Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 17:39:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9867870.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_SRR9867870 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9867870.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 17:39:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9867870.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,202,037
Mapped reads	2,029,548 / 92.17%
Unmapped reads	172,489 / 7.83%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,058 / 0.41%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	105,030 / 4.77%
Duplication rate	3.9%
Clipped reads	2,036,602 / 92.49%

2.2. ACGT Content

Number/percentage of A's	30,781,313 / 25.71%
Number/percentage of C's	23,534,110 / 19.66%
Number/percentage of T's	37,232,614 / 31.1%
Number/percentage of G's	28,148,629 / 23.51%
Number/percentage of N's	16,327 / 0.01%
GC Percentage	43.17%

2.3. Coverage

Mean	0.0387

Standard Deviation	0.352

2.4. Mapping Quality

Mean Mapping Quality	45.68

2.5. Mismatches and indels

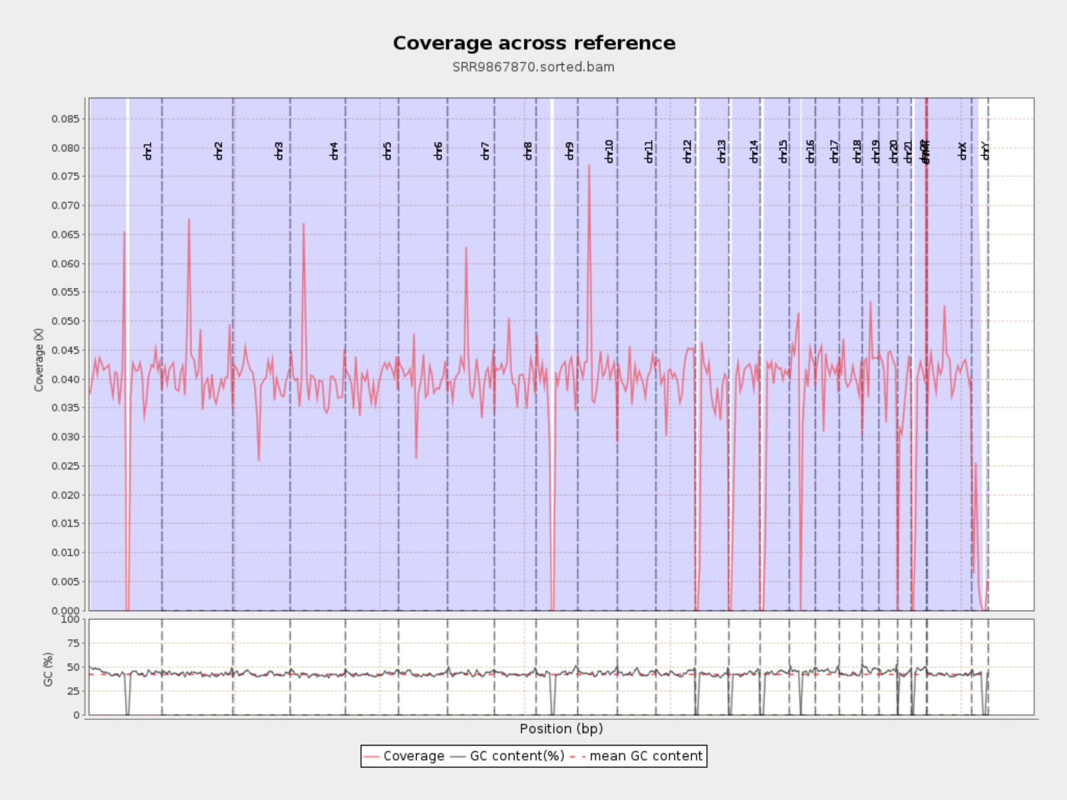
General error rate	0.51%
Mismatches	601,189
Insertions	7,241
Mapped reads with at least one insertion	0.35%
Deletions	22,223
Mapped reads with at least one deletion	1.09%
Homopolymer indels	44.35%

2.6. Chromosome stats

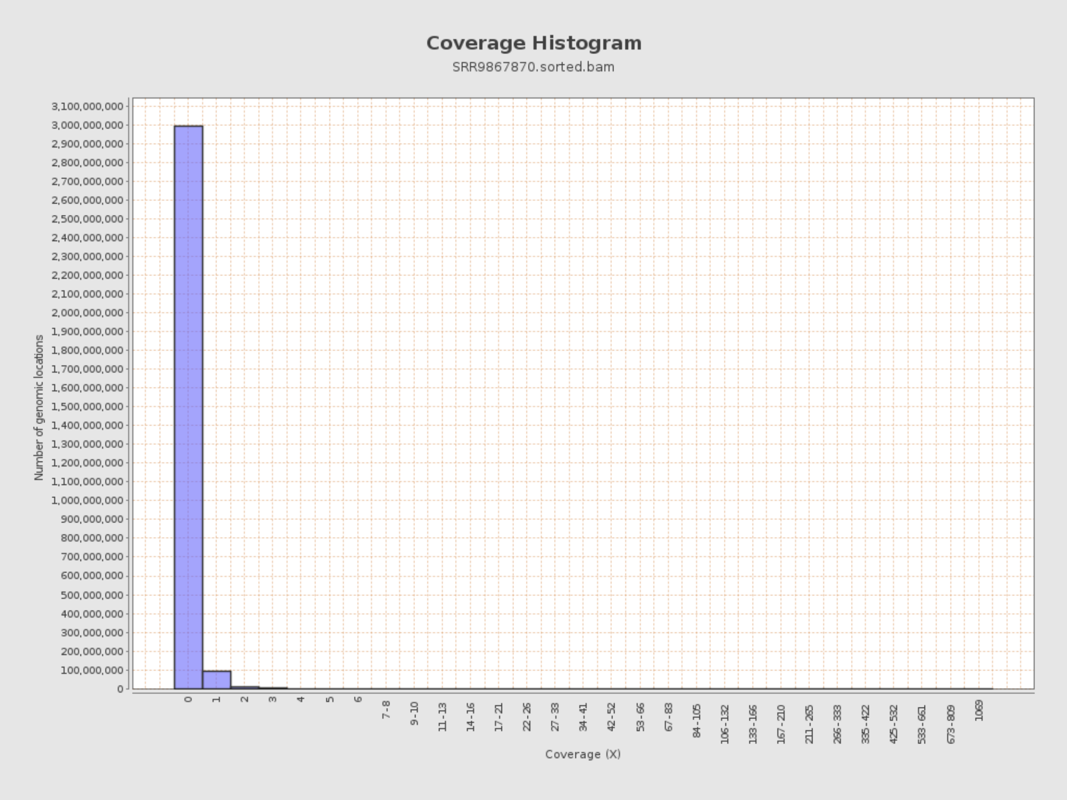
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9707949	0.0389	0.6165
chr2	243199373	10095755	0.0415	0.514
chr3	198022430	7872902	0.0398	0.2232
chr4	191154276	7644291	0.04	0.2656
chr5	180915260	7213365	0.0399	0.2251
chr6	171115067	6836818	0.04	0.2626
chr7	159138663	6552578	0.0412	0.4127

chr8	146364022	5972810	0.0408	0.3824
chr9	141213431	5051957	0.0358	0.2879
chr10	135534747	5836993	0.0431	0.3636
chr11	135006516	5429682	0.0402	0.307
chr12	133851895	5476068	0.0409	0.2303
chr13	115169878	3764191	0.0327	0.2031
chr14	107349540	3641227	0.0339	0.2154
chr15	102531392	3427885	0.0334	0.205
chr16	90354753	3577226	0.0396	0.2428
chr17	81195210	3355846	0.0413	0.2463
chr18	78077248	3192238	0.0409	0.5426
chr19	59128983	2561388	0.0433	0.4735
chr20	63025520	2612487	0.0415	0.2359
chr21	48129895	1595237	0.0331	0.239
chr22	51304566	1458047	0.0284	0.1894
chrMT	16571	25315	1.5277	1.4108
chrX	155270560	6442800	0.0415	0.2562
chrY	59373566	403404	0.0068	0.2363

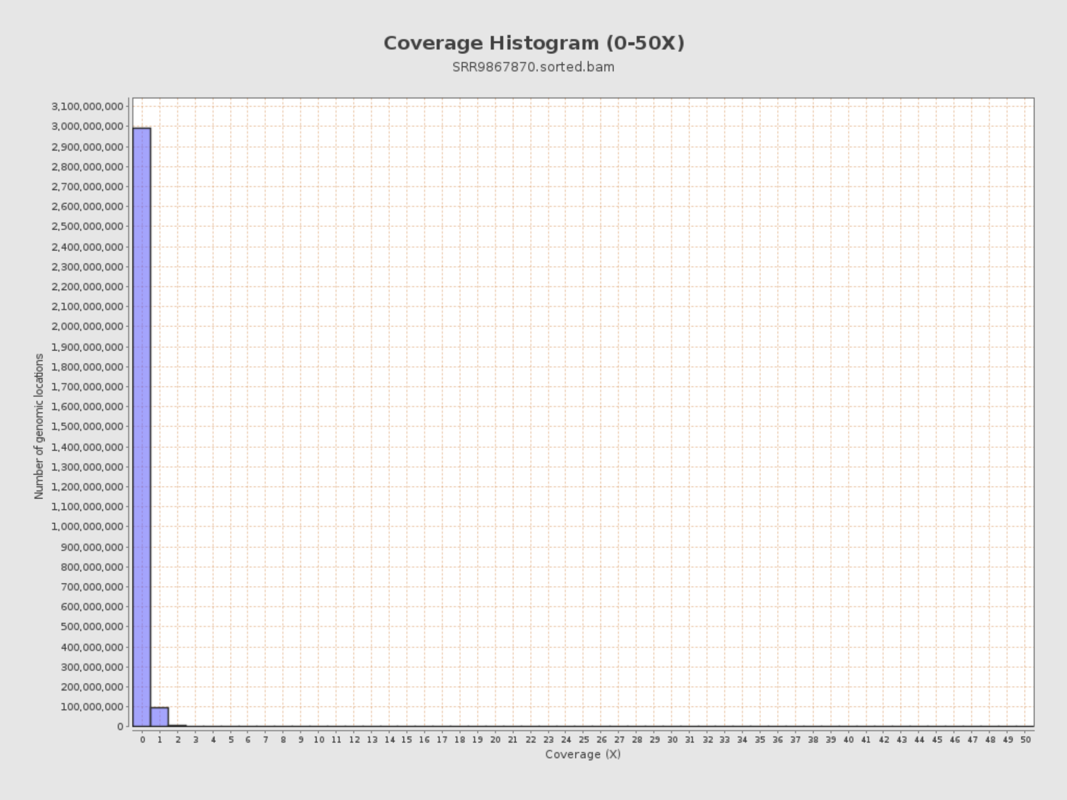
3. Results : Coverage across reference



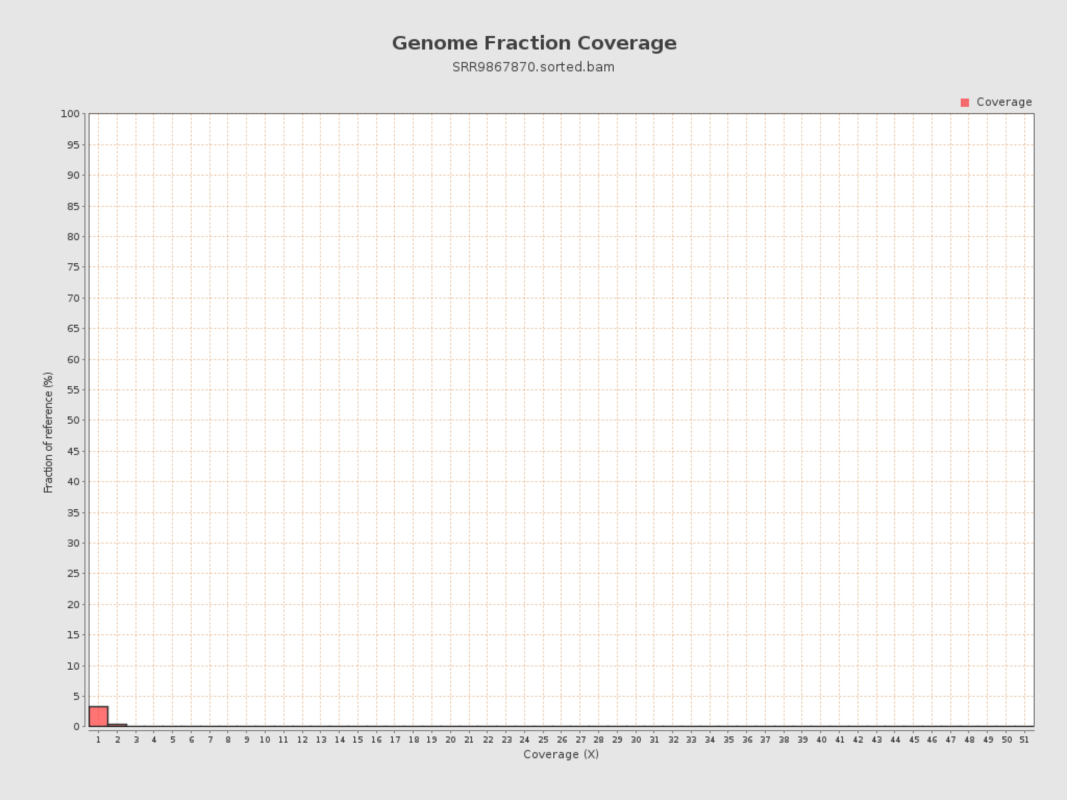
4. Results : Coverage Histogram



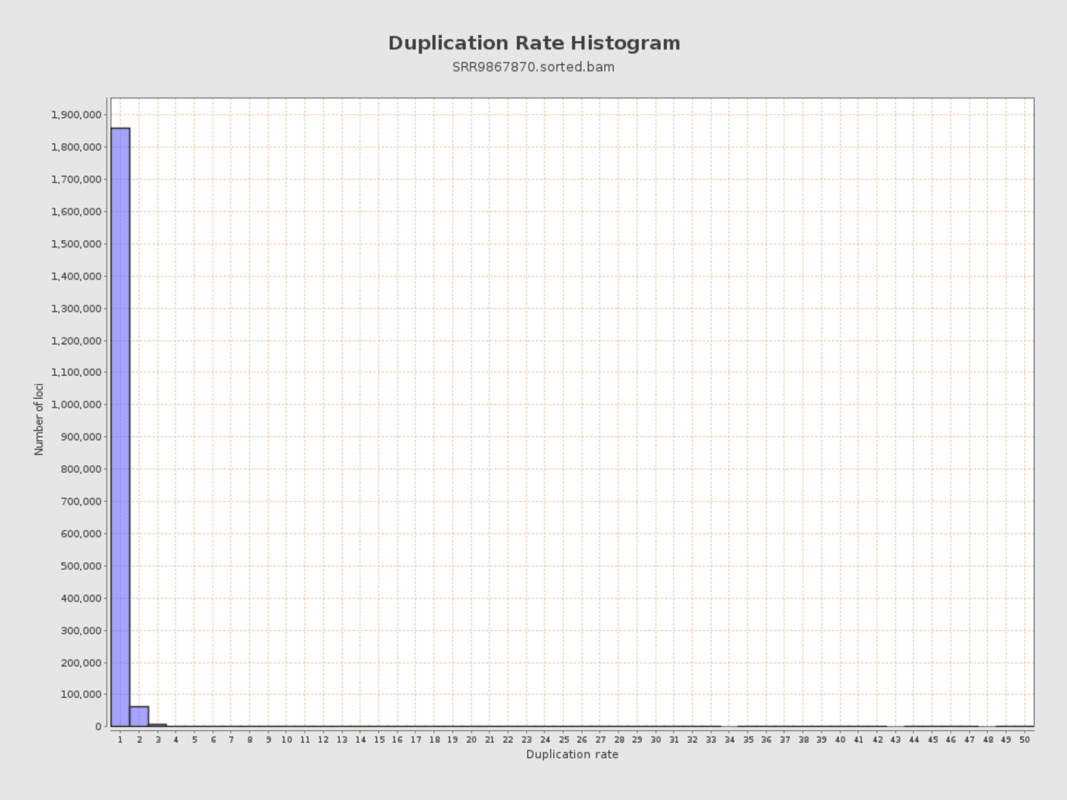
5. Results : Coverage Histogram (0-50X)



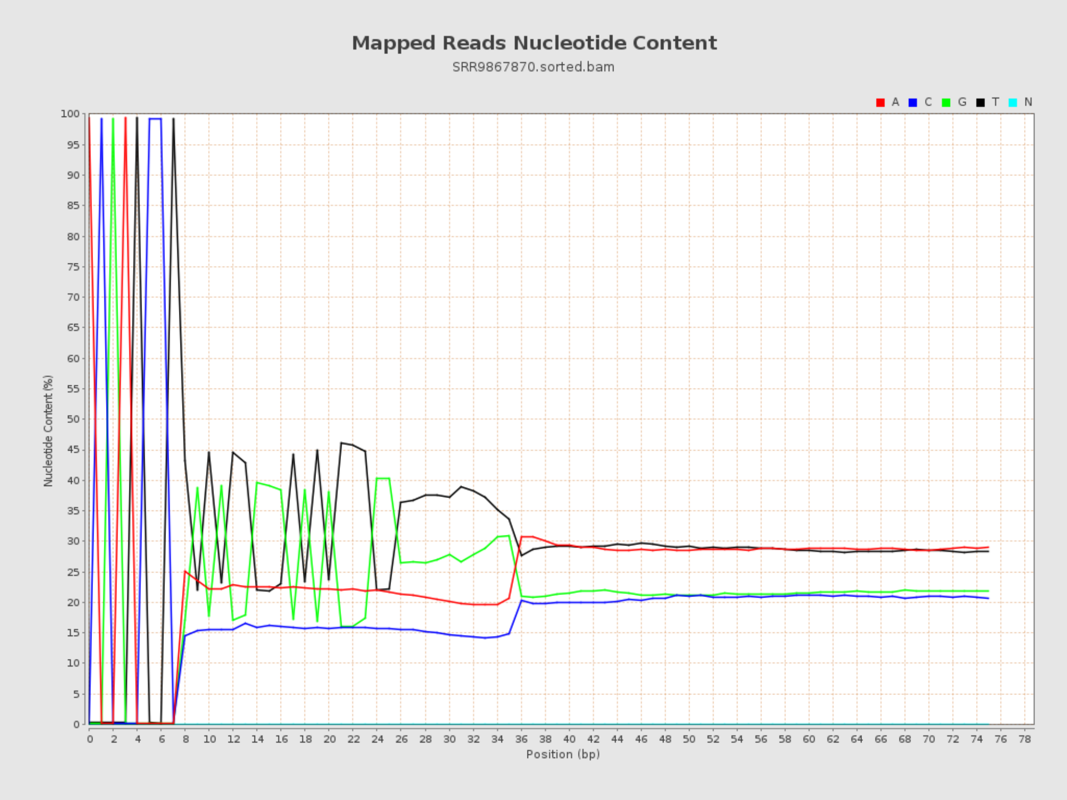
6. Results : Genome Fraction Coverage



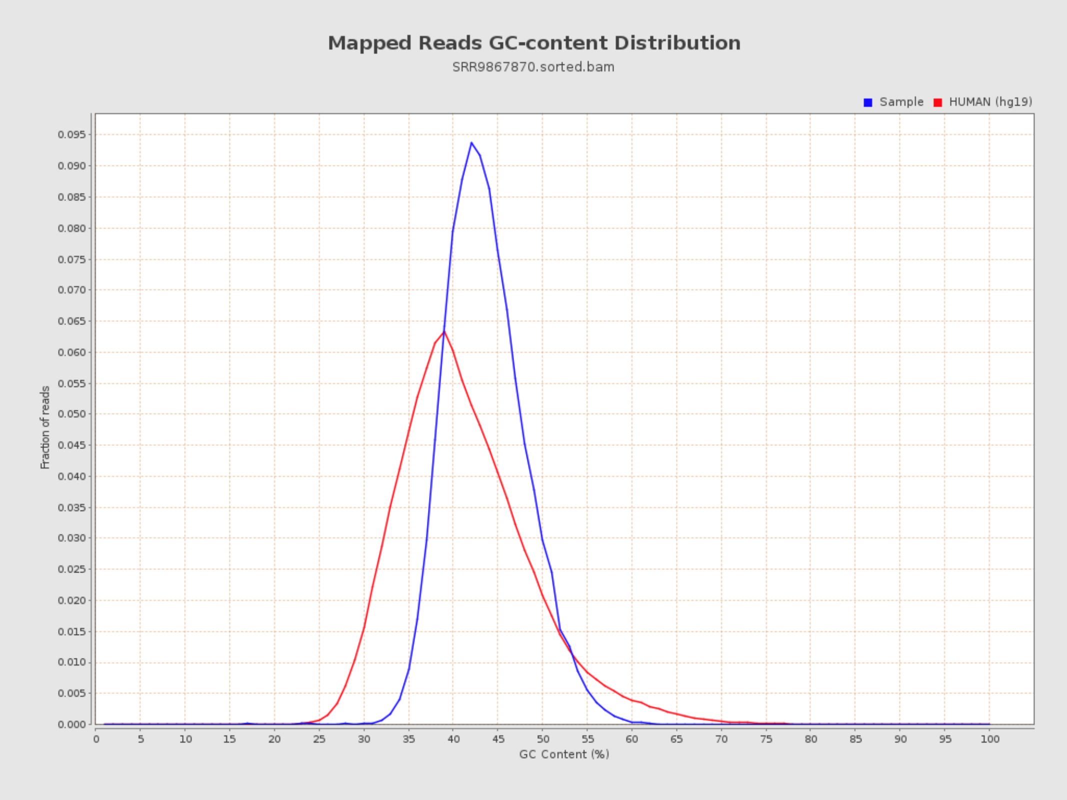
7. Results : Duplication Rate Histogram



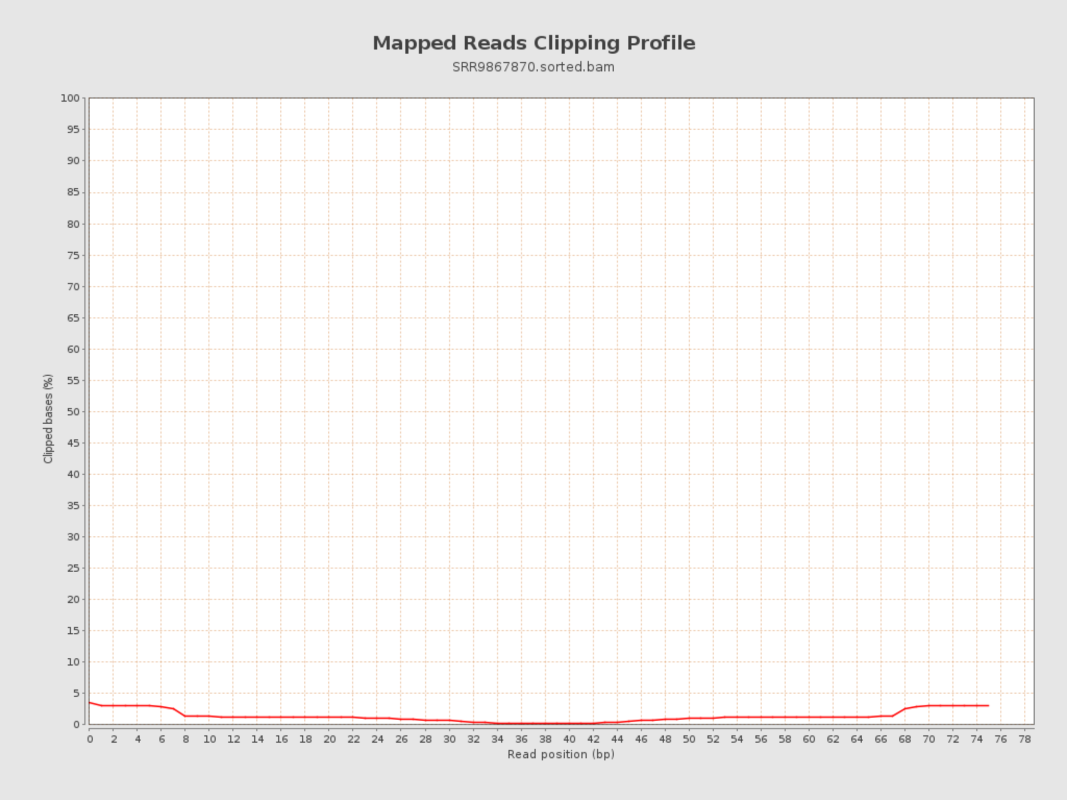
8. Results : Mapped Reads Nucleotide Content



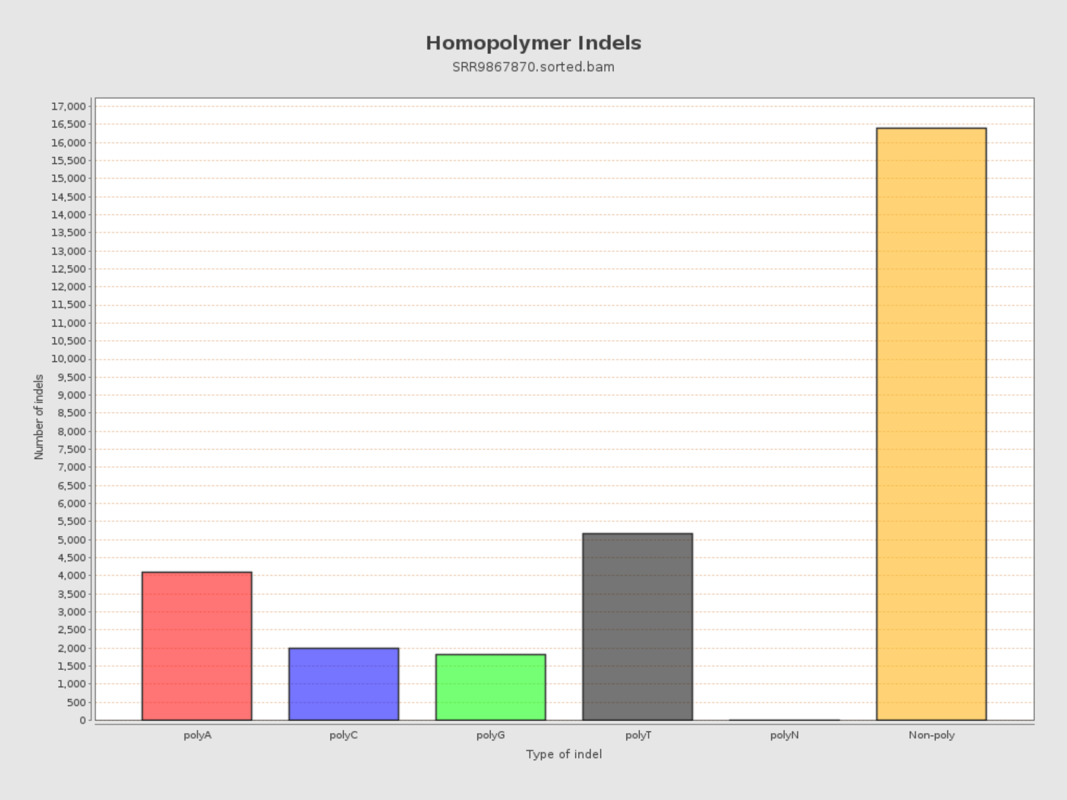
9. Results : Mapped Reads GC-content Distribution



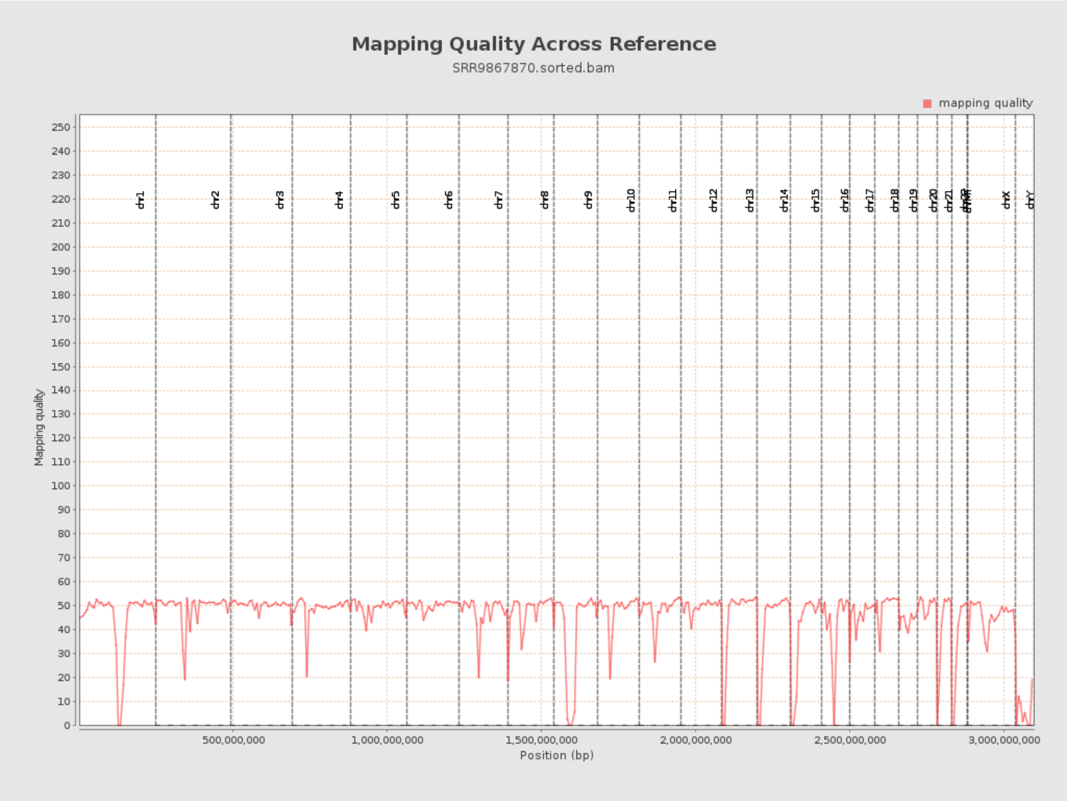
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram