Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 03:39:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9867836.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_SRR9867836 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9867836.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 03:39:00 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9867836.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	20,381,577
Mapped reads	19,570,451 / 96.02%
Unmapped reads	811,126 / 3.98%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	97,992 / 0.48%
Read min/max/mean length	30 / 101 / 101.18
Duplicated reads (estimated)	1,174,999 / 5.77%
Duplication rate	1.48%
Clipped reads	19,600,320 / 96.17%

2.2. ACGT Content

Number/percentage of A's	484,048,477 / 28.34%
Number/percentage of C's	367,173,071 / 21.49%
Number/percentage of T's	494,088,655 / 28.92%
Number/percentage of G's	362,528,933 / 21.22%
Number/percentage of N's	375,862 / 0.02%
GC Percentage	42.72%

2.3. Coverage

Mean	0.5519

Standard Deviation	6.9692

2.4. Mapping Quality

Mean Mapping Quality	50.29

2.5. Mismatches and indels

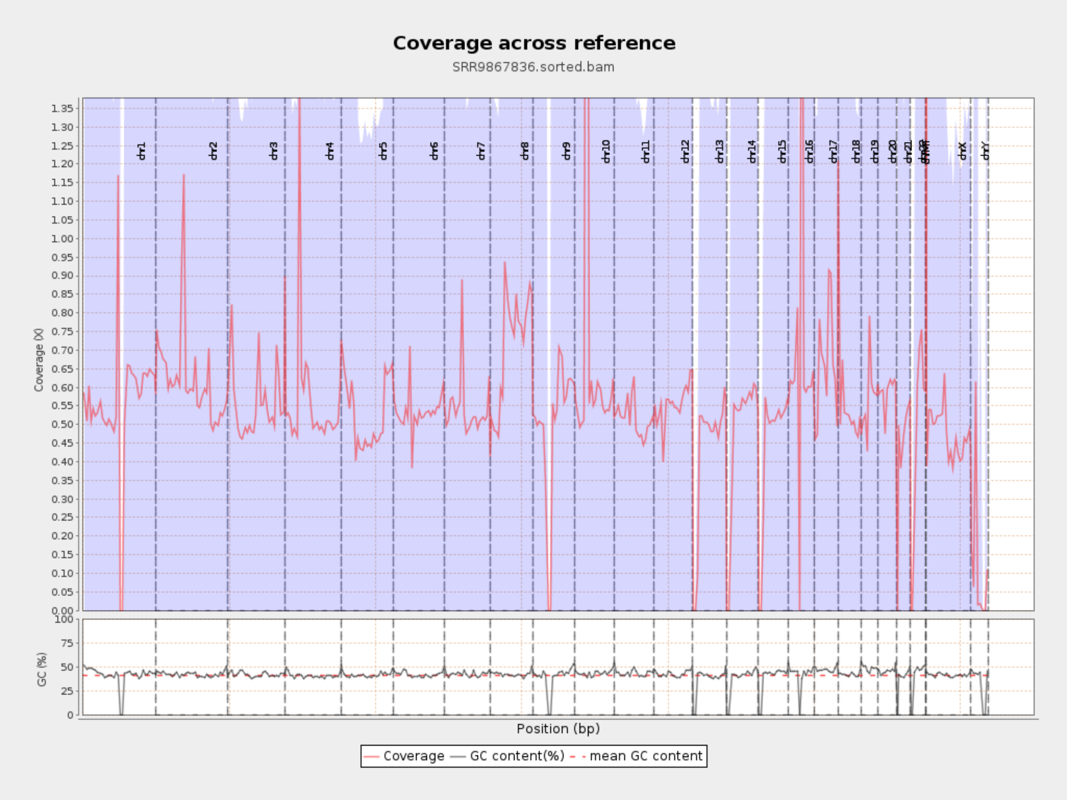
General error rate	0.54%
Mismatches	8,677,395
Insertions	171,125
Mapped reads with at least one insertion	0.86%
Deletions	167,873
Mapped reads with at least one deletion	0.83%
Homopolymer indels	33.68%

2.6. Chromosome stats

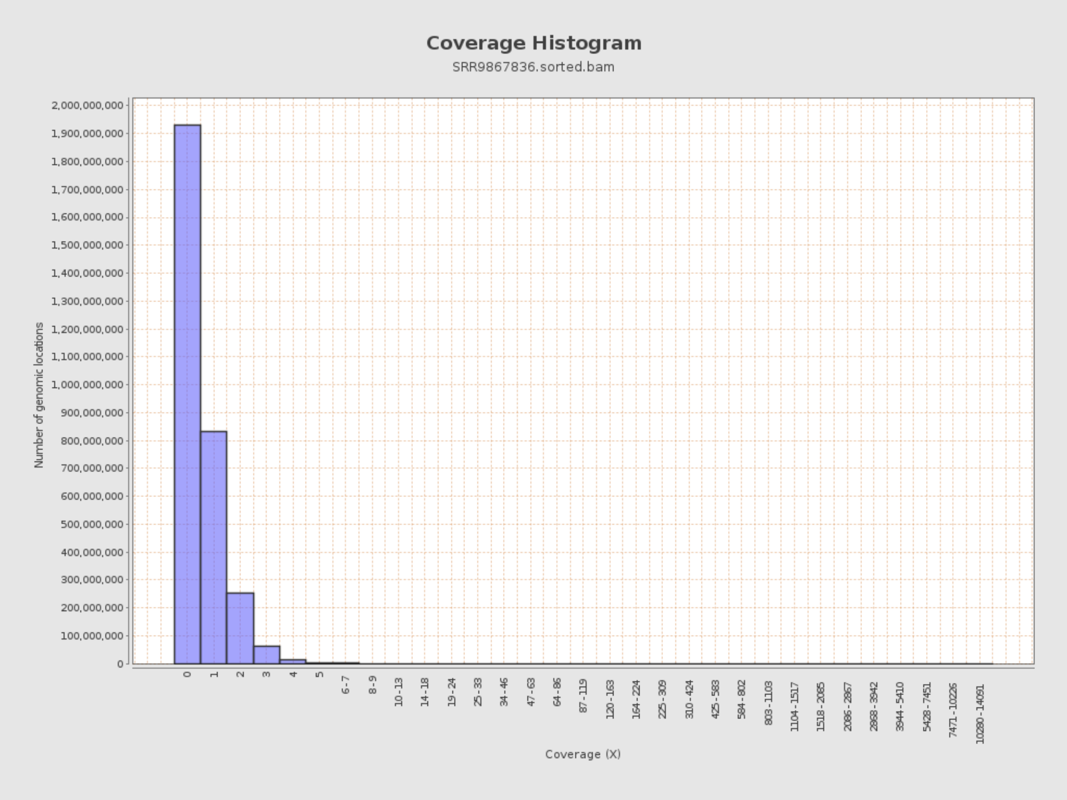
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	138523700	0.5558	12.4894
chr2	243199373	152239172	0.626	4.3688
chr3	198022430	110615123	0.5586	4.3149
chr4	191154276	107714323	0.5635	5.3199
chr5	180915260	95891846	0.53	0.8788
chr6	171115067	91394097	0.5341	2.1672
chr7	159138663	86701650	0.5448	5.7142

chr8	146364022	104902508	0.7167	2.9821
chr9	141213431	69781399	0.4942	2.8134
chr10	135534747	97753590	0.7212	21.6326
chr11	135006516	69747517	0.5166	2.2259
chr12	133851895	74250754	0.5547	1.0858
chr13	115169878	49234131	0.4275	0.7242
chr14	107349540	51330083	0.4782	0.9927
chr15	102531392	44367640	0.4327	0.7417
chr16	90354753	67571891	0.7479	12.3335
chr17	81195210	54134452	0.6667	2.4052
chr18	78077248	43337371	0.5551	5.8094
chr19	59128983	33846754	0.5724	8.0396
chr20	63025520	37032144	0.5876	1.7531
chr21	48129895	21540813	0.4476	3.7667
chr22	51304566	23604212	0.4601	0.8905
chrMT	16571	2223816	134.1993	58.2168
chrX	155270560	73653579	0.4744	1.5538
chrY	59373566	7256619	0.1222	6.2991

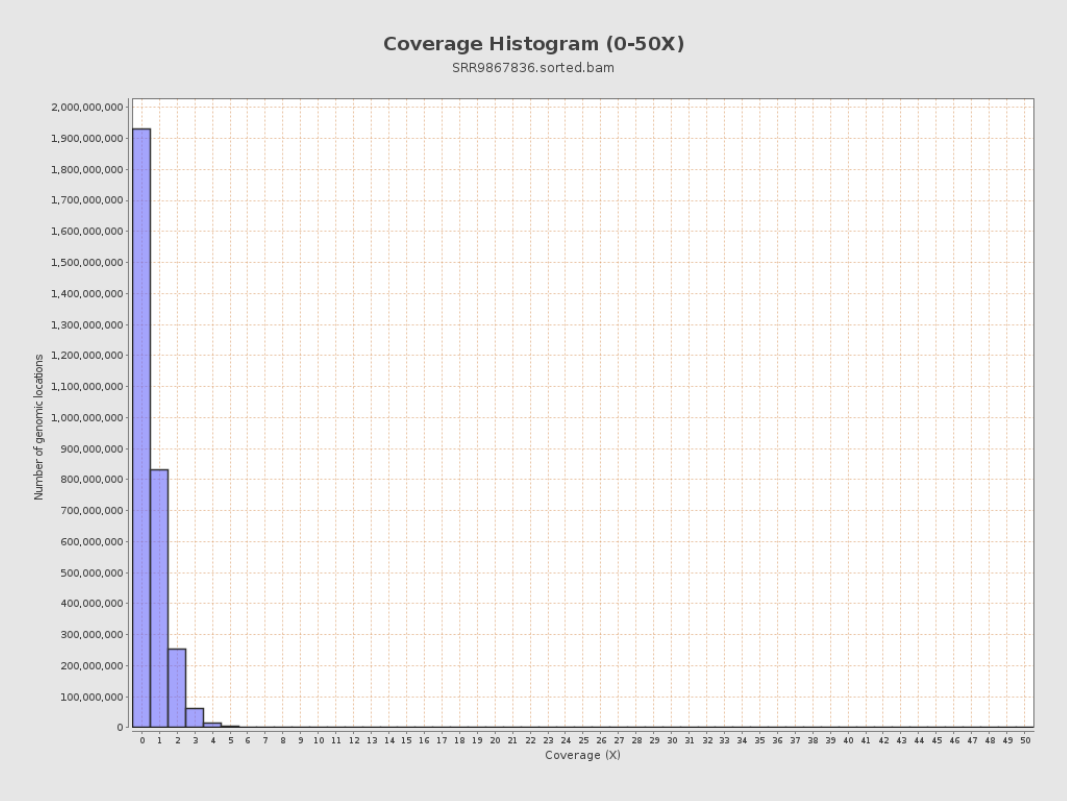
3. Results : Coverage across reference



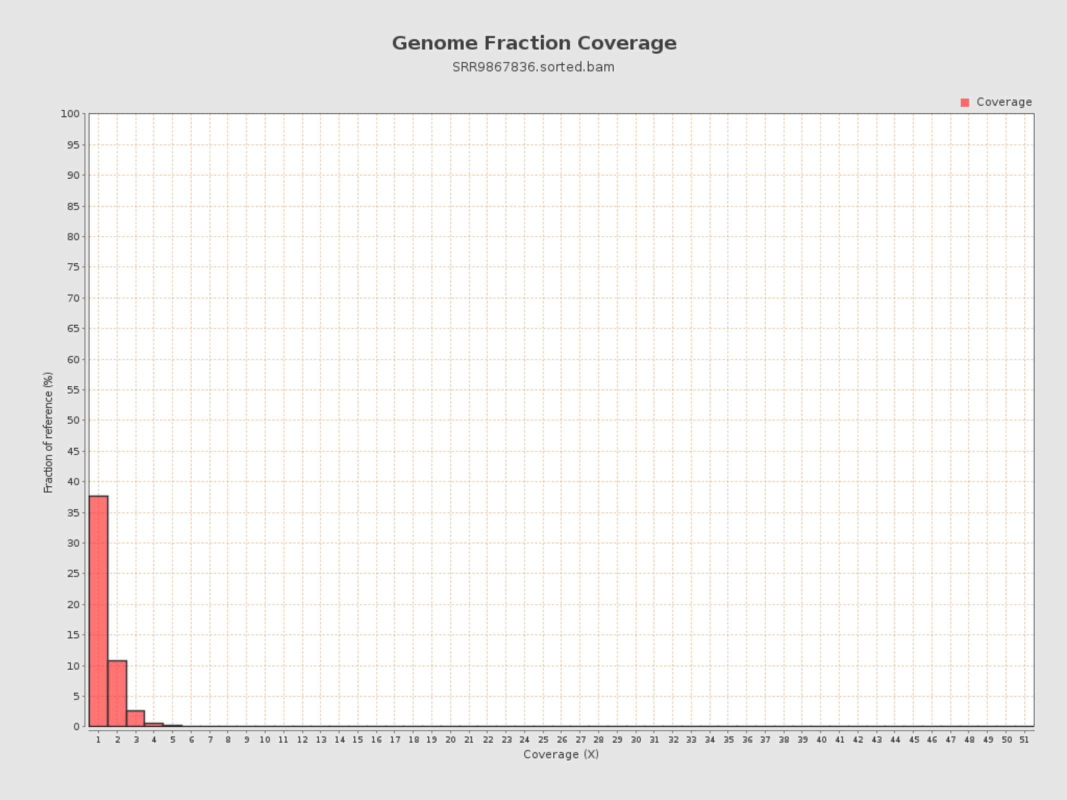
4. Results : Coverage Histogram



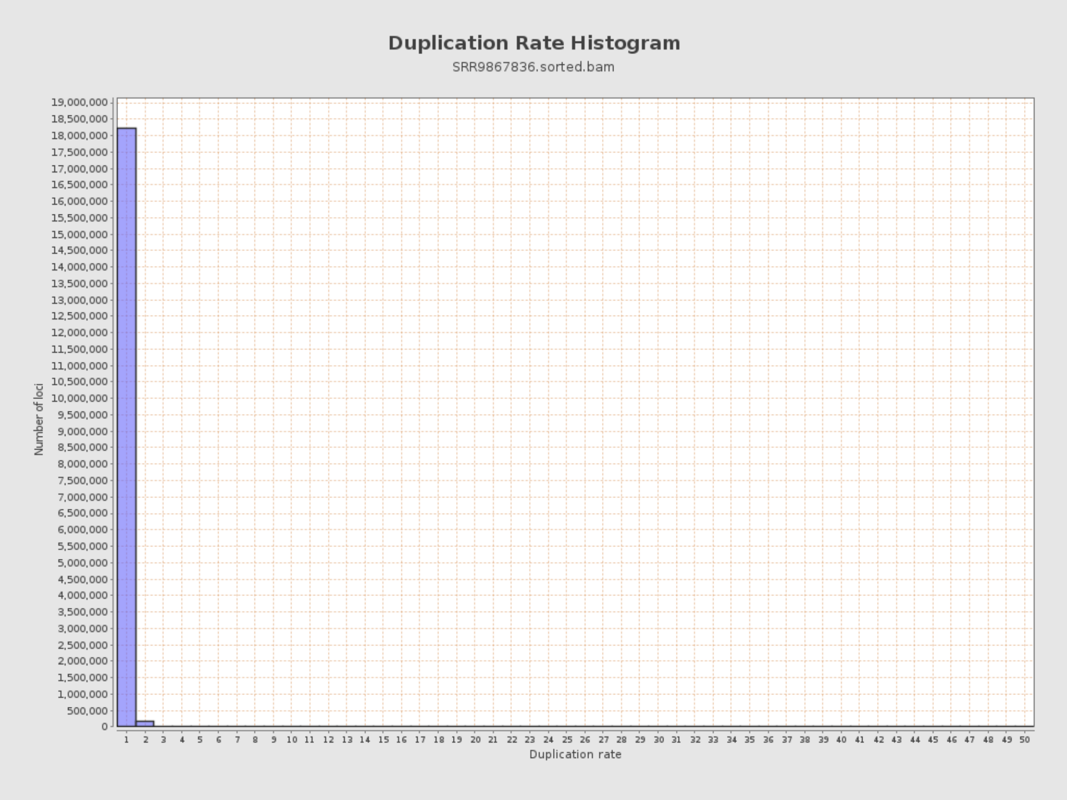
5. Results : Coverage Histogram (0-50X)



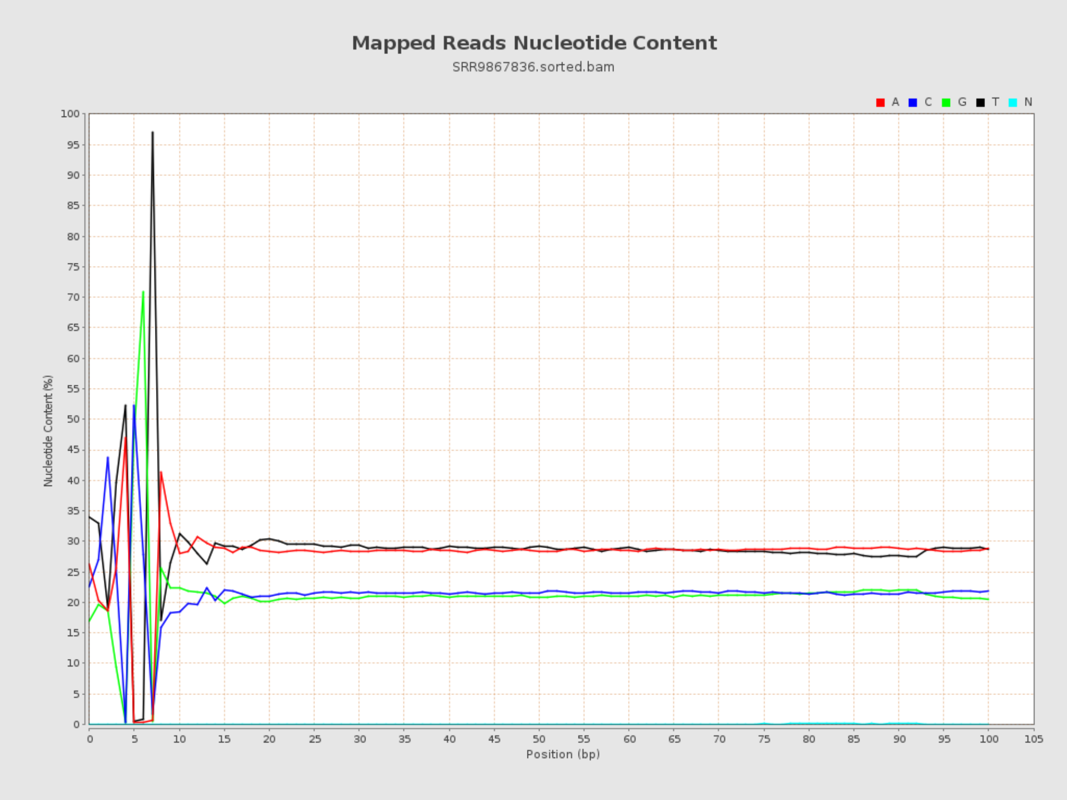
6. Results : Genome Fraction Coverage



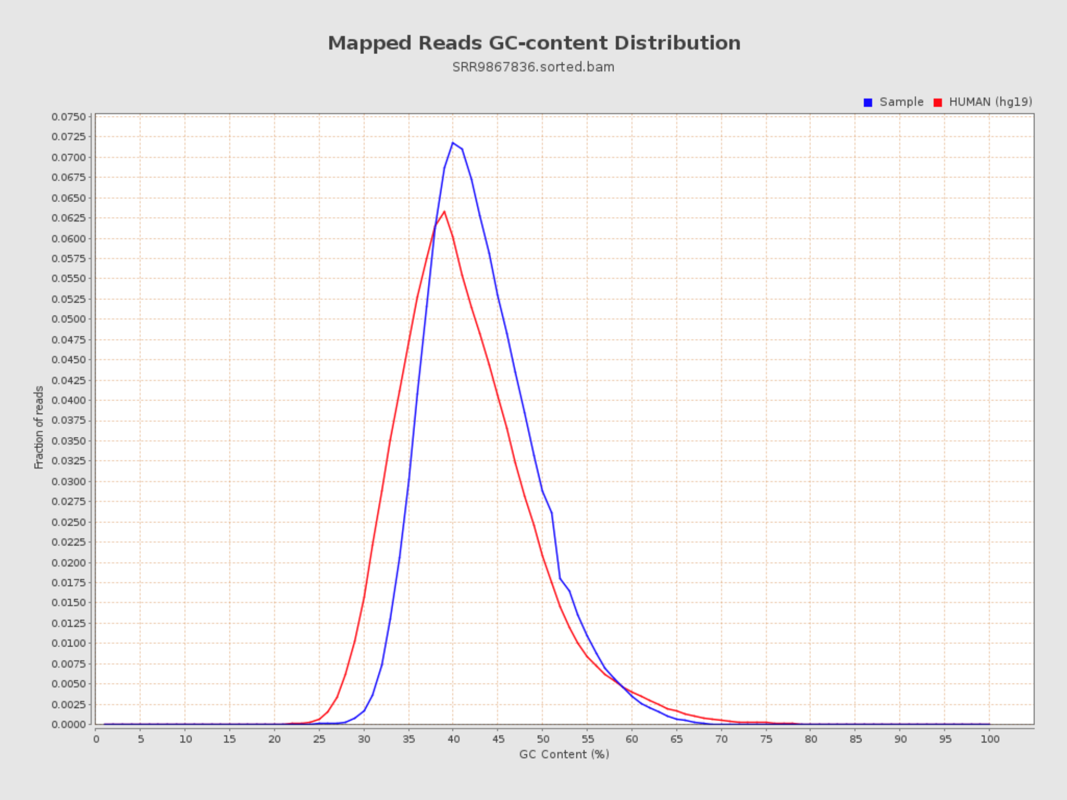
7. Results : Duplication Rate Histogram



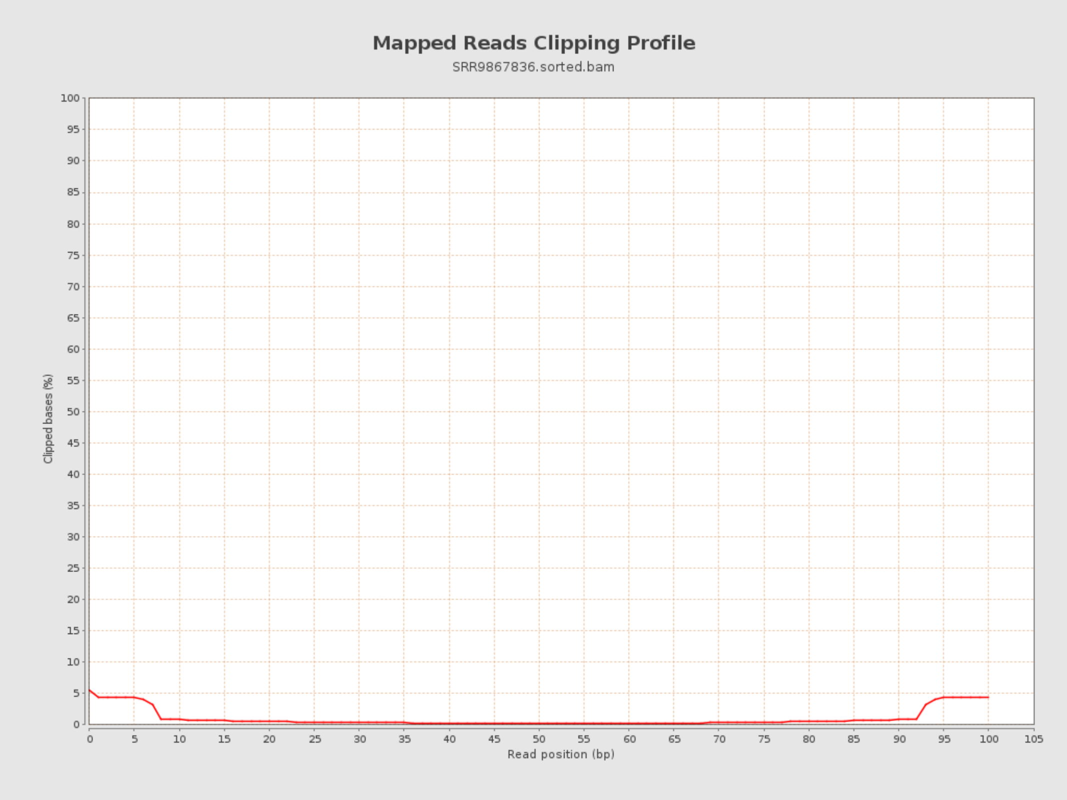
8. Results : Mapped Reads Nucleotide Content



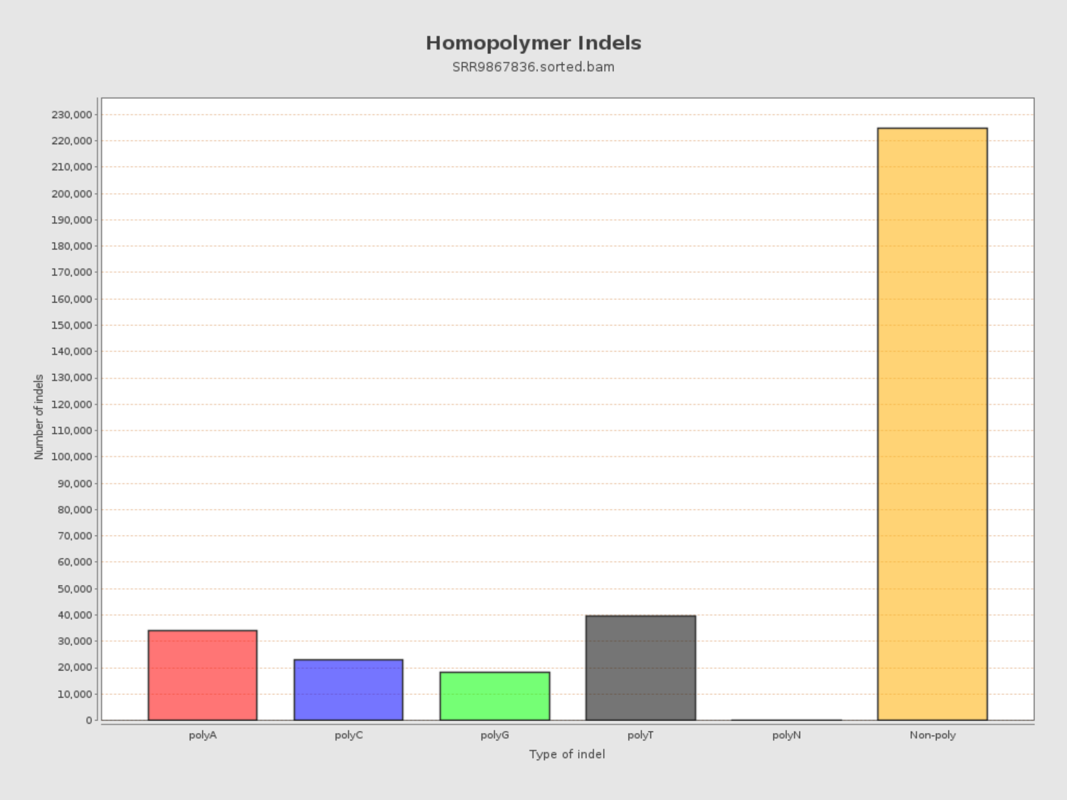
9. Results : Mapped Reads GC-content Distribution



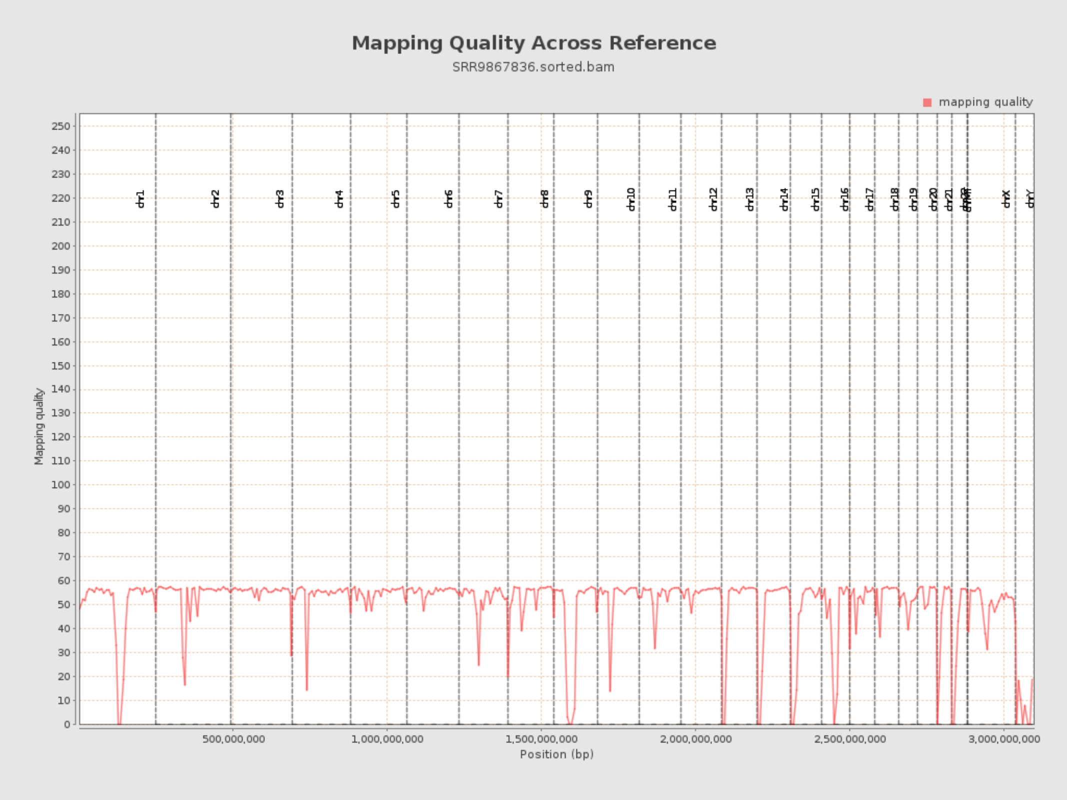
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram