Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 15:48:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9867858.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_SRR9867858 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9867858.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 15:48:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9867858.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,025,163
Mapped reads	2,777,089 / 91.8%
Unmapped reads	248,074 / 8.2%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,505 / 0.41%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	174,785 / 5.78%
Duplication rate	4.68%
Clipped reads	2,780,994 / 91.93%

2.2. ACGT Content

Number/percentage of A's	41,074,562 / 25.07%
Number/percentage of C's	33,363,806 / 20.37%
Number/percentage of T's	52,476,694 / 32.03%
Number/percentage of G's	36,882,658 / 22.51%
Number/percentage of N's	21,749 / 0.01%
GC Percentage	42.88%

2.3. Coverage

Mean	0.0529

Standard Deviation	0.4718

2.4. Mapping Quality

Mean Mapping Quality	45.79

2.5. Mismatches and indels

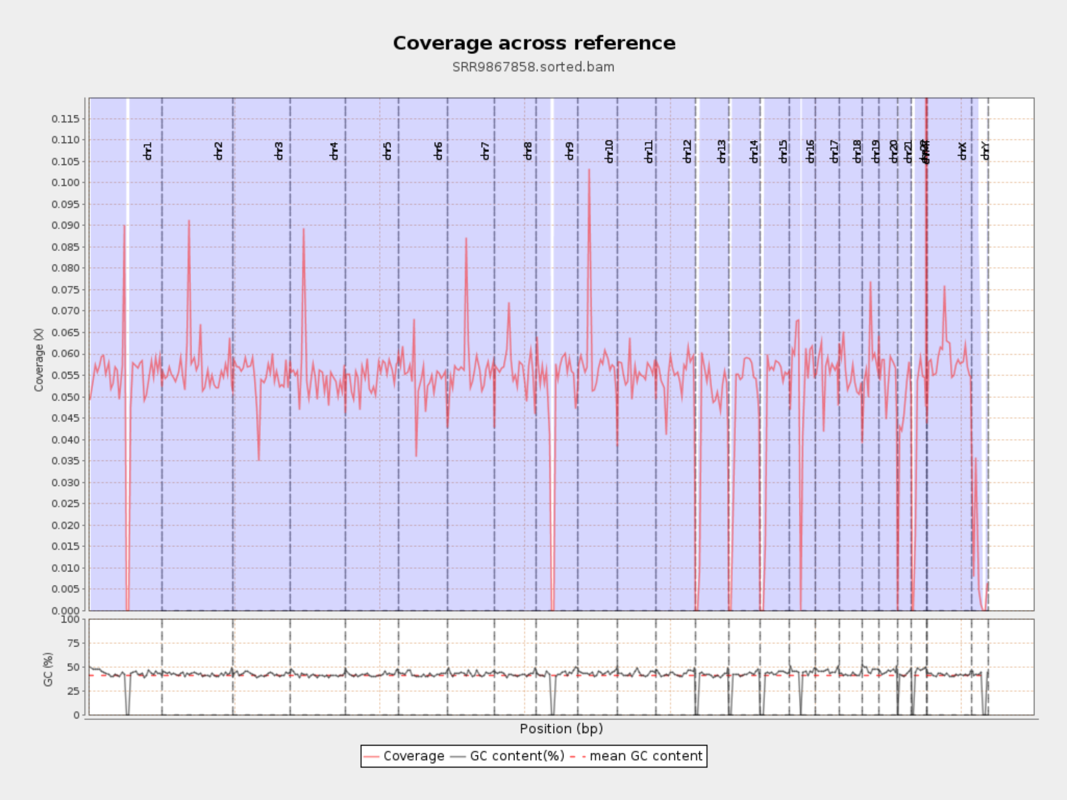
General error rate	0.52%
Mismatches	829,823
Insertions	11,607
Mapped reads with at least one insertion	0.42%
Deletions	31,103
Mapped reads with at least one deletion	1.11%
Homopolymer indels	44.01%

2.6. Chromosome stats

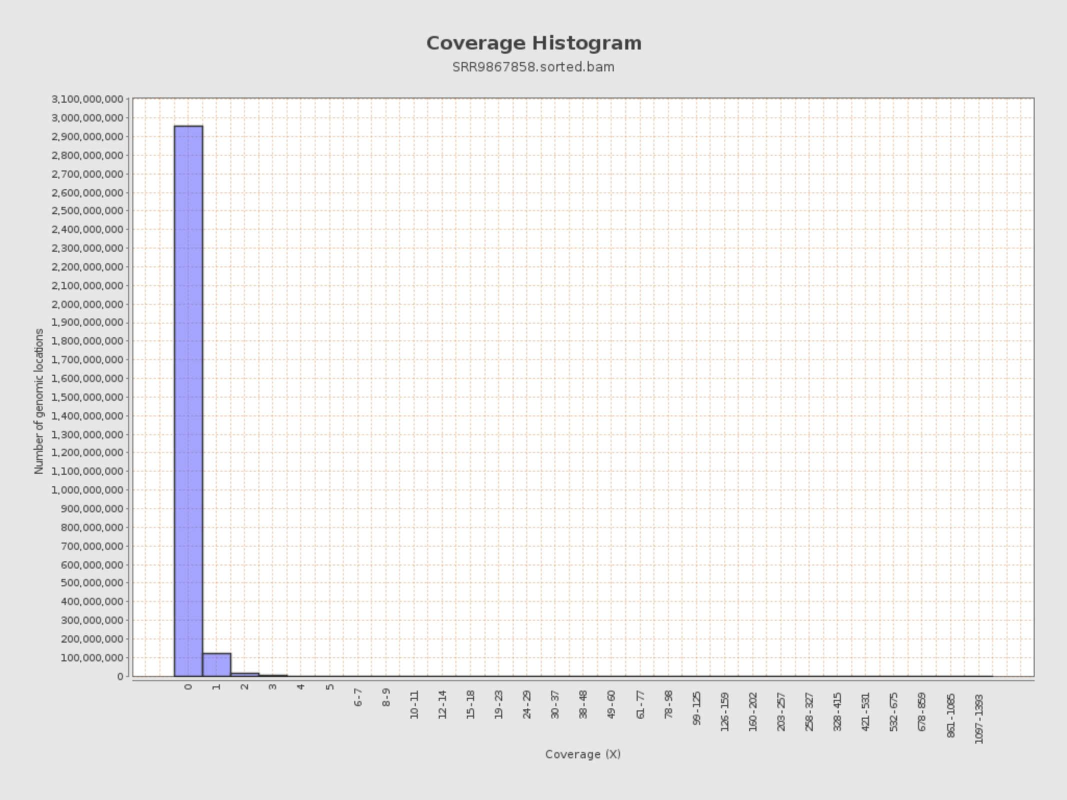
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13216924	0.053	0.8935
chr2	243199373	13864490	0.057	0.67
chr3	198022430	10829497	0.0547	0.2693
chr4	191154276	10532997	0.0551	0.3303
chr5	180915260	9875011	0.0546	0.2722
chr6	171115067	9310371	0.0544	0.3256
chr7	159138663	9089302	0.0571	0.5679

chr8	146364022	8280092	0.0566	0.5229
chr9	141213431	6919369	0.049	0.3692
chr10	135534747	8011737	0.0591	0.4677
chr11	135006516	7489713	0.0555	0.3886
chr12	133851895	7375180	0.0551	0.2764
chr13	115169878	5102712	0.0443	0.2458
chr14	107349540	4956130	0.0462	0.264
chr15	102531392	4667172	0.0455	0.2462
chr16	90354753	4821508	0.0534	0.3007
chr17	81195210	4528451	0.0558	0.2941
chr18	78077248	4338539	0.0556	0.7476
chr19	59128983	3434892	0.0581	0.6865
chr20	63025520	3462133	0.0549	0.2812
chr21	48129895	2127860	0.0442	0.2972
chr22	51304566	1949707	0.038	0.225
chrMT	16571	25964	1.5668	1.6156
chrX	155270560	9107861	0.0587	0.3249
chrY	59373566	551176	0.0093	0.3568

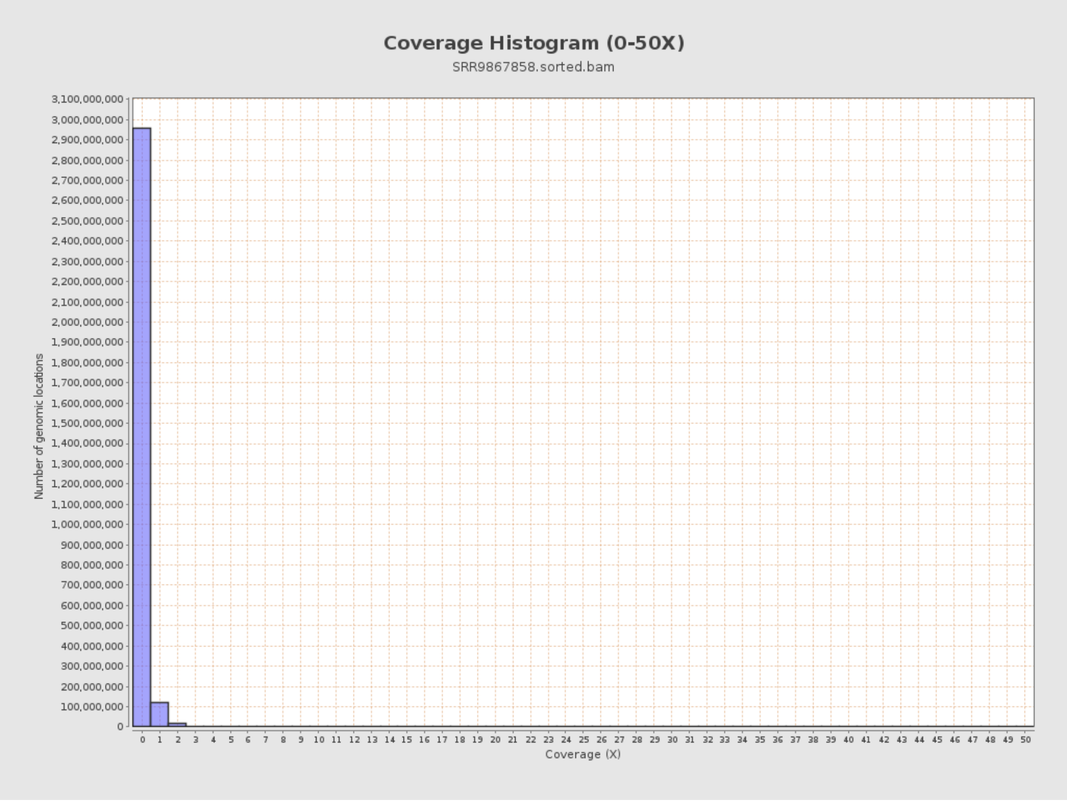
3. Results : Coverage across reference



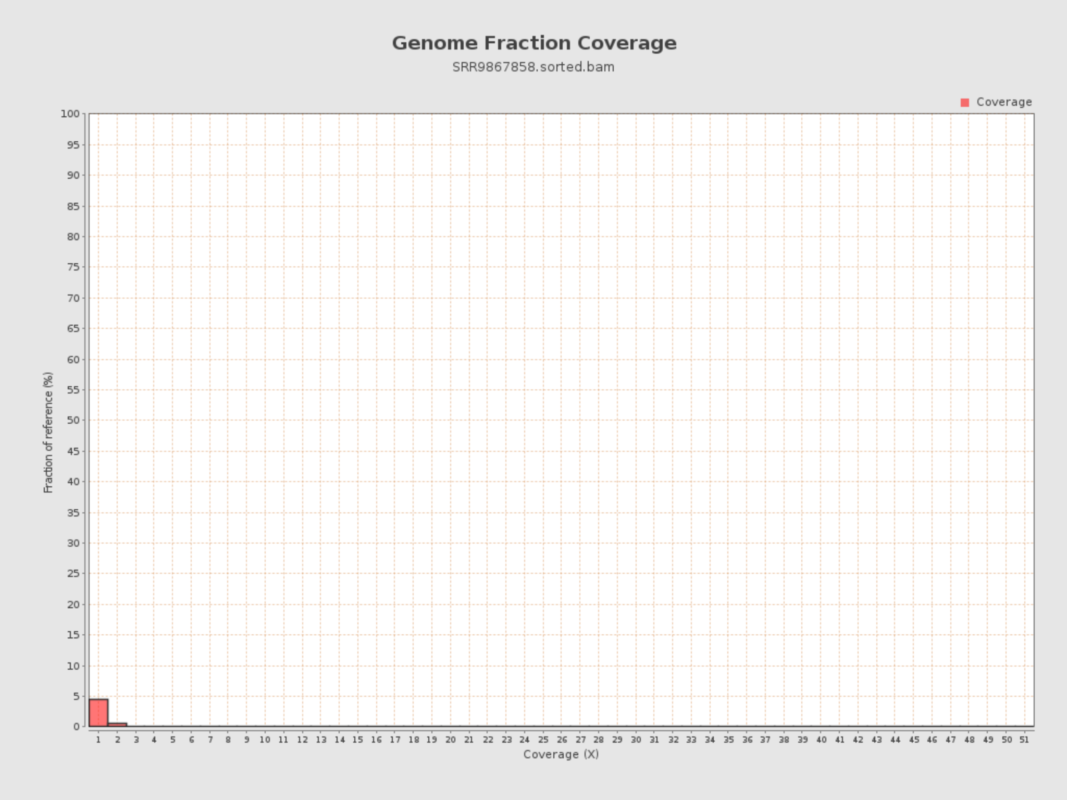
4. Results : Coverage Histogram



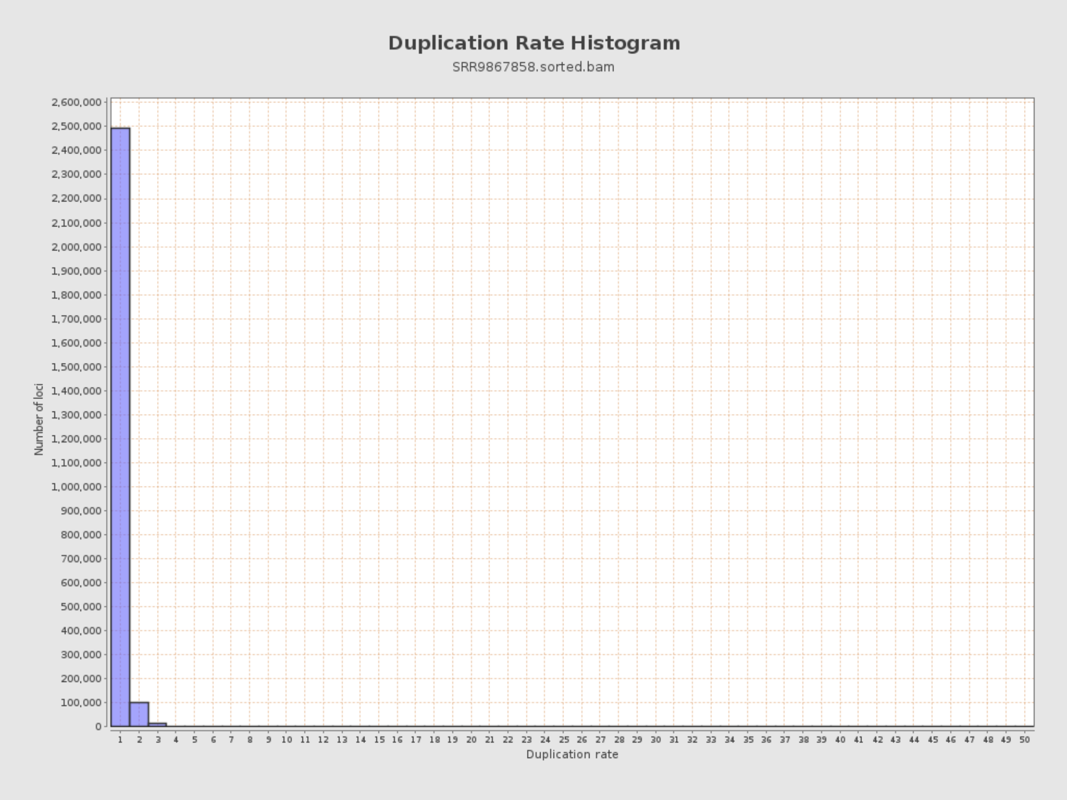
5. Results : Coverage Histogram (0-50X)



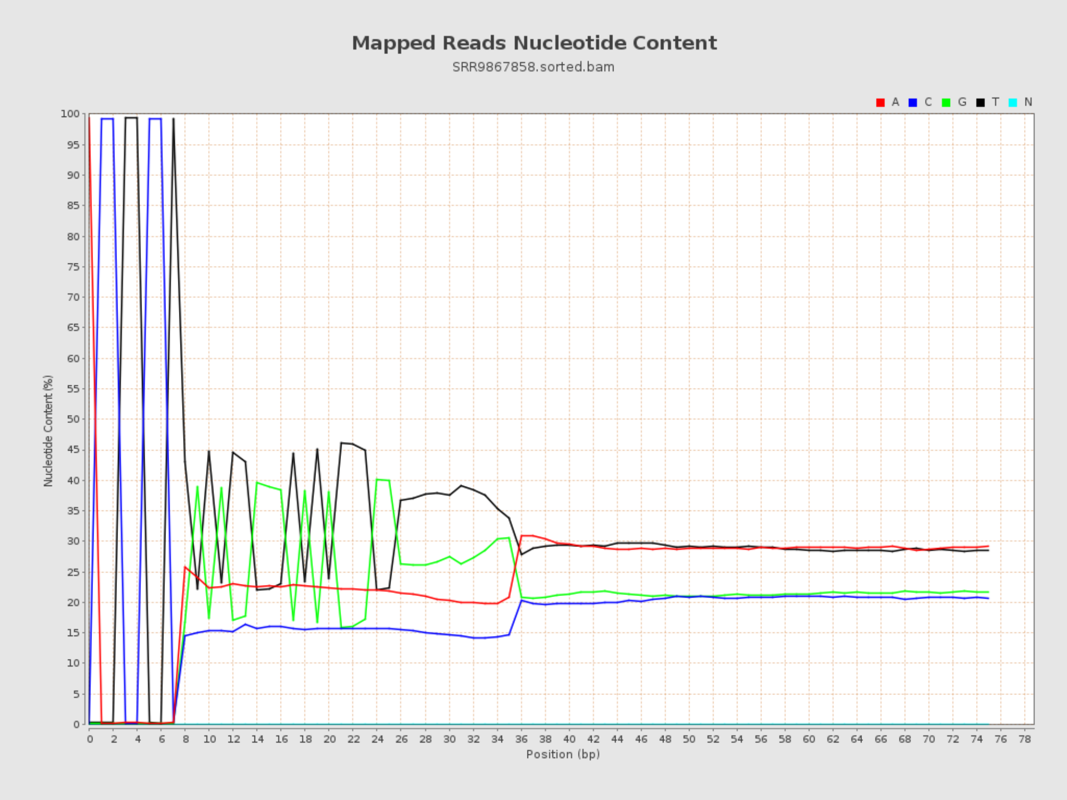
6. Results : Genome Fraction Coverage



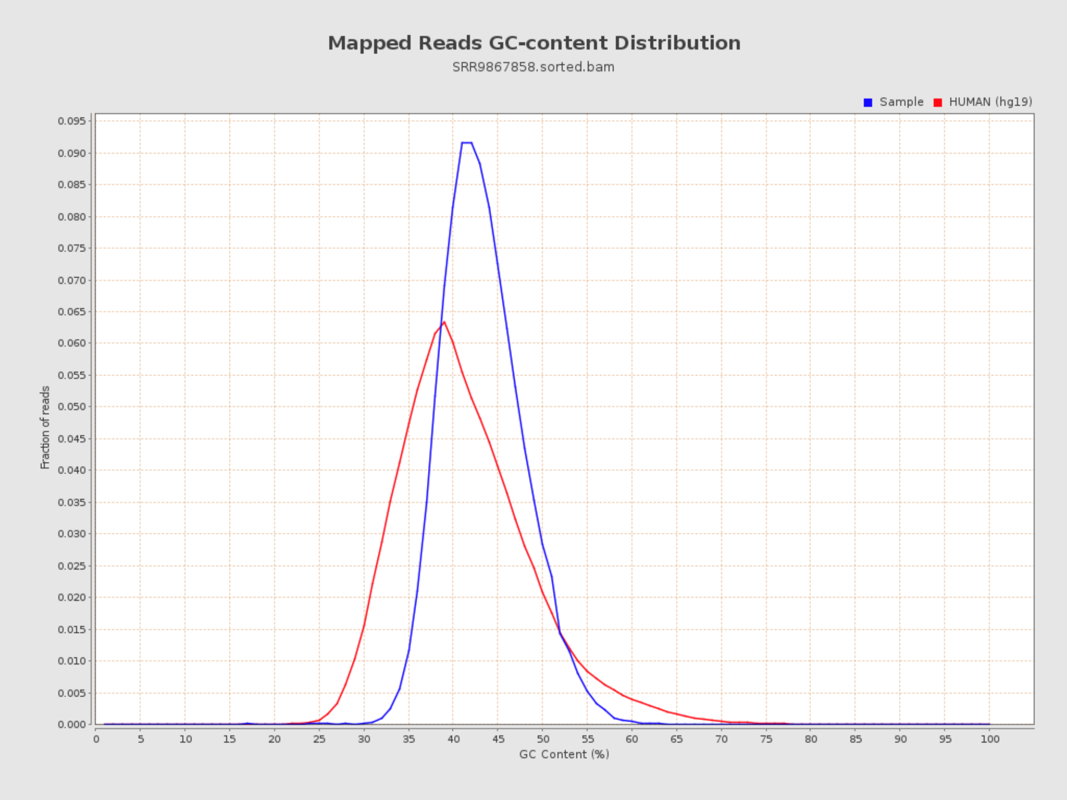
7. Results : Duplication Rate Histogram



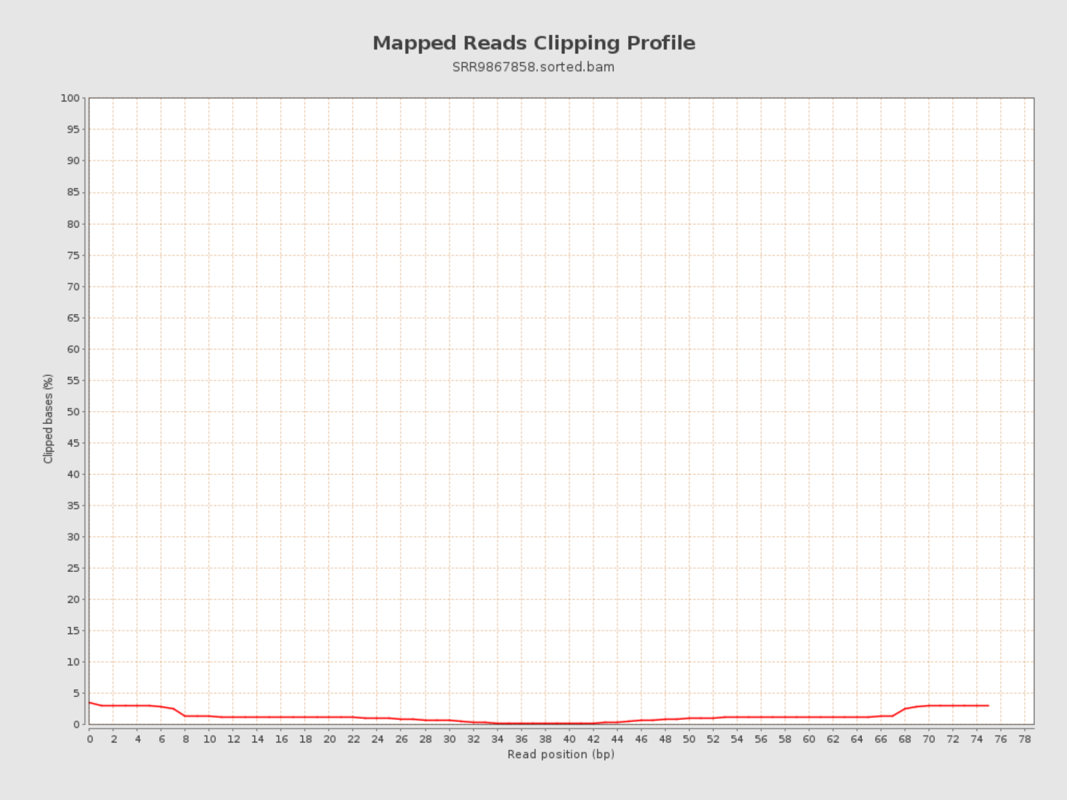
8. Results : Mapped Reads Nucleotide Content



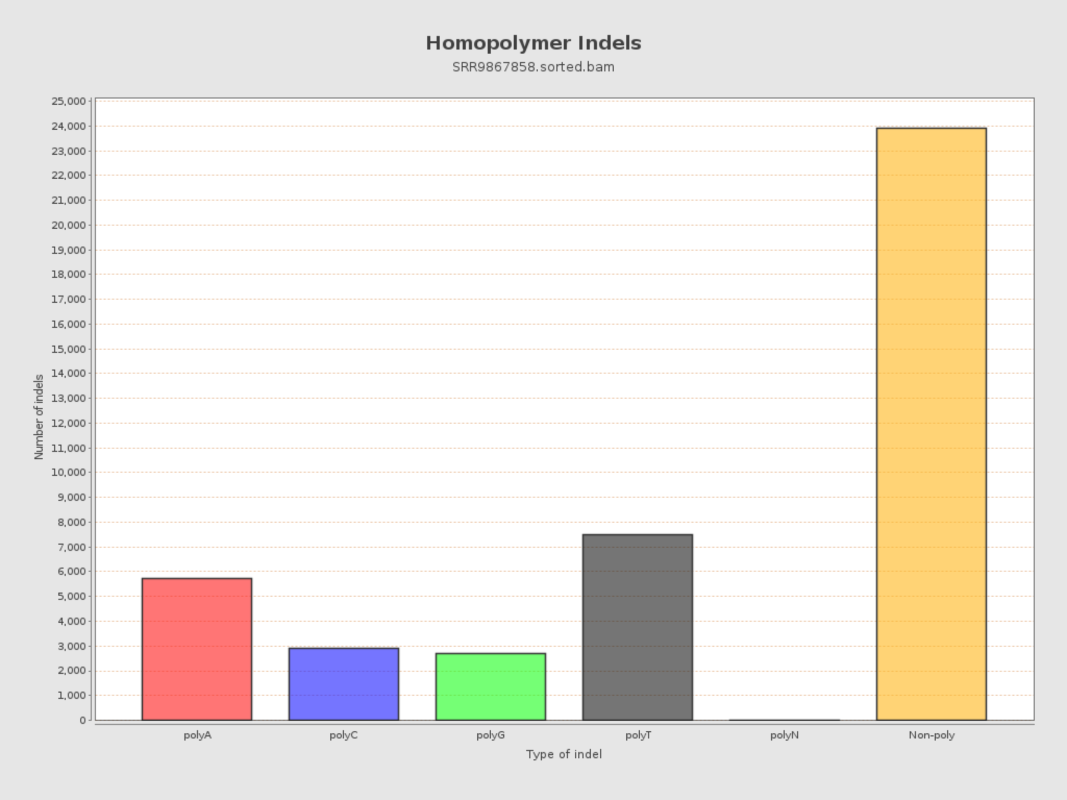
9. Results : Mapped Reads GC-content Distribution



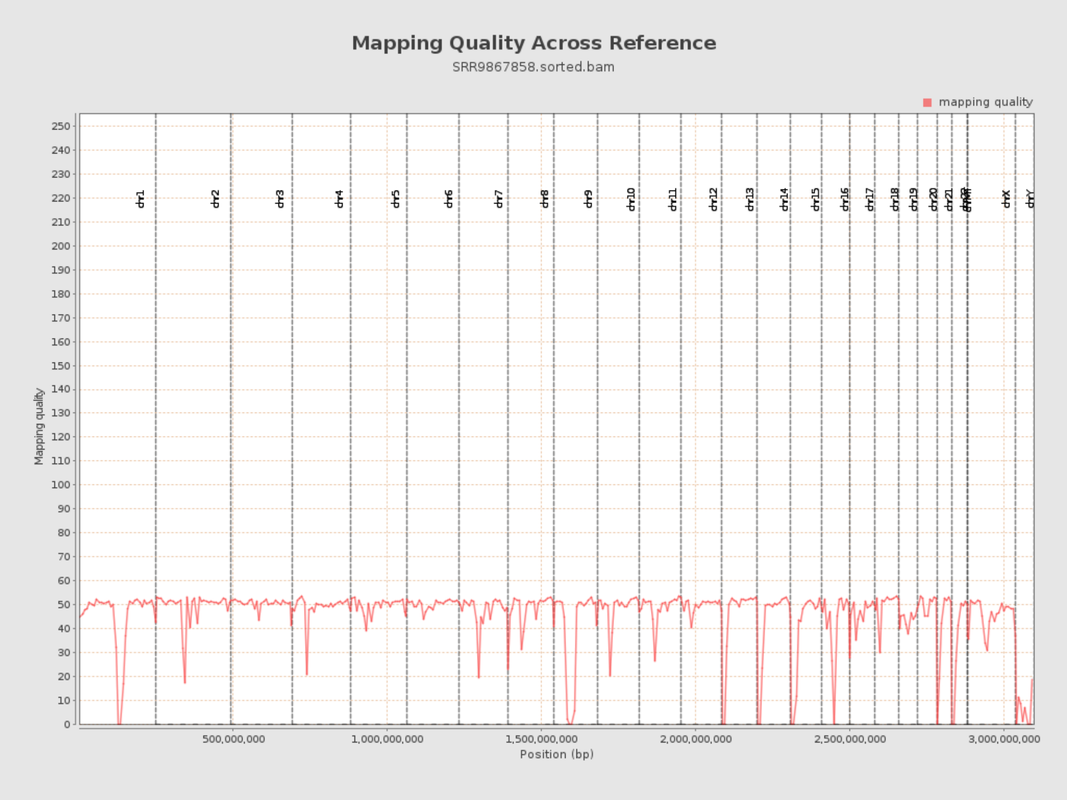
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram