987	0.0511	0.4173
chr11	135006516	6512579	0.0482	0.348
chr12	133851895	6149483	0.0459	0.2453
chr13	115169878	4416676	0.0383	0.2223
chr14	107349540	4235189	0.0395	0.2327
chr15	102531392	4120038	0.0402	0.2281
chr16	90354753	4225342	0.0468	0.2708
chr17	81195210	3945780	0.0486	0.2716
chr18	78077248	3844486	0.0492	0.6767
chr19	59128983	3021654	0.0511	0.5737
chr20	63025520	3052877	0.0484	0.2582
chr21	48129895	1890365	0.0393	0.2741
chr22	51304566	1778931	0.0347	0.2117
chrMT	16571	24573	1.4829	1.5193
chrX	155270560	7942857	0.0512	0.2891
chrY	59373566	461776	0.0078	0.2732

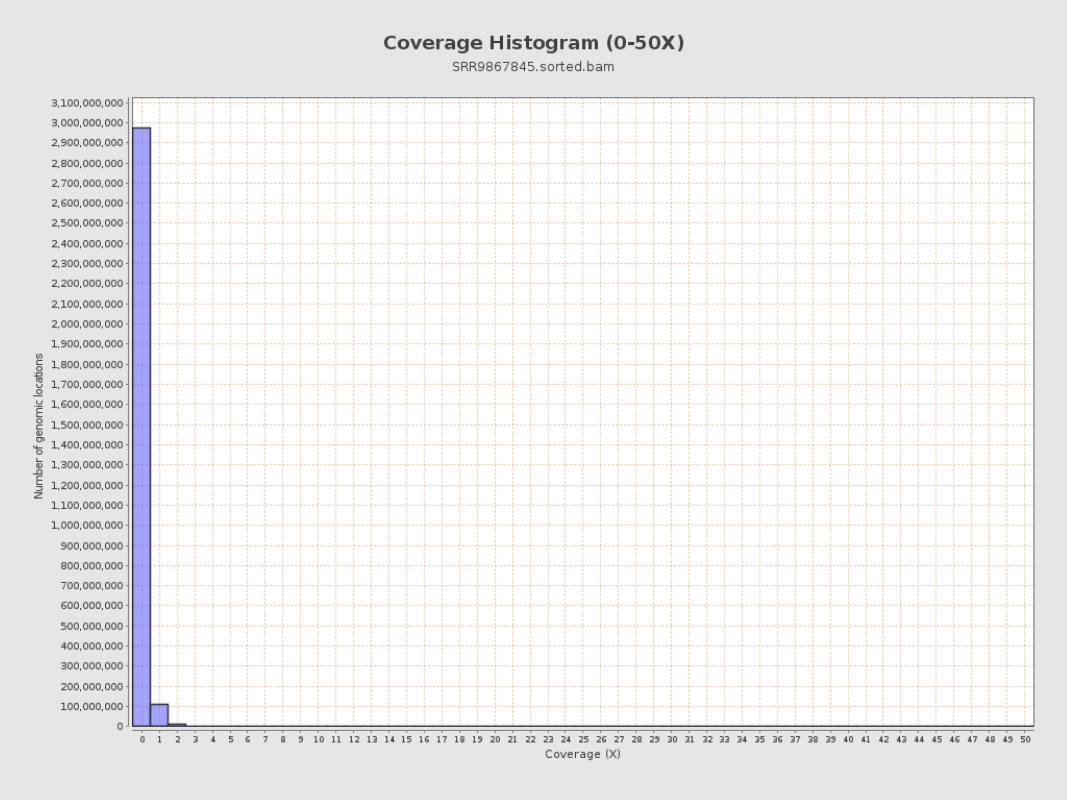
3. Results : Coverage across reference



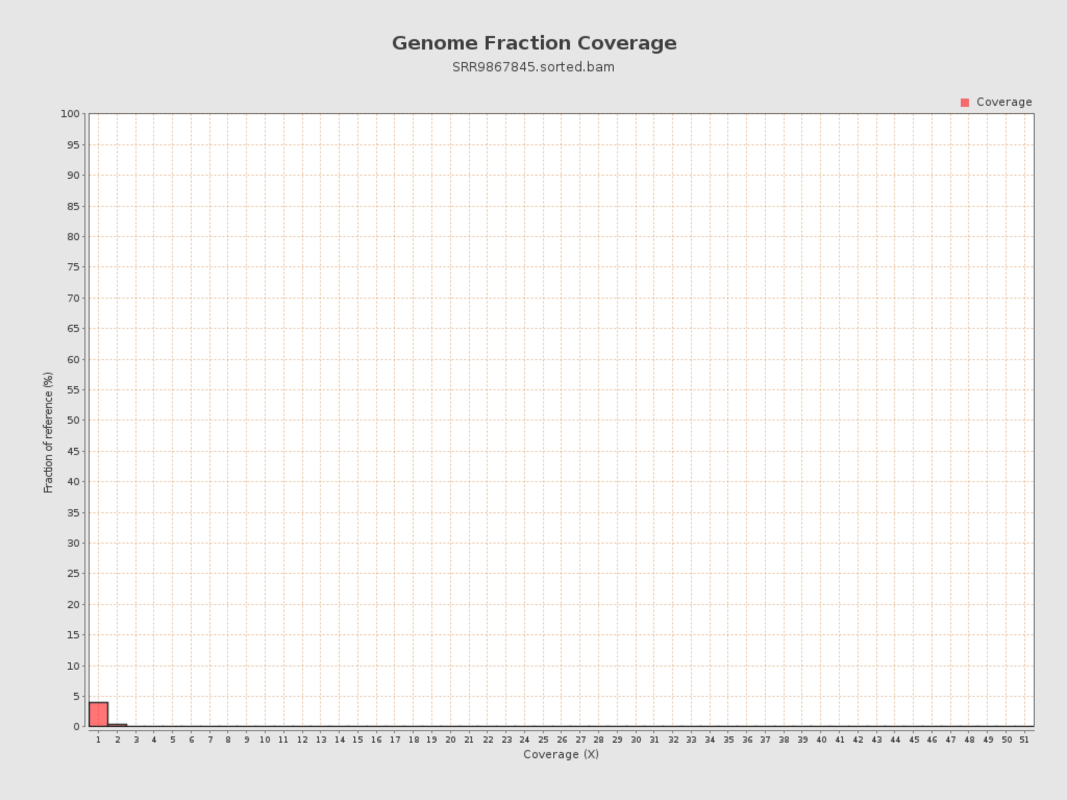
4. Results : Coverage Histogram



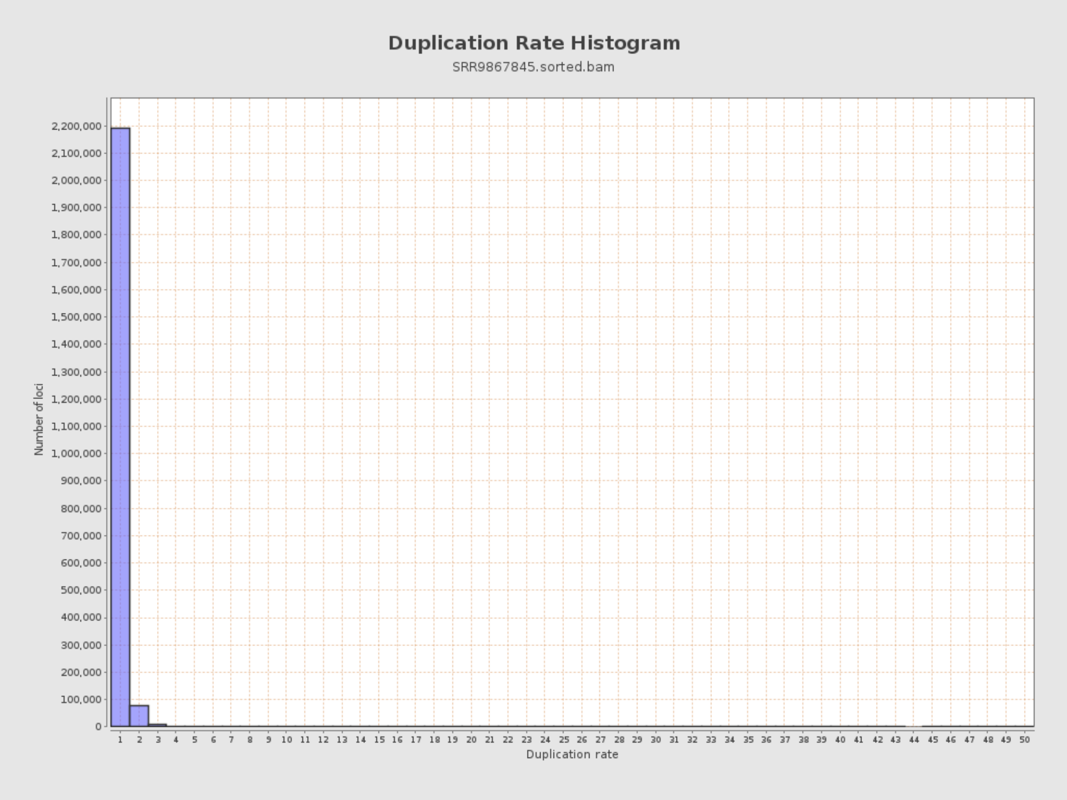
5. Results : Coverage Histogram (0-50X)



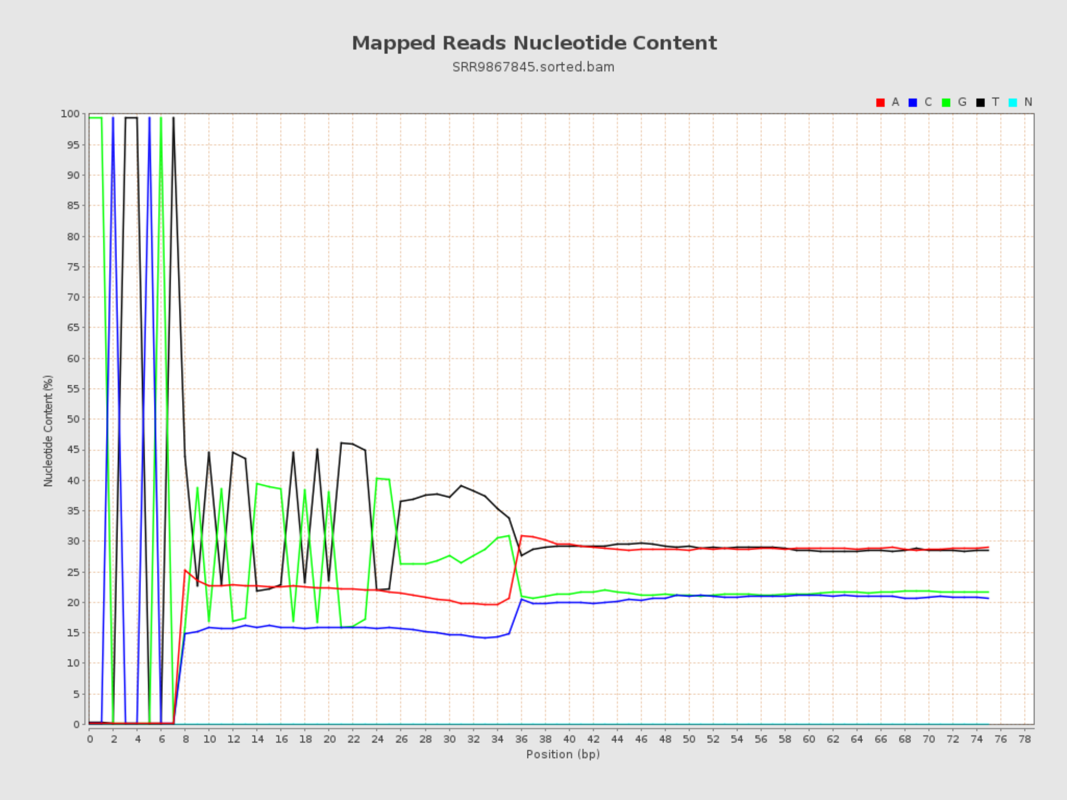
6. Results : Genome Fraction Coverage



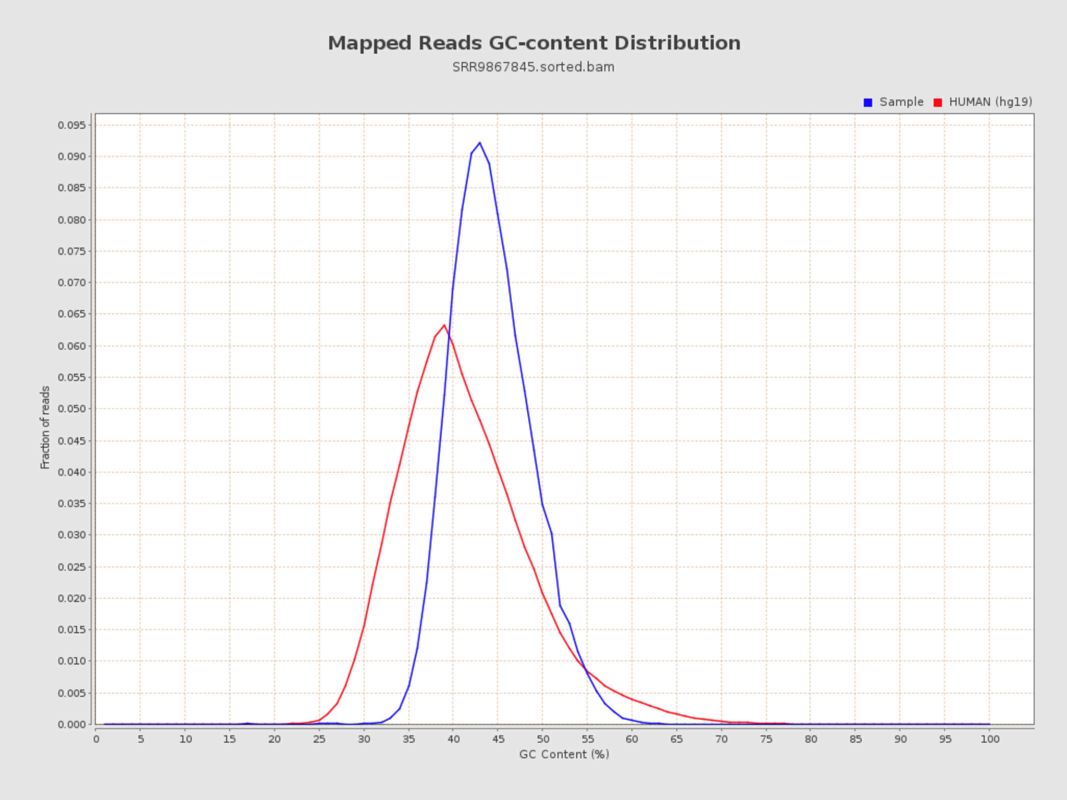
7. Results : Duplication Rate Histogram



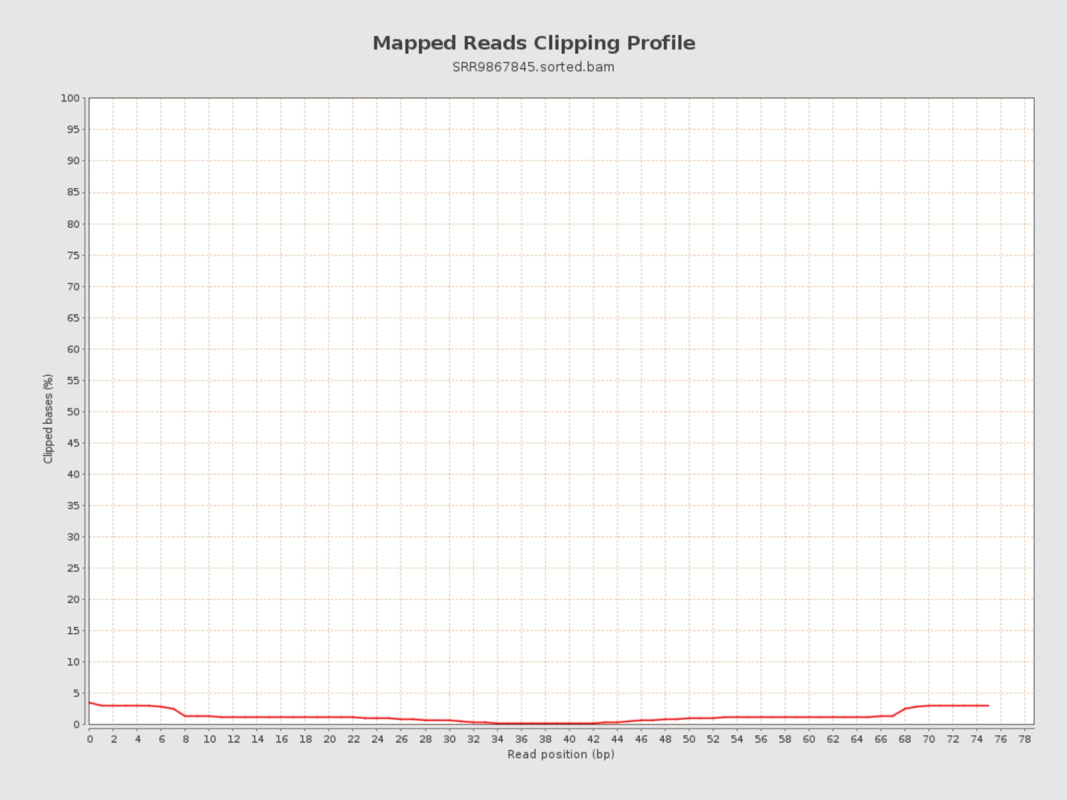
8. Results : Mapped Reads Nucleotide Content



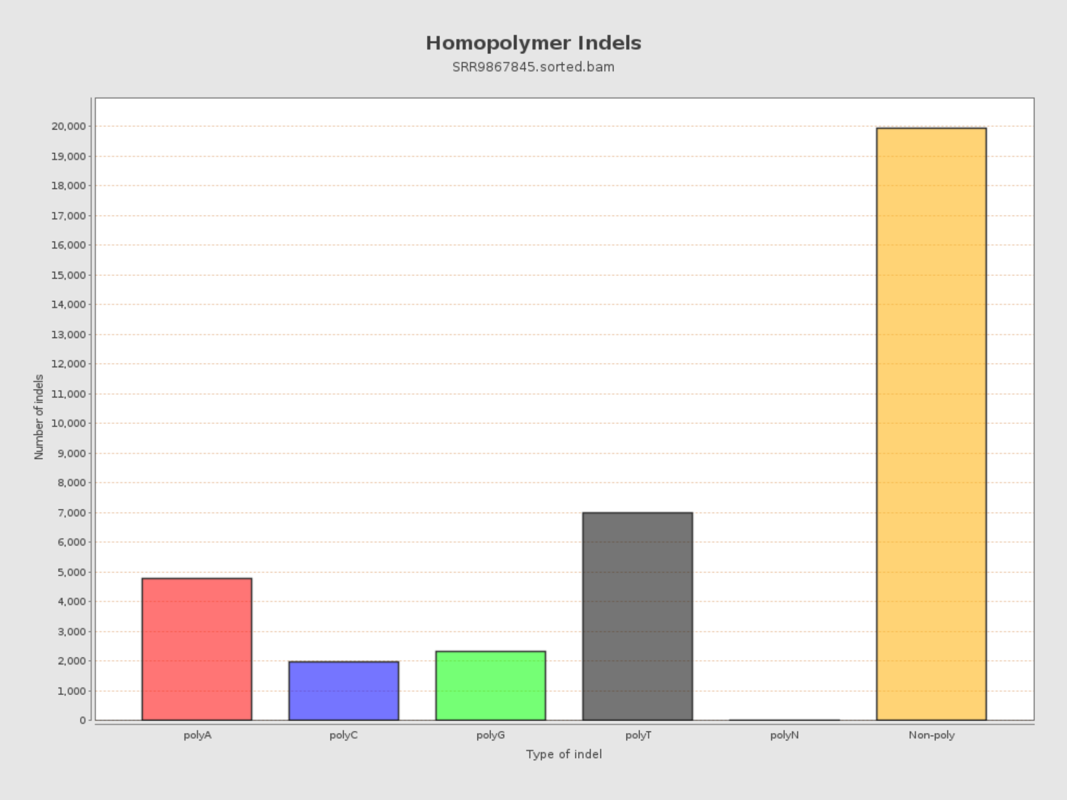
9. Results : Mapped Reads GC-content Distribution



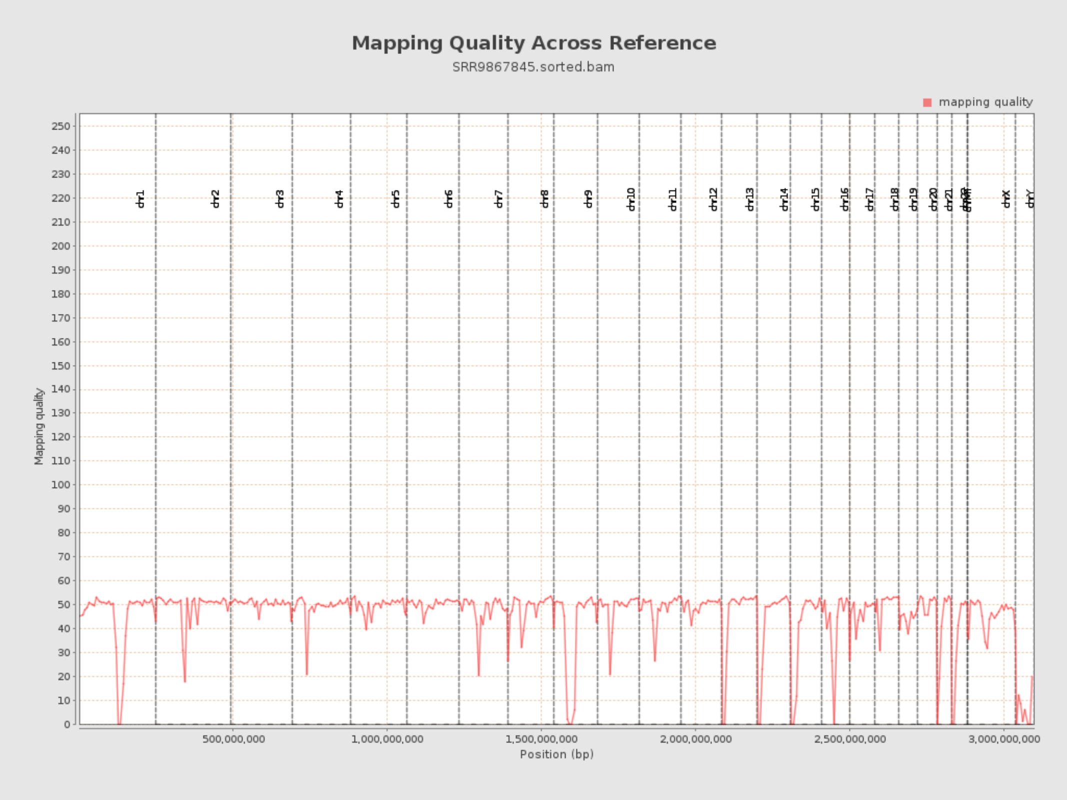
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram