Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 17:19:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9867866.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_SRR9867866 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9867866.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 17:19:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9867866.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	22,597,829
Mapped reads	20,266,524 / 89.68%
Unmapped reads	2,331,305 / 10.32%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	77,148 / 0.34%
Read min/max/mean length	30 / 101 / 101.13
Duplicated reads (estimated)	1,028,396 / 4.55%
Duplication rate	1.54%
Clipped reads	20,275,221 / 89.72%

2.2. ACGT Content

Number/percentage of A's	511,068,854 / 28.23%
Number/percentage of C's	390,731,630 / 21.58%
Number/percentage of T's	511,708,581 / 28.27%
Number/percentage of G's	396,780,559 / 21.92%
Number/percentage of N's	54,808 / 0%
GC Percentage	43.5%

2.3. Coverage

Mean	0.5849

Standard Deviation	6.1657

2.4. Mapping Quality

Mean Mapping Quality	50.48

2.5. Mismatches and indels

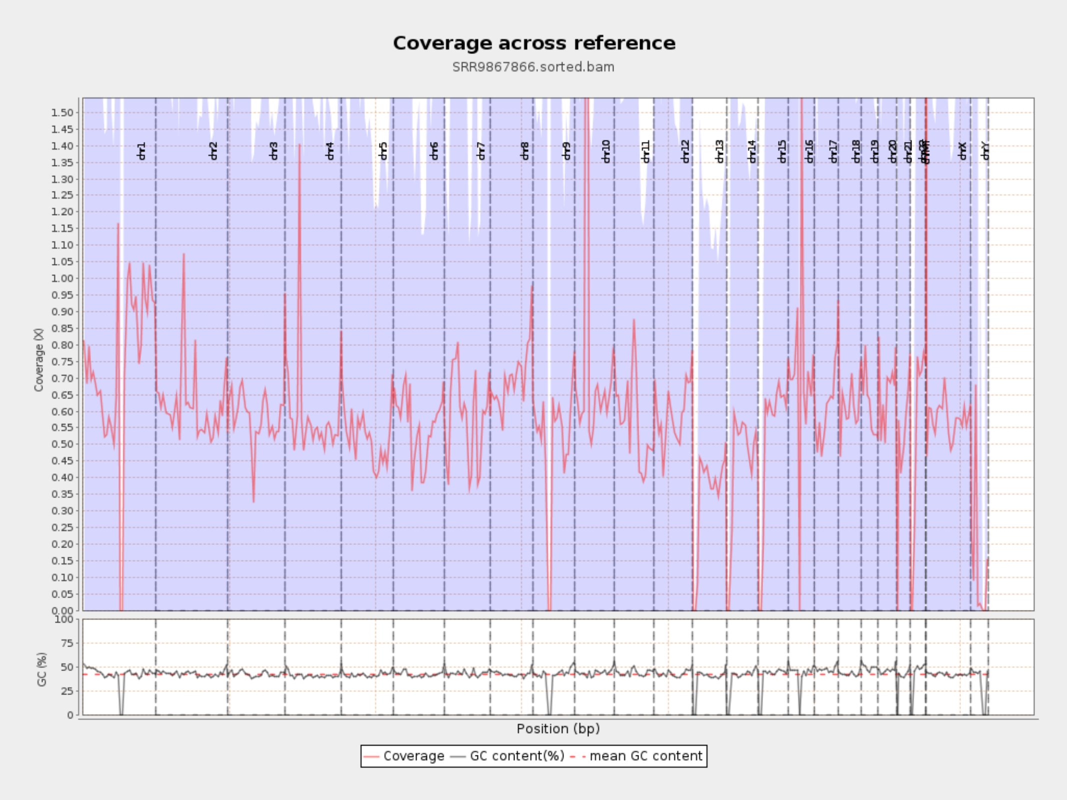
General error rate	0.5%
Mismatches	8,540,197
Insertions	171,963
Mapped reads with at least one insertion	0.83%
Deletions	181,157
Mapped reads with at least one deletion	0.87%
Homopolymer indels	36.1%

2.6. Chromosome stats

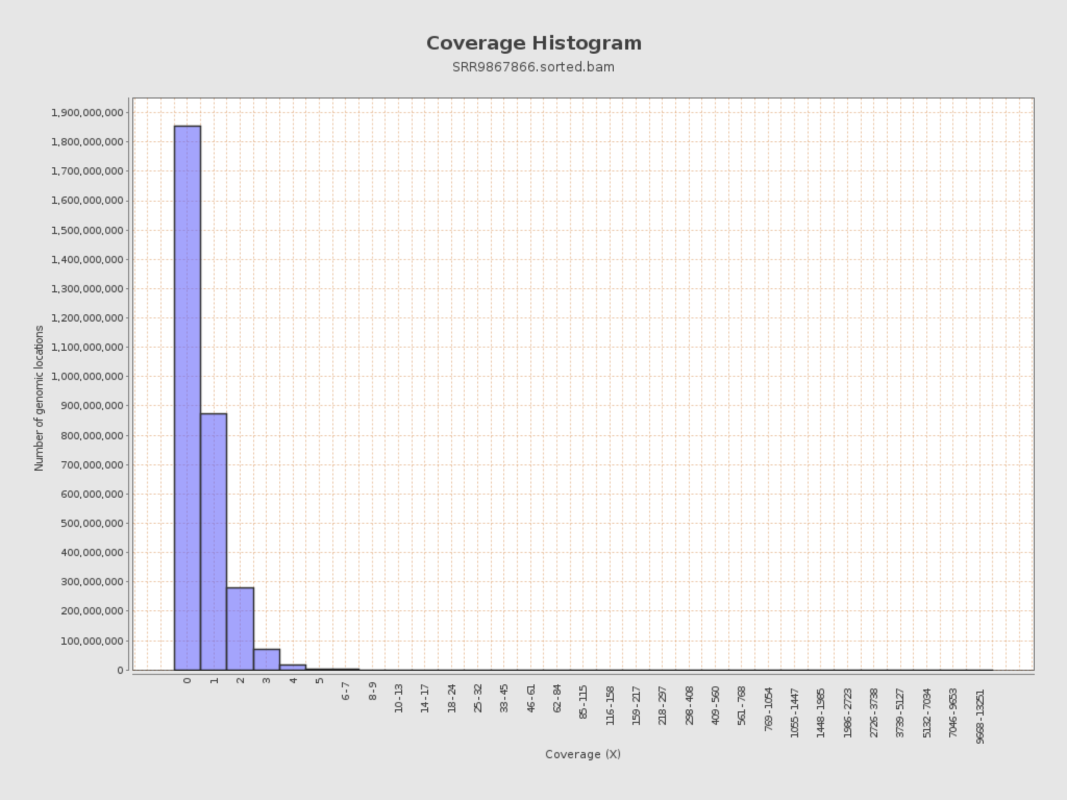
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	184330400	0.7395	12.0108
chr2	243199373	151278484	0.622	3.8442
chr3	198022430	115209514	0.5818	3.6666
chr4	191154276	113705350	0.5948	4.1147
chr5	180915260	95460482	0.5277	0.9324
chr6	171115067	95161177	0.5561	1.7924
chr7	159138663	92765860	0.5829	2.6703

chr8	146364022	102348160	0.6993	2.7121
chr9	141213431	70641186	0.5002	3.4786
chr10	135534747	102059027	0.753	19.4775
chr11	135006516	76738086	0.5684	2.2572
chr12	133851895	79538995	0.5942	0.999
chr13	115169878	39616018	0.344	0.6547
chr14	107349540	46781712	0.4358	1.0307
chr15	102531392	52197742	0.5091	0.8029
chr16	90354753	65268442	0.7224	6.4093
chr17	81195210	48900015	0.6023	1.6606
chr18	78077248	48334451	0.6191	7.5651
chr19	59128983	36799412	0.6224	7.0589
chr20	63025520	41390060	0.6567	1.4896
chr21	48129895	24948861	0.5184	3.0261
chr22	51304566	26207543	0.5108	0.8905
chrMT	16571	2847657	171.8458	54.2005
chrX	155270560	89697270	0.5777	1.6806
chrY	59373566	8579389	0.1445	6.0255

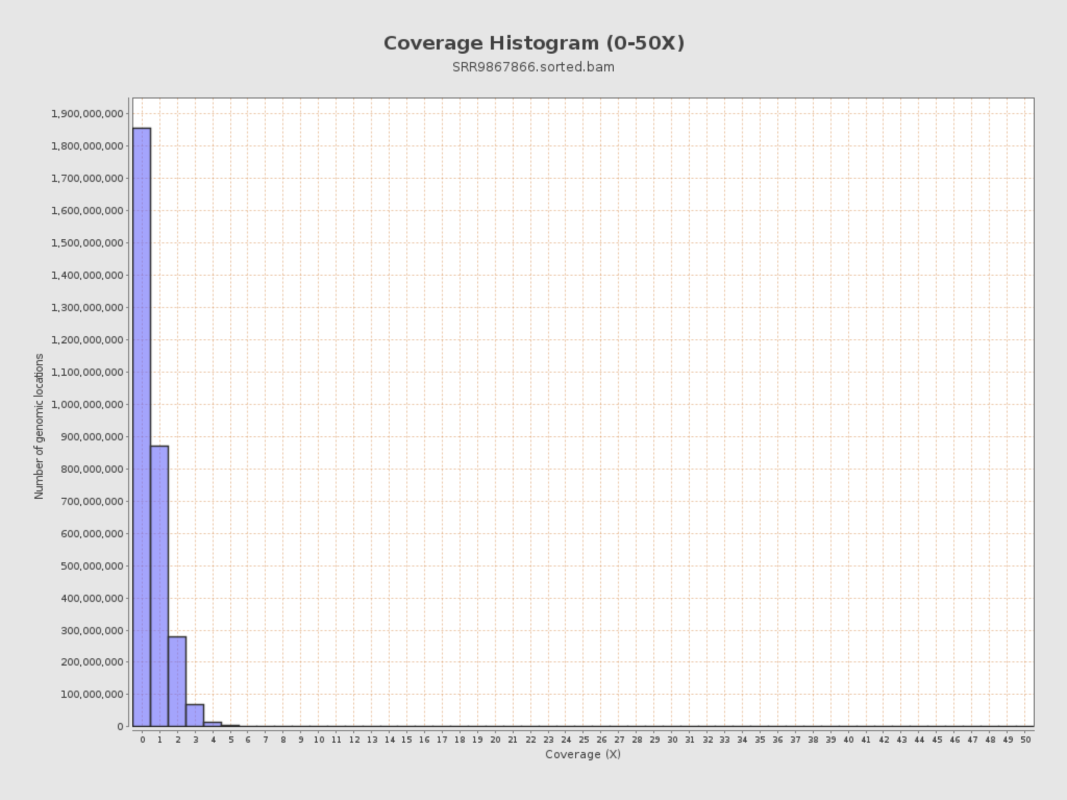
3. Results : Coverage across reference



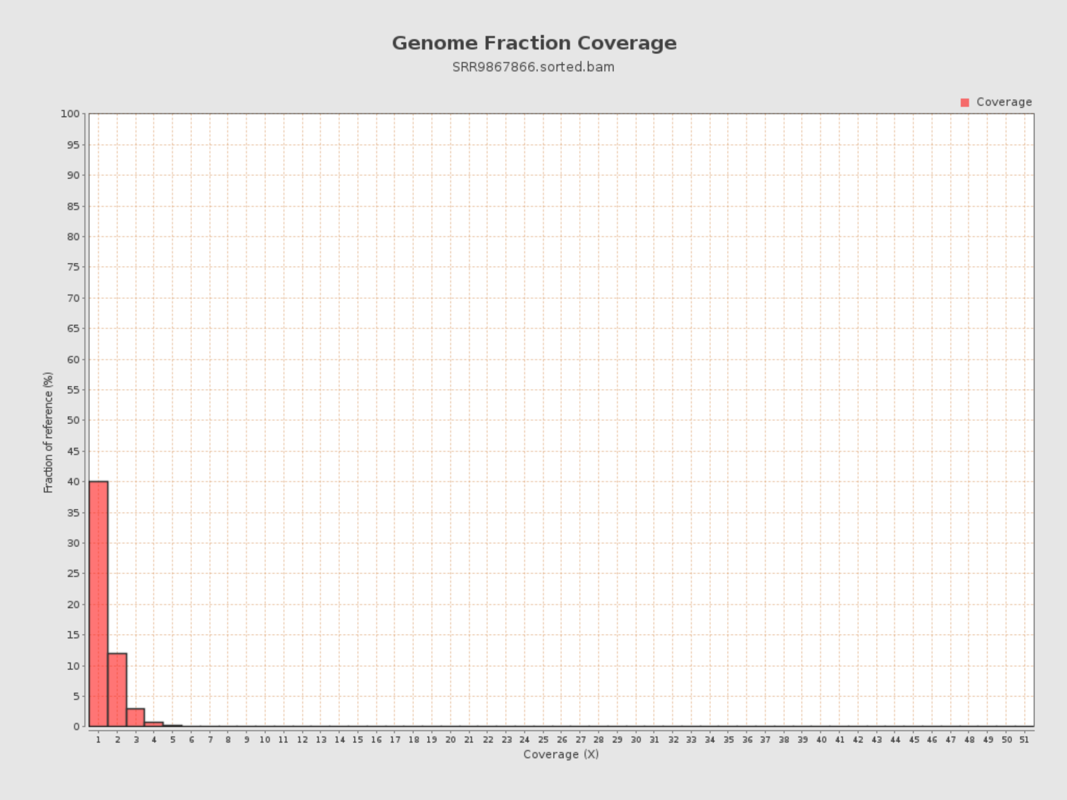
4. Results : Coverage Histogram



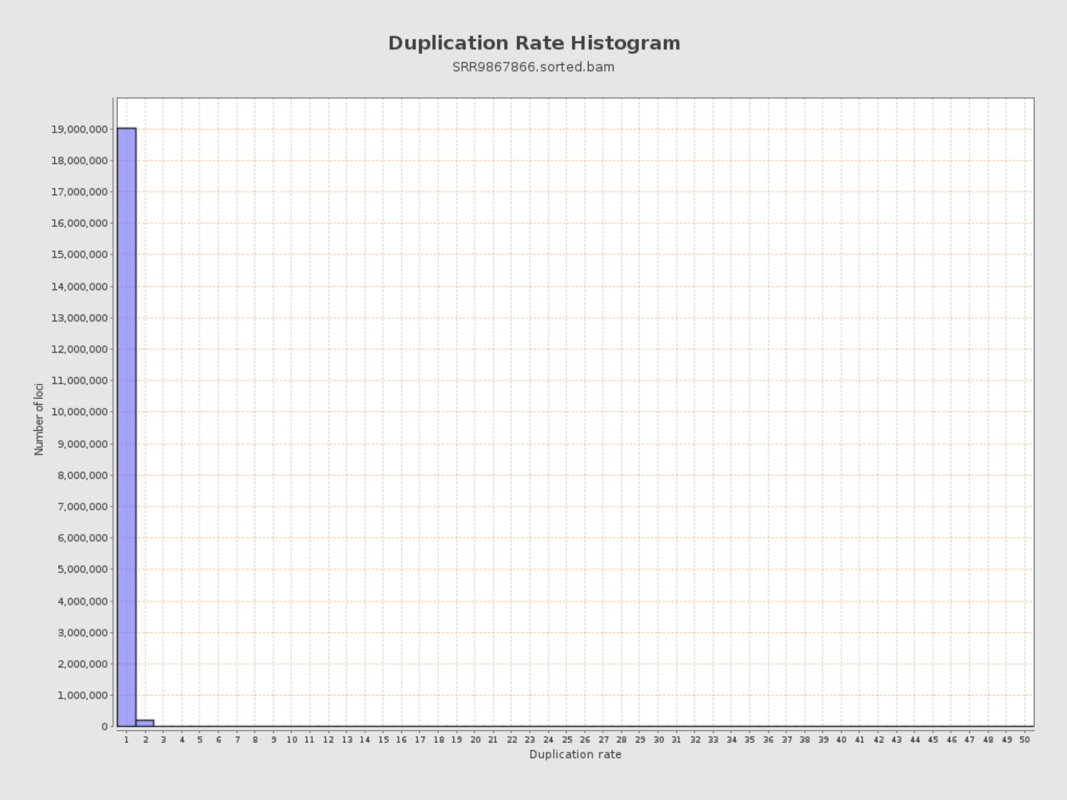
5. Results : Coverage Histogram (0-50X)



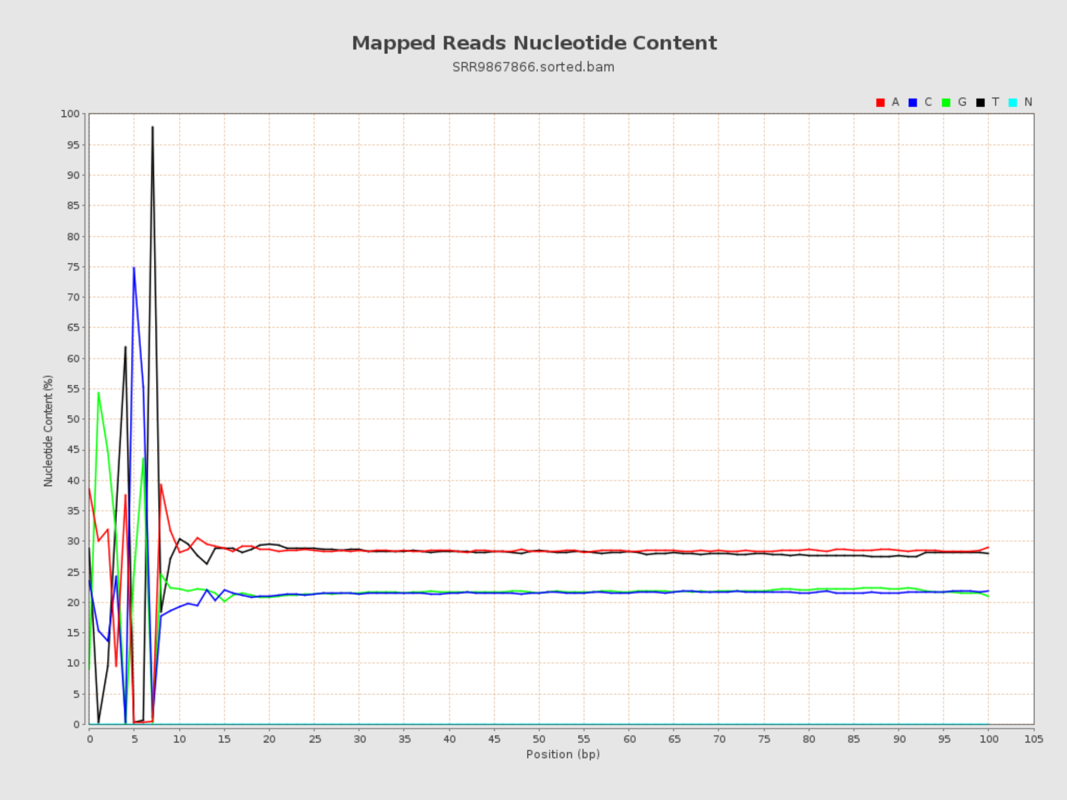
6. Results : Genome Fraction Coverage



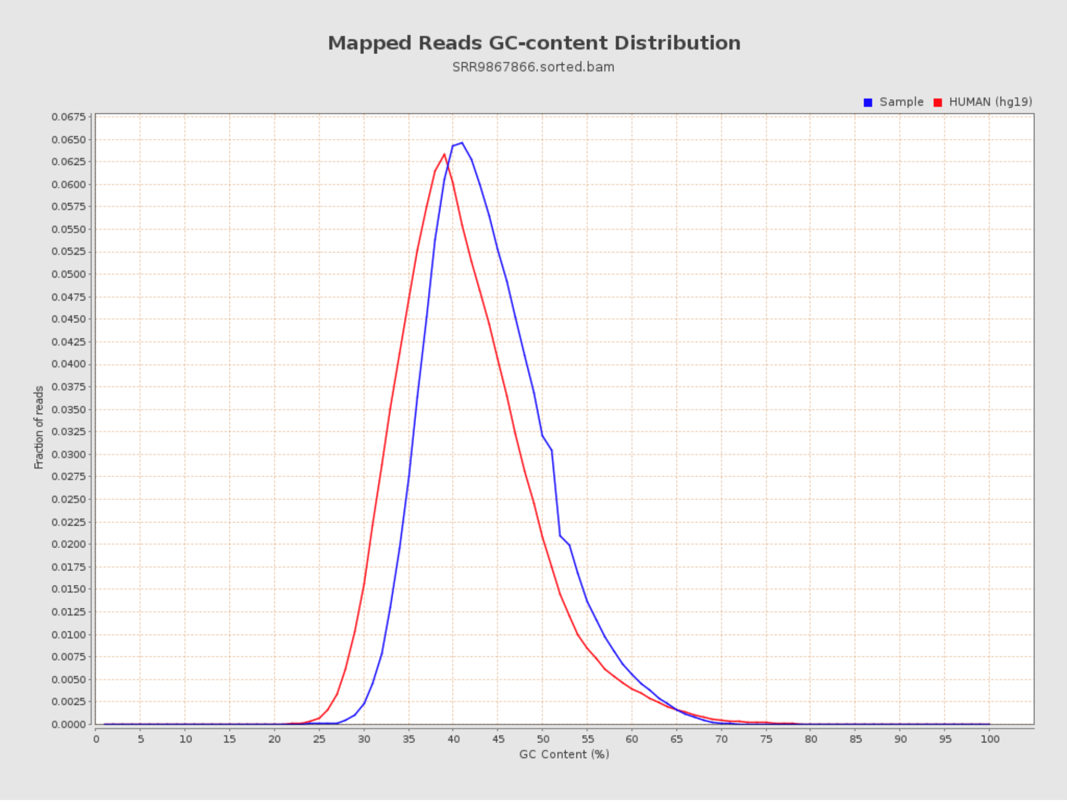
7. Results : Duplication Rate Histogram



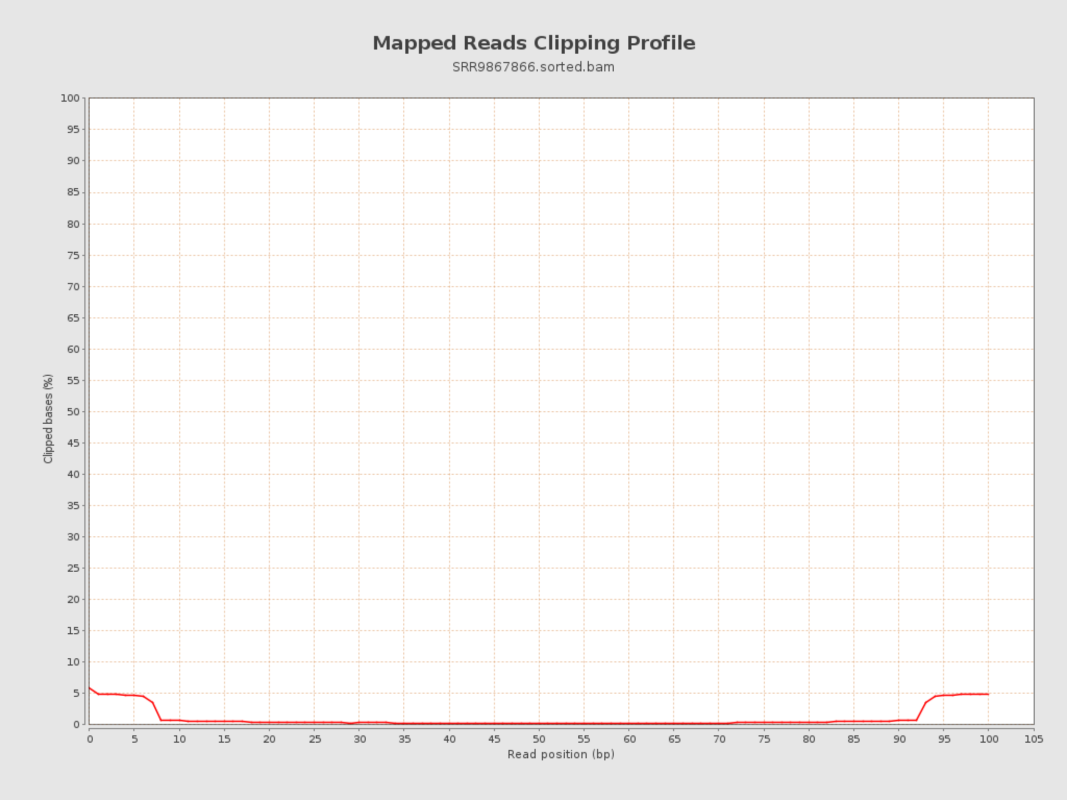
8. Results : Mapped Reads Nucleotide Content



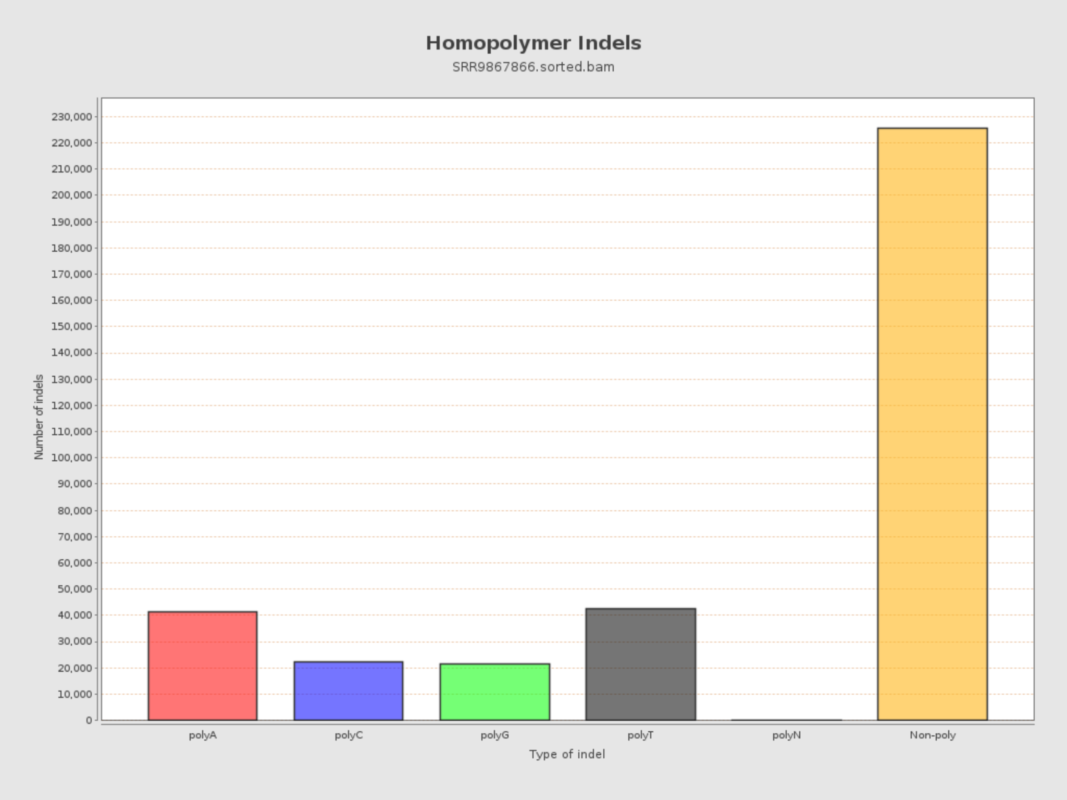
9. Results : Mapped Reads GC-content Distribution



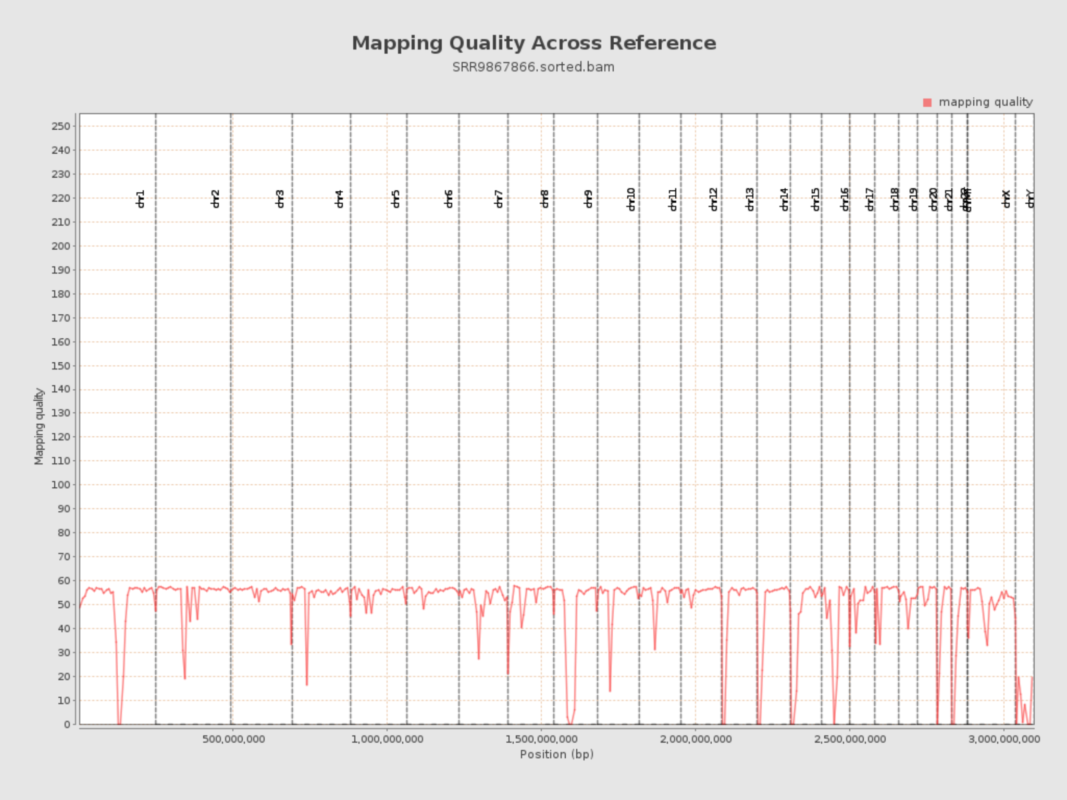
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram