Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 02:58:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9867835.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_SRR9867835 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9867835.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 02:58:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9867835.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	22,222,151
Mapped reads	21,722,634 / 97.75%
Unmapped reads	499,517 / 2.25%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	55,334 / 0.25%
Read min/max/mean length	30 / 101 / 101.1
Duplicated reads (estimated)	1,050,440 / 4.73%
Duplication rate	1.39%
Clipped reads	21,703,441 / 97.67%

2.2. ACGT Content

Number/percentage of A's	533,076,909 / 28.03%
Number/percentage of C's	413,648,443 / 21.75%
Number/percentage of T's	534,188,598 / 28.08%
Number/percentage of G's	420,752,364 / 22.12%
Number/percentage of N's	415,038 / 0.02%
GC Percentage	43.87%

2.3. Coverage

Mean	0.6146

Standard Deviation	7.0939

2.4. Mapping Quality

Mean Mapping Quality	50.22

2.5. Mismatches and indels

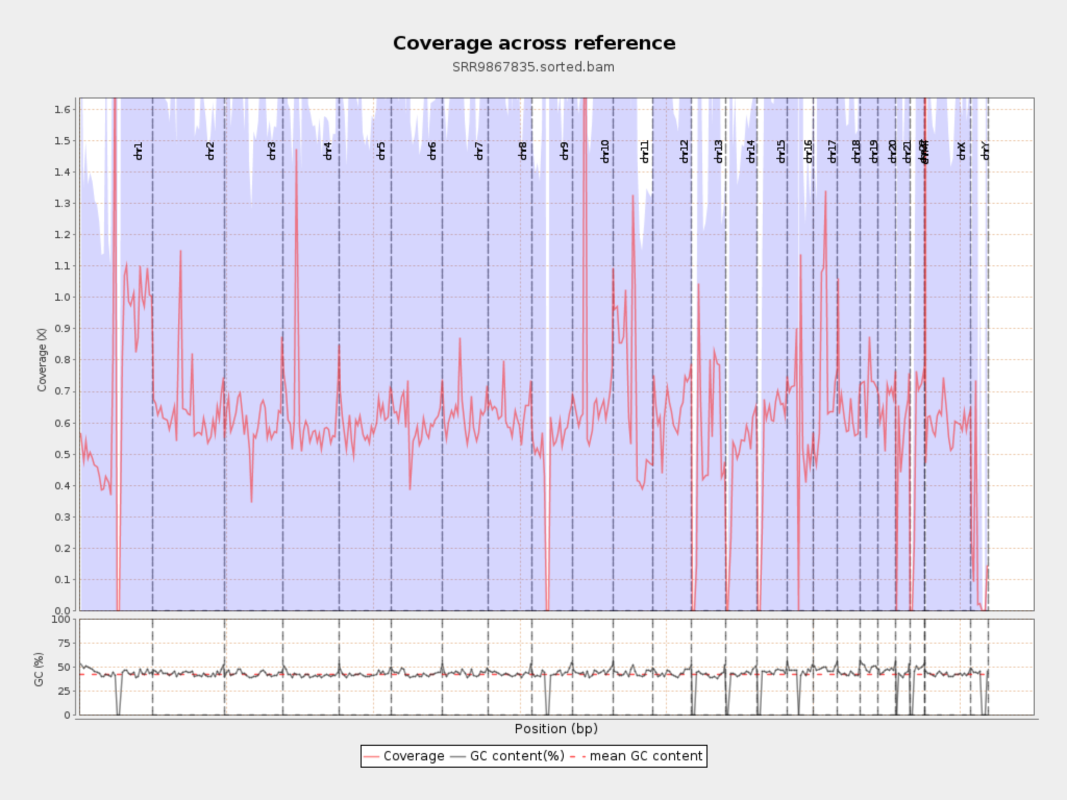
General error rate	0.47%
Mismatches	8,501,184
Insertions	178,847
Mapped reads with at least one insertion	0.81%
Deletions	185,214
Mapped reads with at least one deletion	0.83%
Homopolymer indels	34.88%

2.6. Chromosome stats

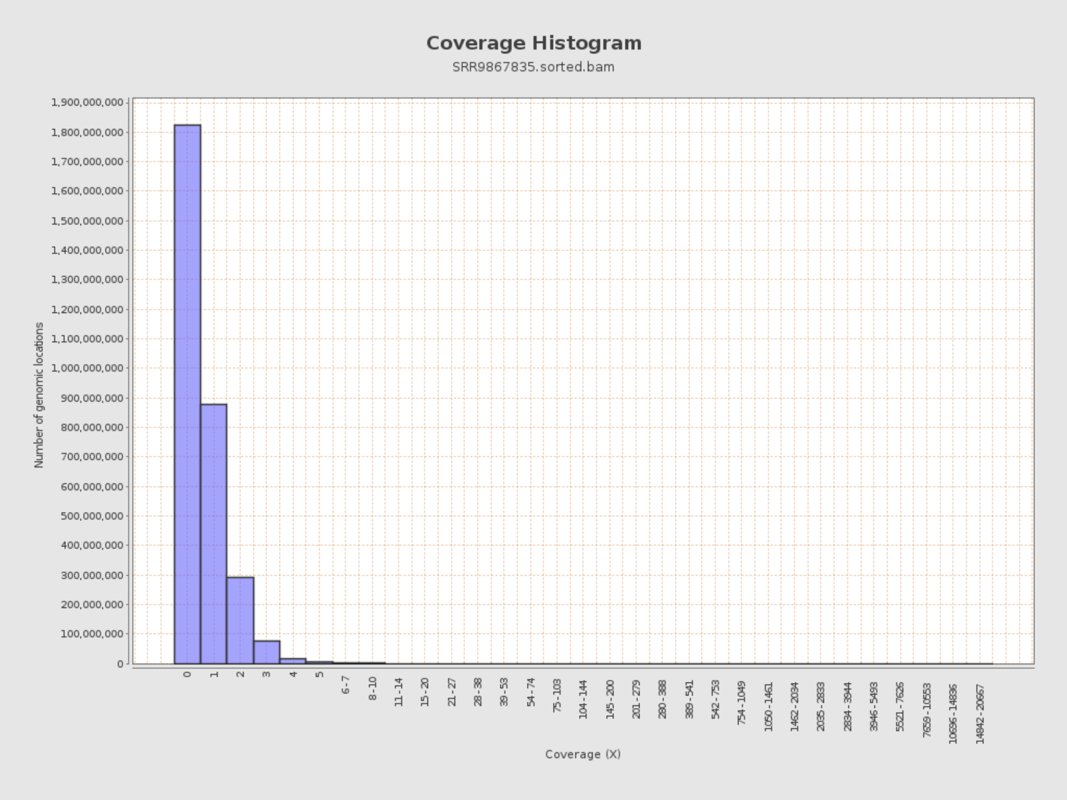
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	178801489	0.7174	19.2524
chr2	243199373	156704973	0.6443	4.295
chr3	198022430	118654861	0.5992	2.6008
chr4	191154276	118674791	0.6208	4.2918
chr5	180915260	108536156	0.5999	1.0004
chr6	171115067	102720609	0.6003	2.0968
chr7	159138663	100231975	0.6298	4.7163

chr8	146364022	92311199	0.6307	3.2883
chr9	141213431	69973657	0.4955	3.015
chr10	135534747	100987785	0.7451	14.2796
chr11	135006516	97064211	0.719	3.4038
chr12	133851895	86607347	0.647	1.017
chr13	115169878	61073441	0.5303	0.8543
chr14	107349540	49373675	0.4599	0.9838
chr15	102531392	54082821	0.5275	0.8302
chr16	90354753	54979669	0.6085	4.2157
chr17	81195210	62548692	0.7703	2.224
chr18	78077248	49497403	0.634	6.9374
chr19	59128983	42776074	0.7234	10.9464
chr20	63025520	41642916	0.6607	1.521
chr21	48129895	26218118	0.5447	3.1847
chr22	51304566	26047558	0.5077	0.8775
chrMT	16571	1324756	79.9442	27.2687
chrX	155270560	92752893	0.5974	1.9611
chrY	59373566	8955978	0.1508	6.9253

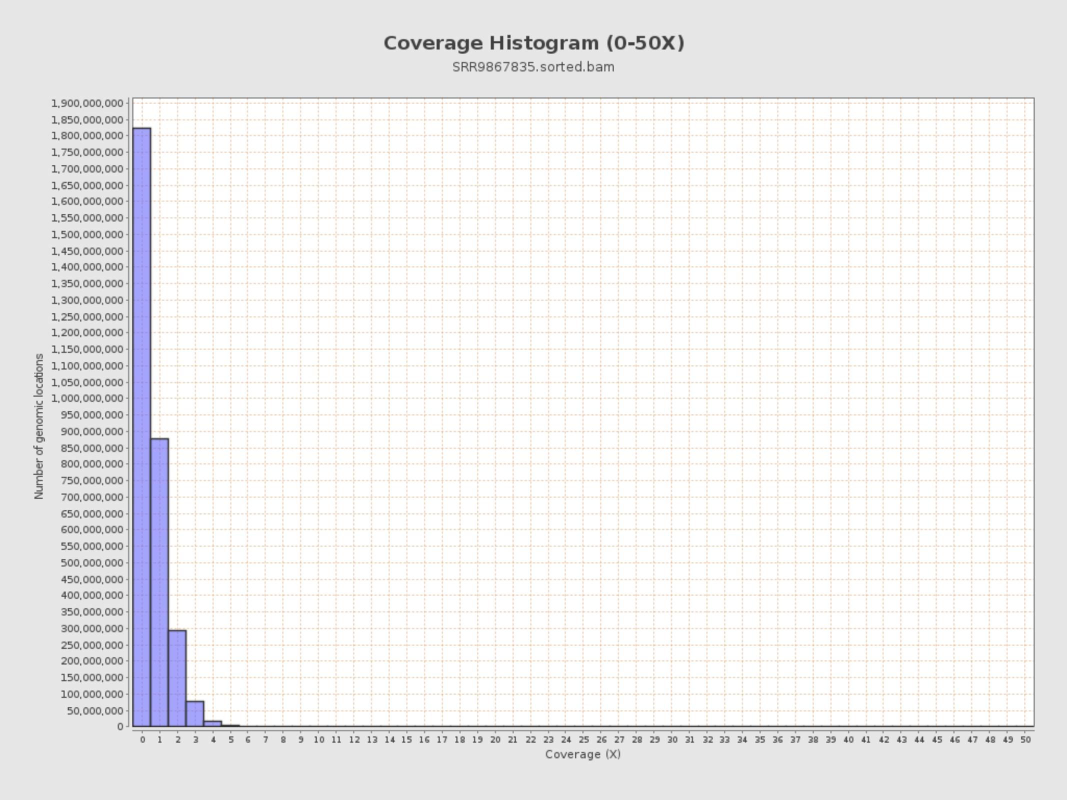
3. Results : Coverage across reference



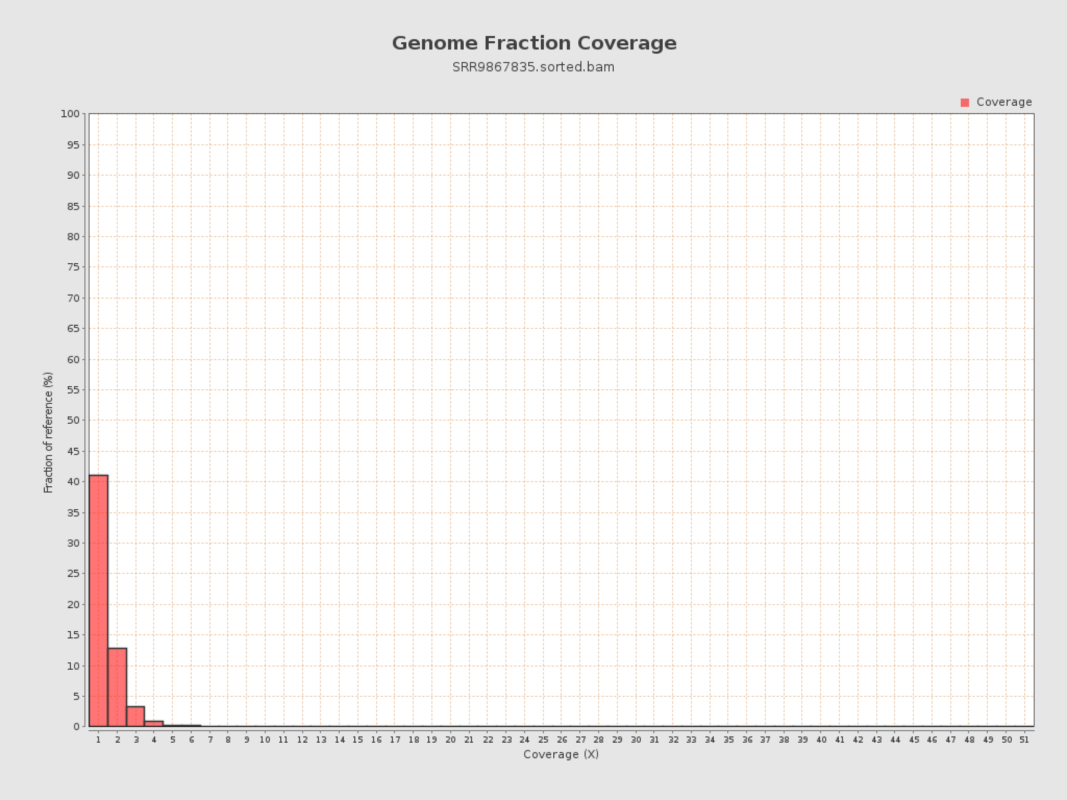
4. Results : Coverage Histogram



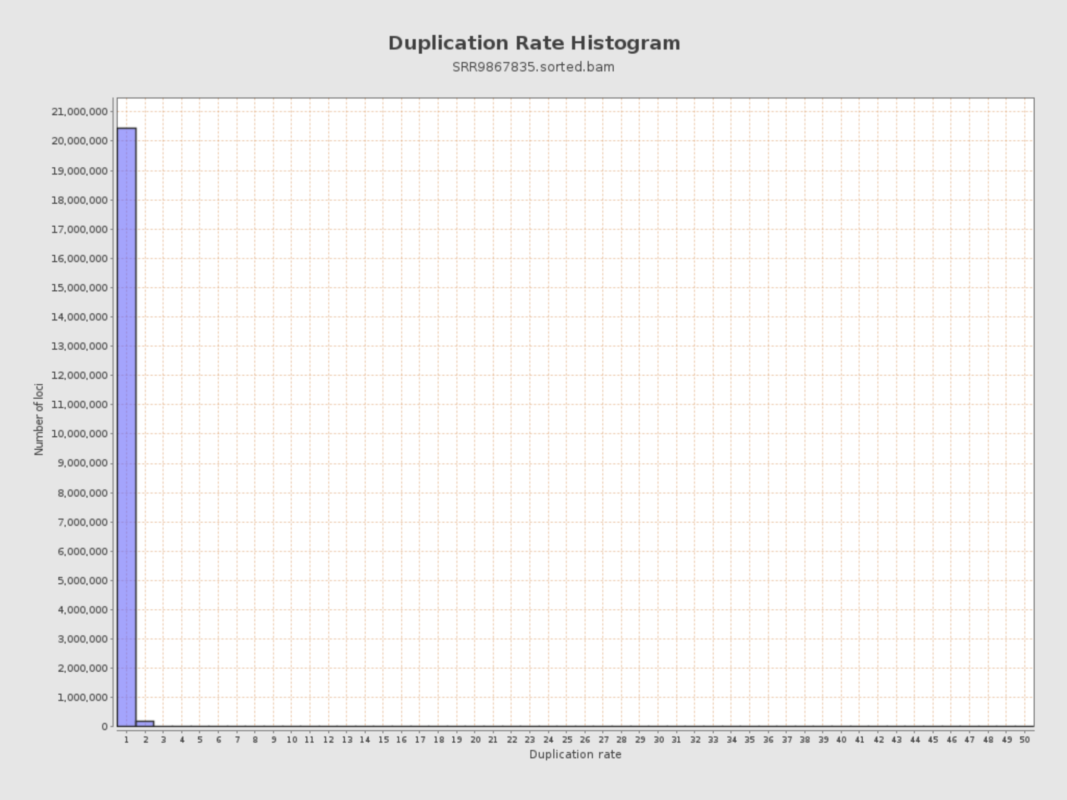
5. Results : Coverage Histogram (0-50X)



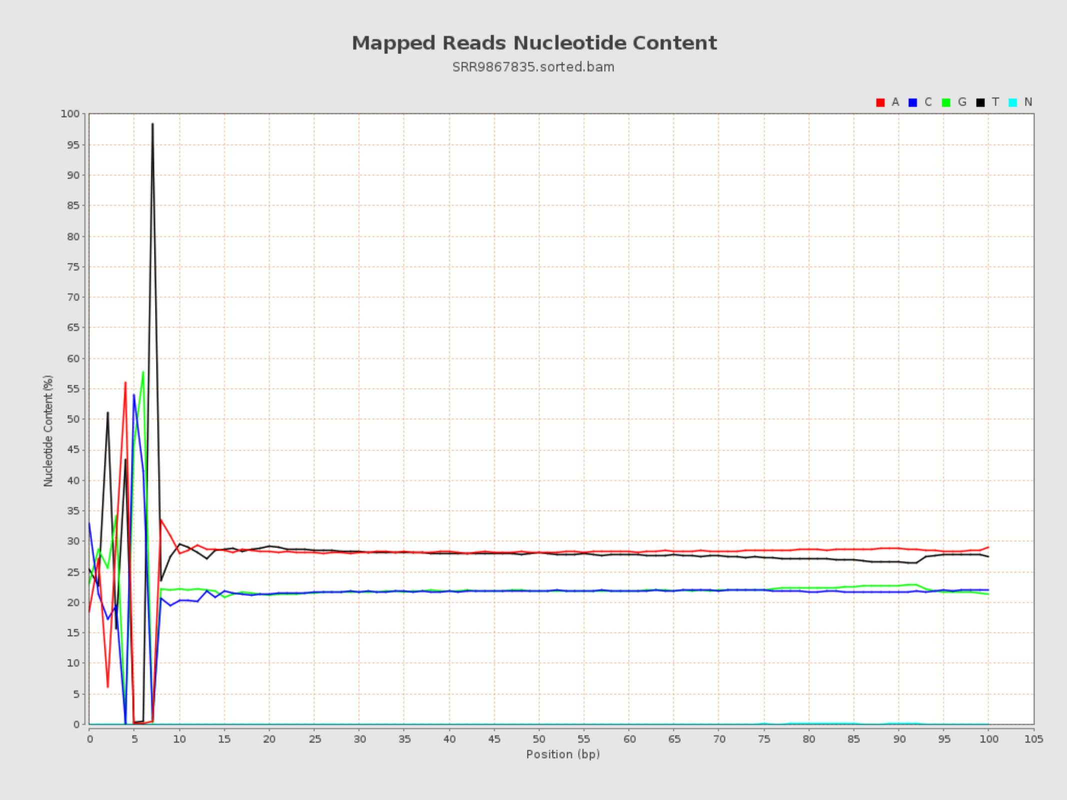
6. Results : Genome Fraction Coverage



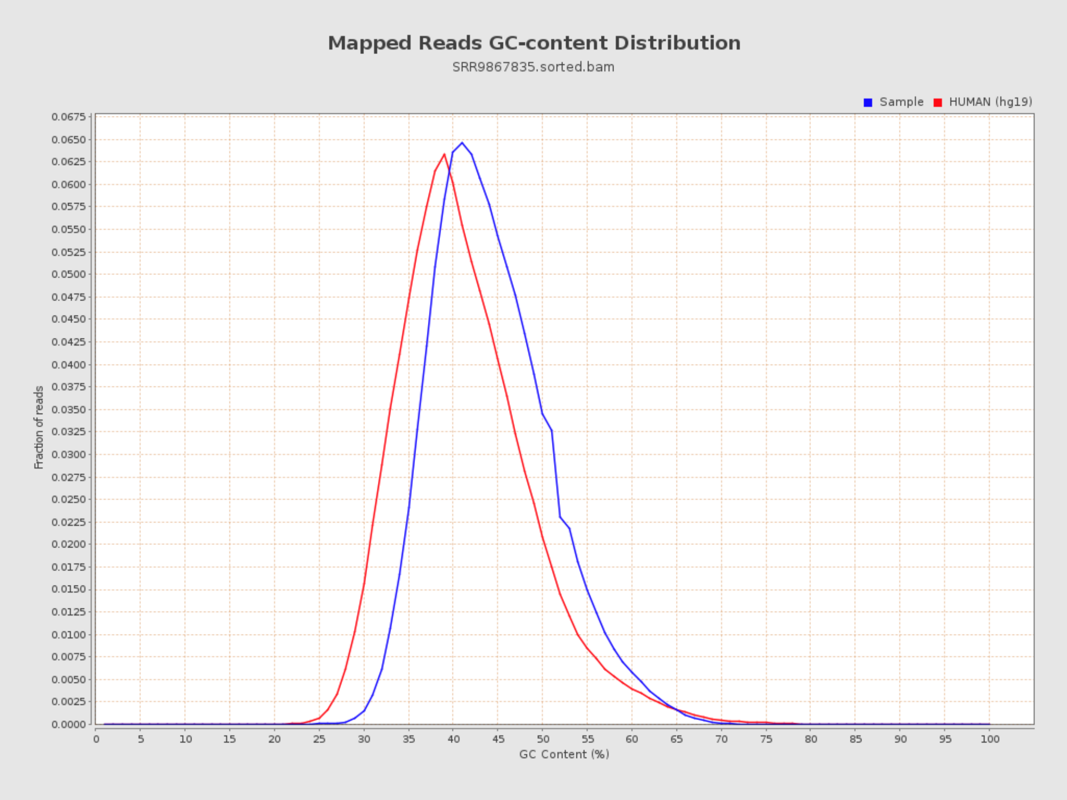
7. Results : Duplication Rate Histogram



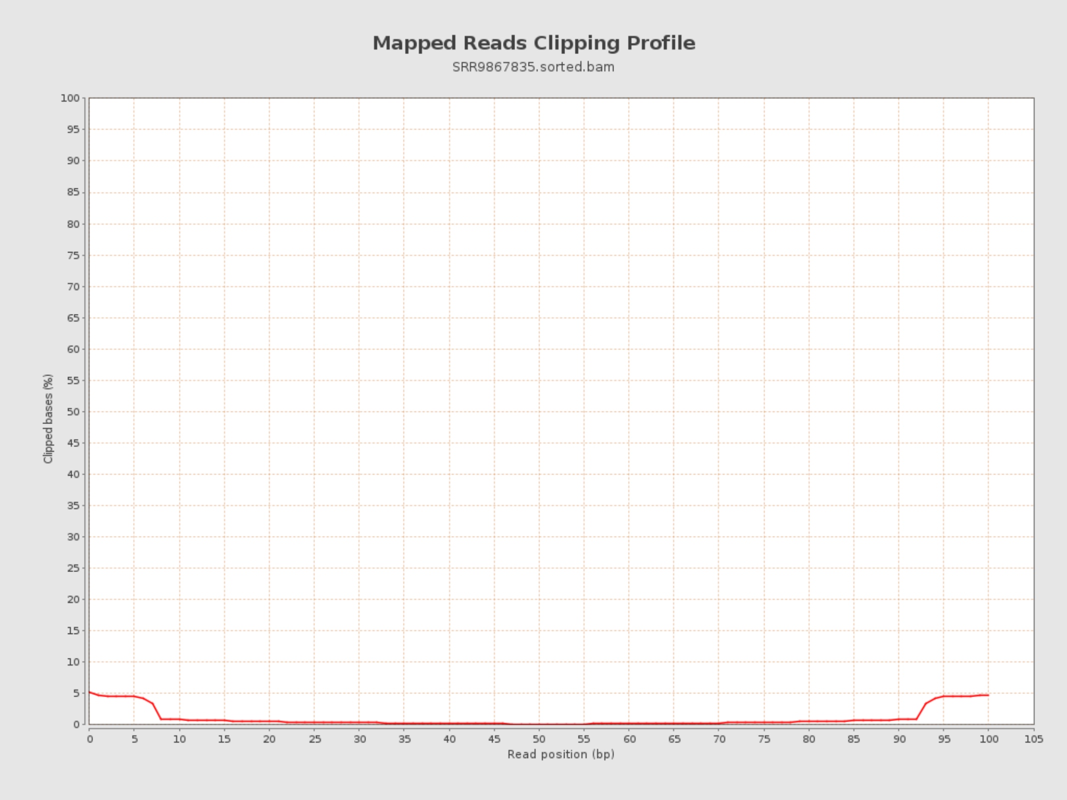
8. Results : Mapped Reads Nucleotide Content



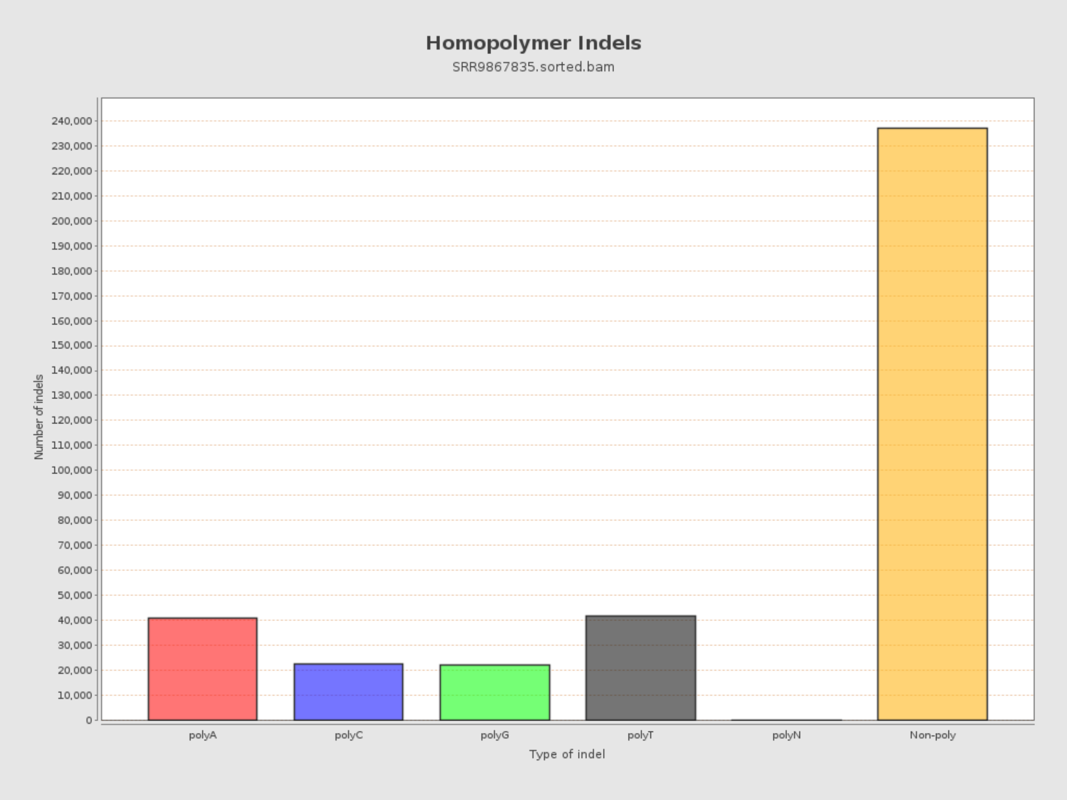
9. Results : Mapped Reads GC-content Distribution



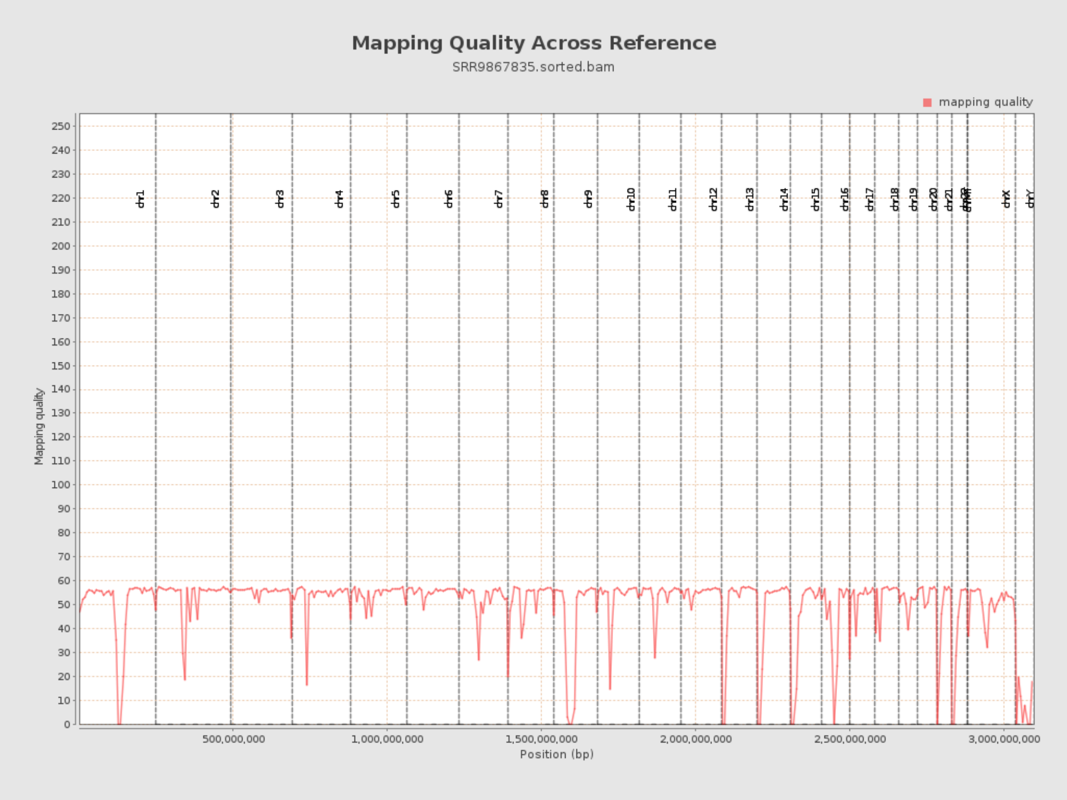
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram