Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 13:14:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080967.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_SRR3080967 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080967.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 13:14:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080967.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,871,390
Mapped reads	5,066,629 / 86.29%
Unmapped reads	804,761 / 13.71%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	61,632 / 1.05%
Read min/max/mean length	30 / 76 / 76.37
Duplicated reads (estimated)	429,384 / 7.31%
Duplication rate	6.76%
Clipped reads	2,099,662 / 35.76%

2.2. ACGT Content

Number/percentage of A's	97,182,175 / 28.37%
Number/percentage of C's	60,549,273 / 17.68%
Number/percentage of T's	111,394,164 / 32.52%
Number/percentage of G's	72,744,886 / 21.24%
Number/percentage of N's	677,544 / 0.2%
GC Percentage	38.91%

2.3. Coverage

Mean	0.1107

Standard Deviation	0.7157

2.4. Mapping Quality

Mean Mapping Quality	47.15

2.5. Mismatches and indels

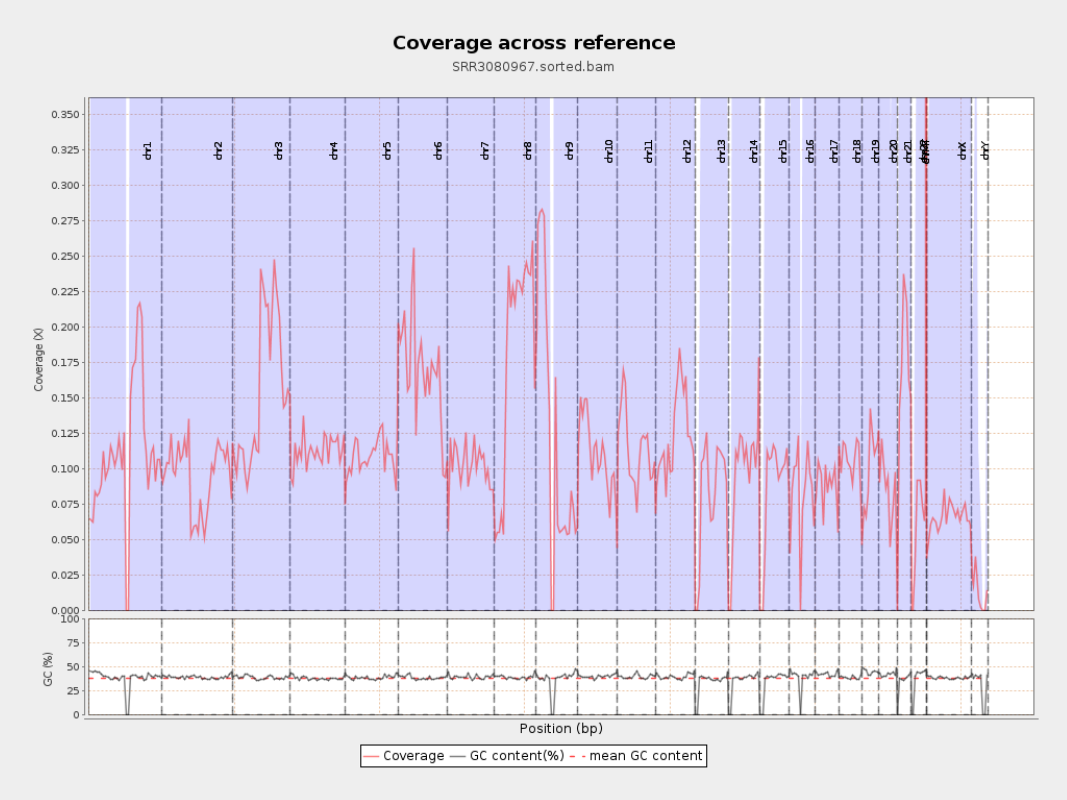
General error rate	1.01%
Mismatches	3,428,350
Insertions	27,091
Mapped reads with at least one insertion	0.53%
Deletions	76,675
Mapped reads with at least one deletion	1.5%
Homopolymer indels	49.51%

2.6. Chromosome stats

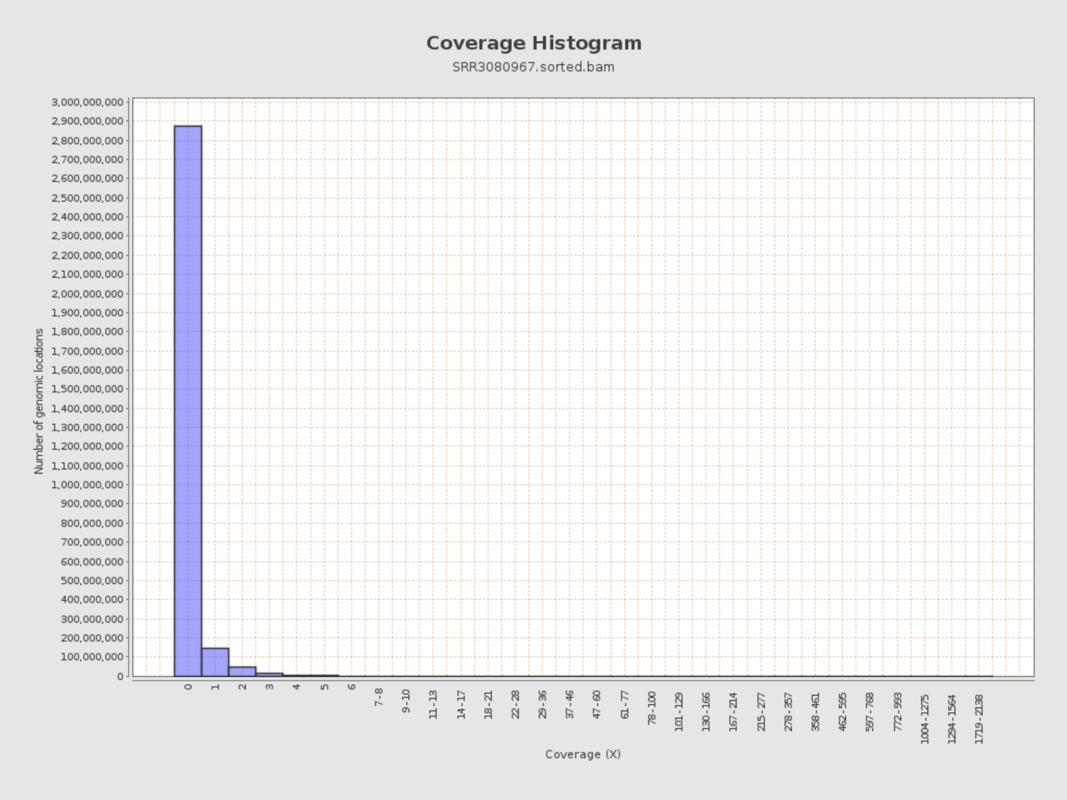
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	27563029	0.1106	1.0103
chr2	243199373	23191813	0.0954	0.636
chr3	198022430	30628258	0.1547	0.5642
chr4	191154276	21492748	0.1124	0.4972
chr5	180915260	19673514	0.1087	0.469
chr6	171115067	28888881	0.1688	0.824
chr7	159138663	16355252	0.1028	0.6259

chr8	146364022	26408900	0.1804	1.4541
chr9	141213431	17130841	0.1213	0.8299
chr10	135534747	15162743	0.1119	0.6055
chr11	135006516	15278544	0.1132	0.6299
chr12	133851895	16749896	0.1251	0.523
chr13	115169878	9223734	0.0801	0.4005
chr14	107349540	10067713	0.0938	0.5229
chr15	102531392	8805329	0.0859	0.4138
chr16	90354753	7501013	0.083	0.4952
chr17	81195210	7056009	0.0869	0.4542
chr18	78077248	8327281	0.1067	1.3586
chr19	59128983	5951246	0.1006	0.8035
chr20	63025520	5465875	0.0867	0.4454
chr21	48129895	7906724	0.1643	0.6624
chr22	51304566	2894948	0.0564	0.3307
chrMT	16571	85314	5.1484	4.1249
chrX	155270560	10136634	0.0653	0.4026
chrY	59373566	727273	0.0122	0.2143

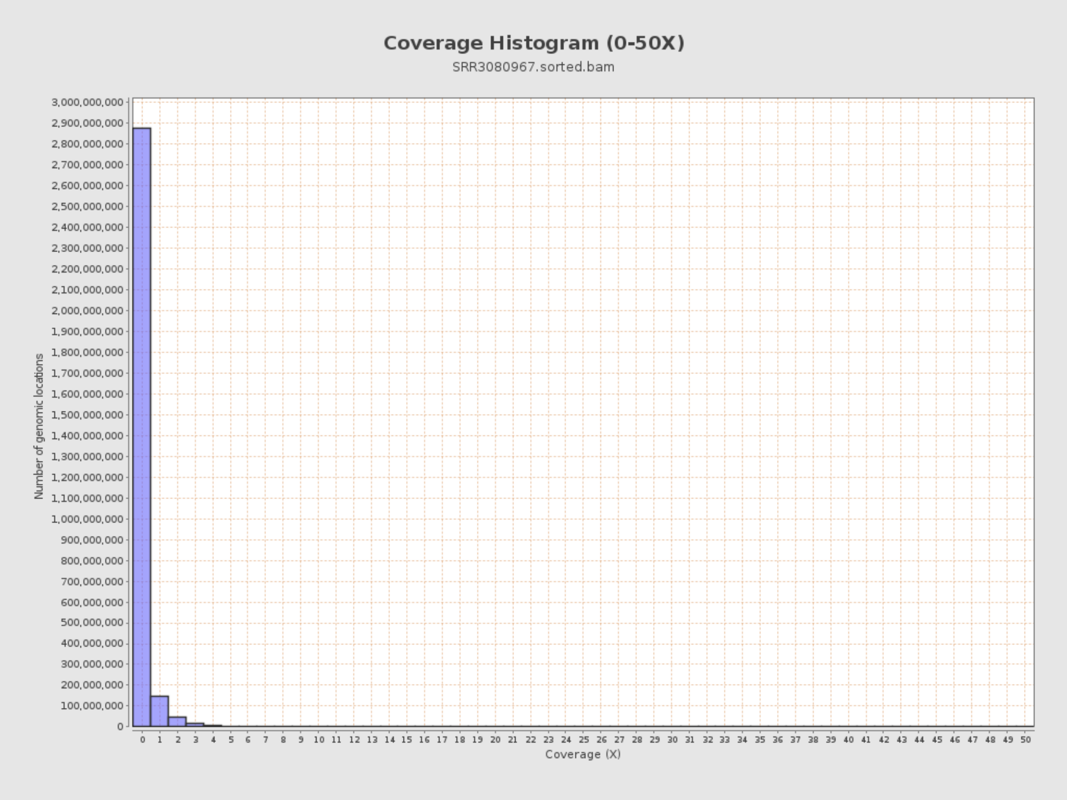
3. Results : Coverage across reference



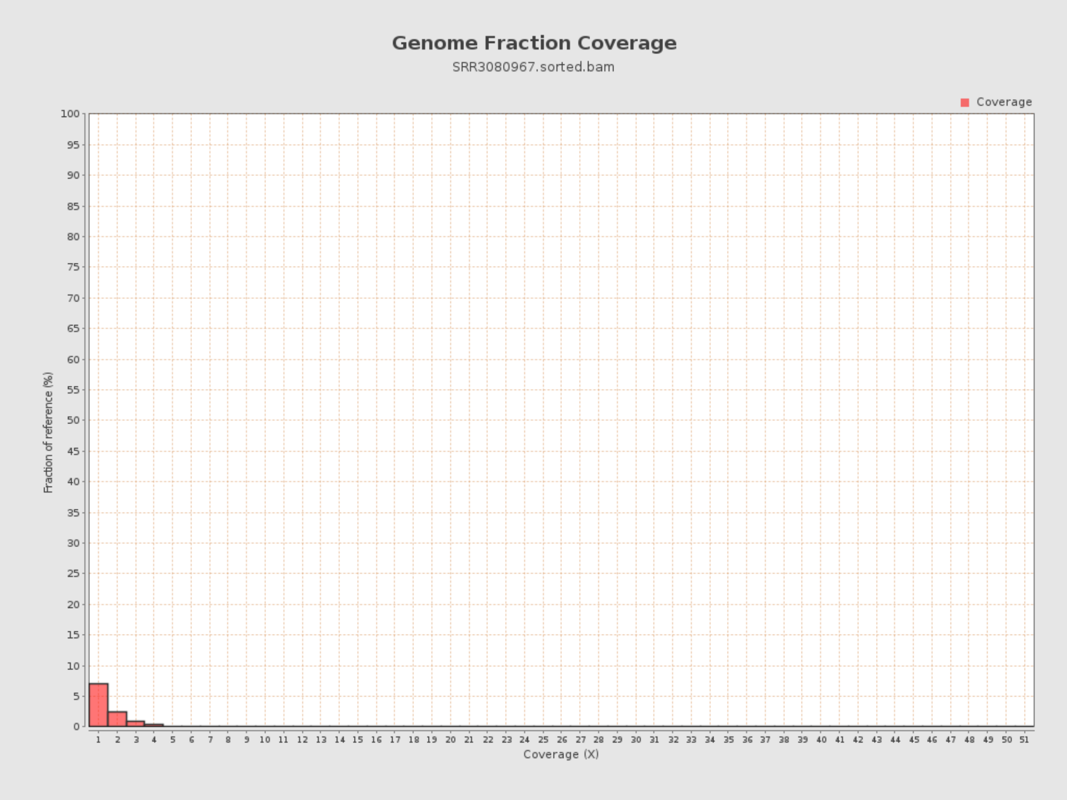
4. Results : Coverage Histogram



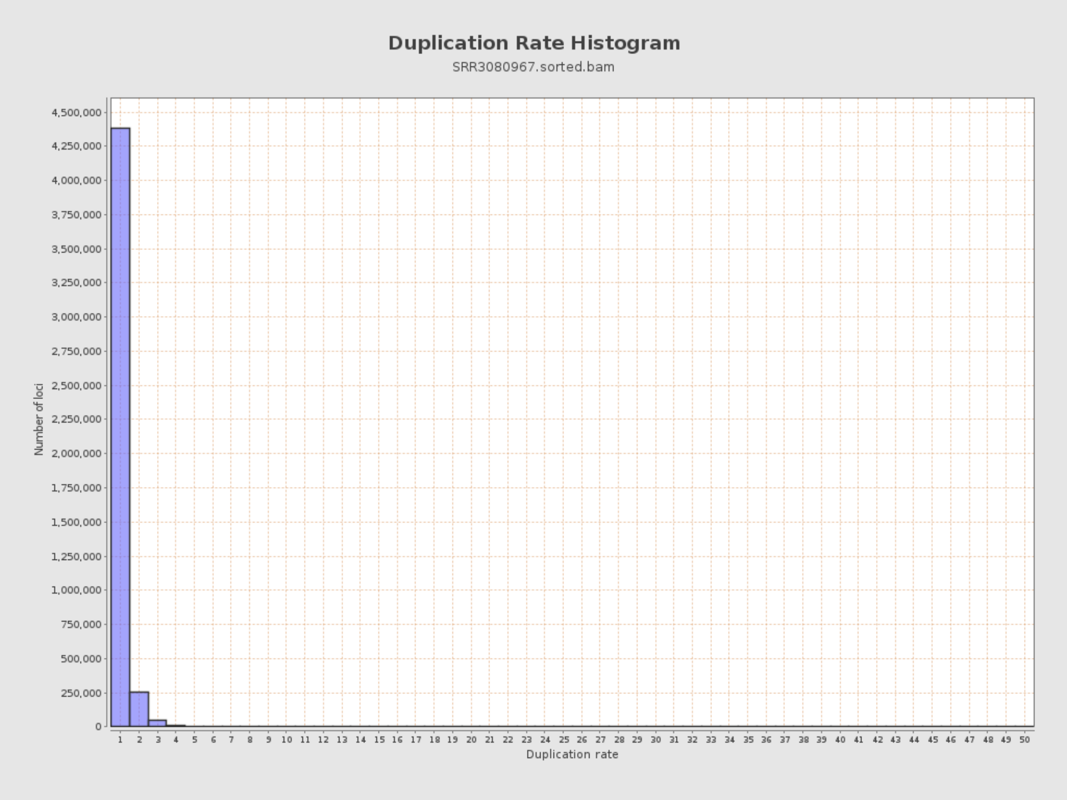
5. Results : Coverage Histogram (0-50X)



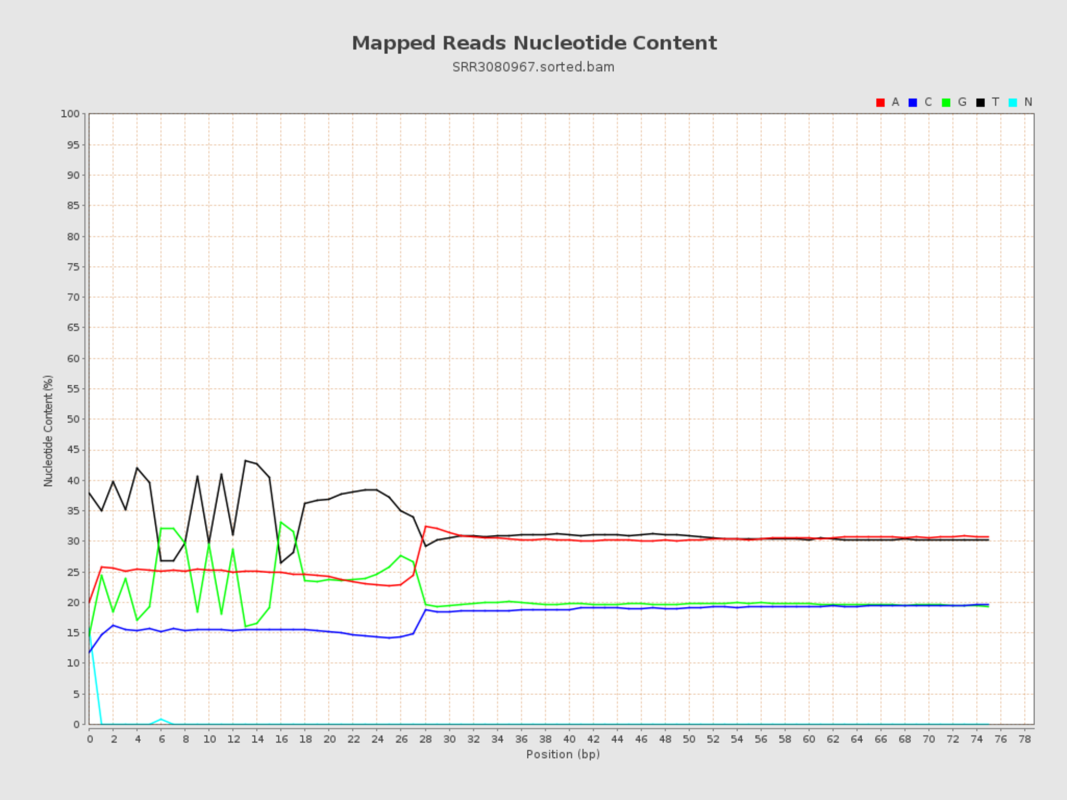
6. Results : Genome Fraction Coverage



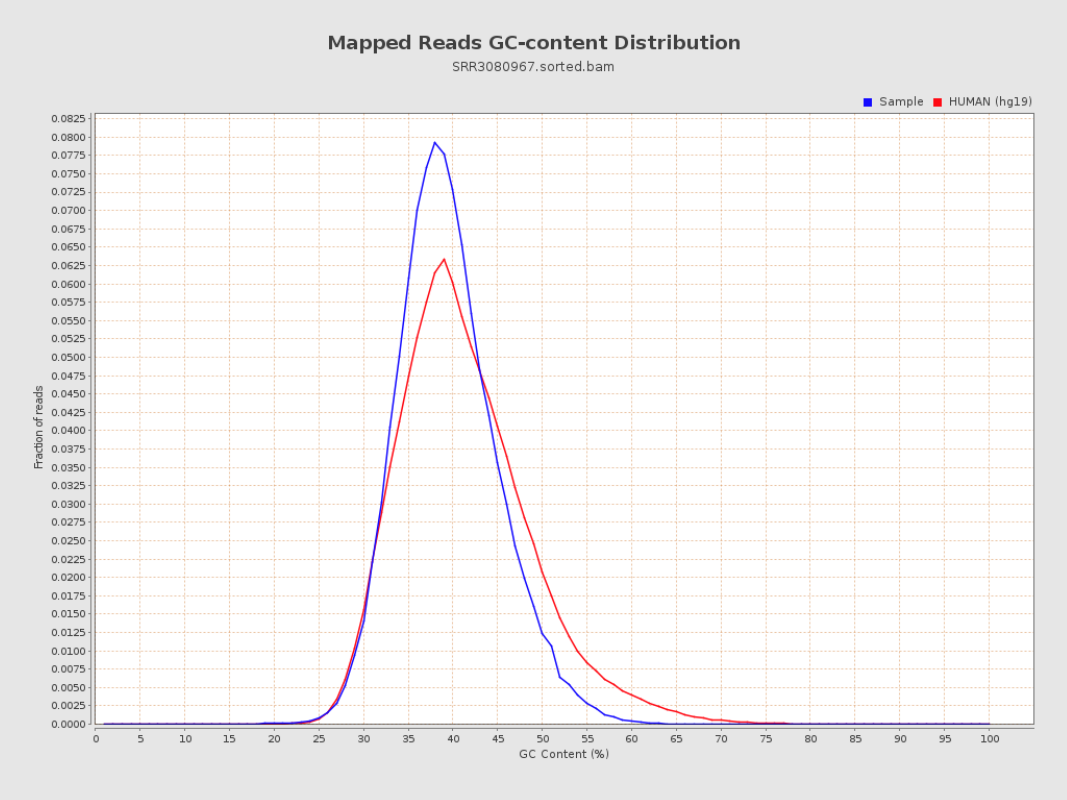
7. Results : Duplication Rate Histogram



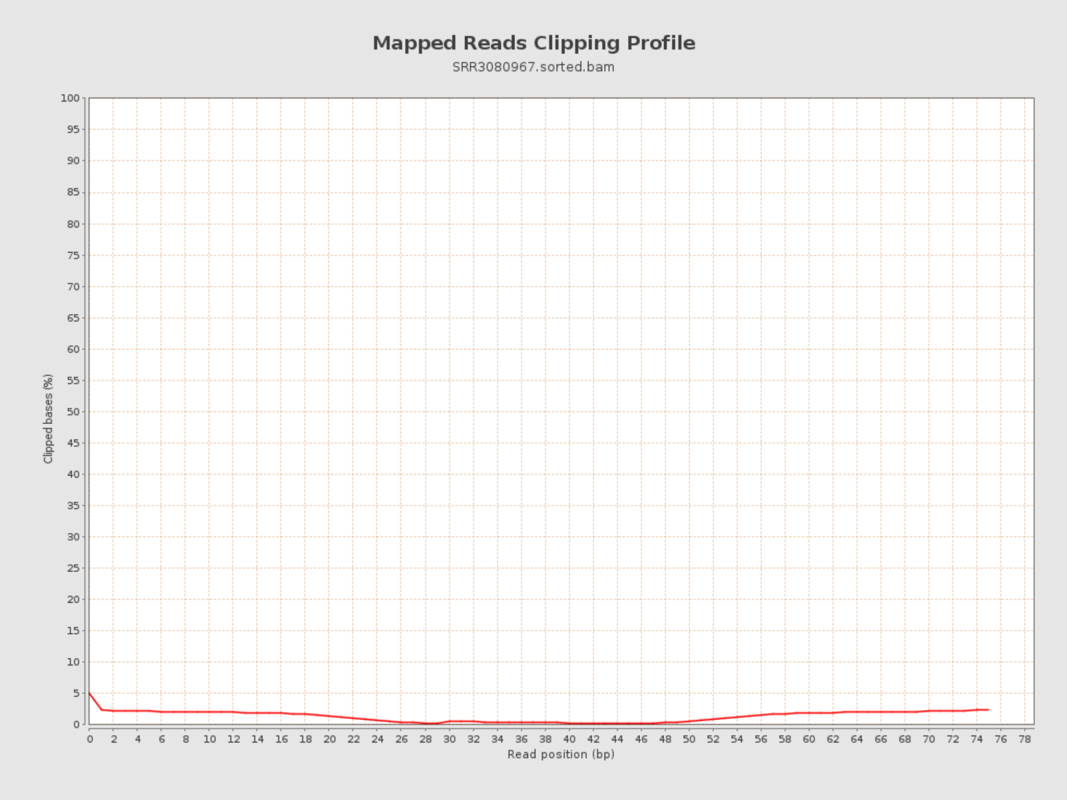
8. Results : Mapped Reads Nucleotide Content



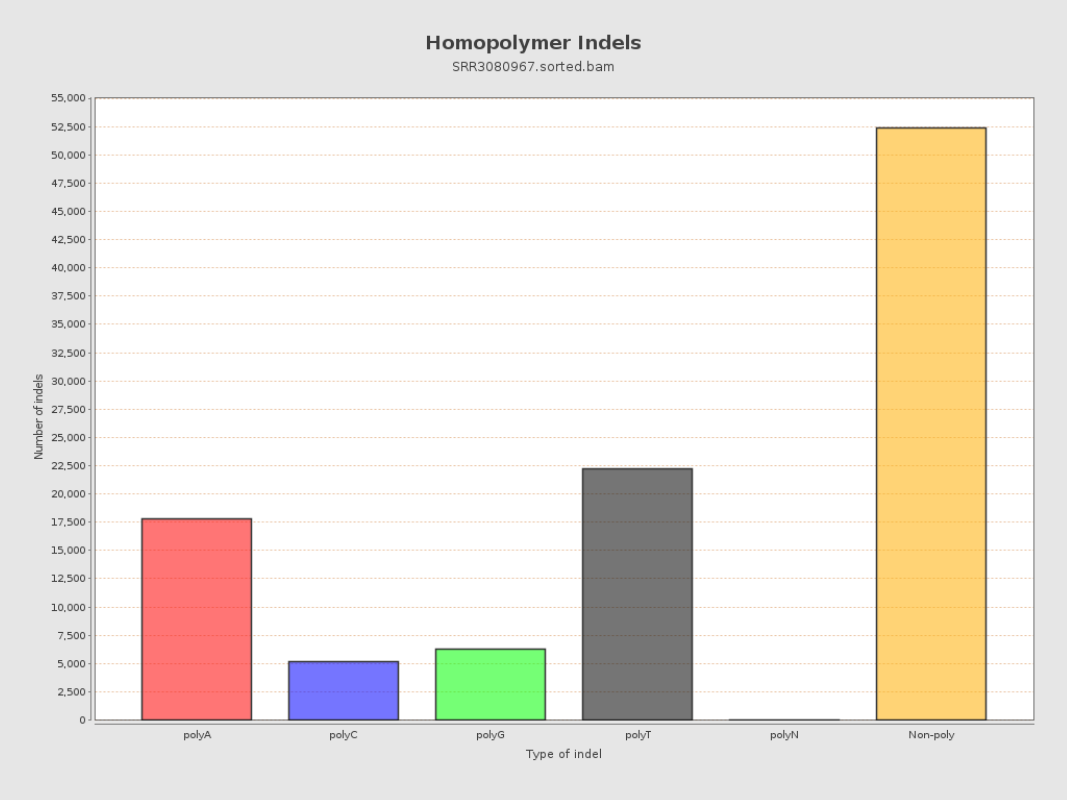
9. Results : Mapped Reads GC-content Distribution



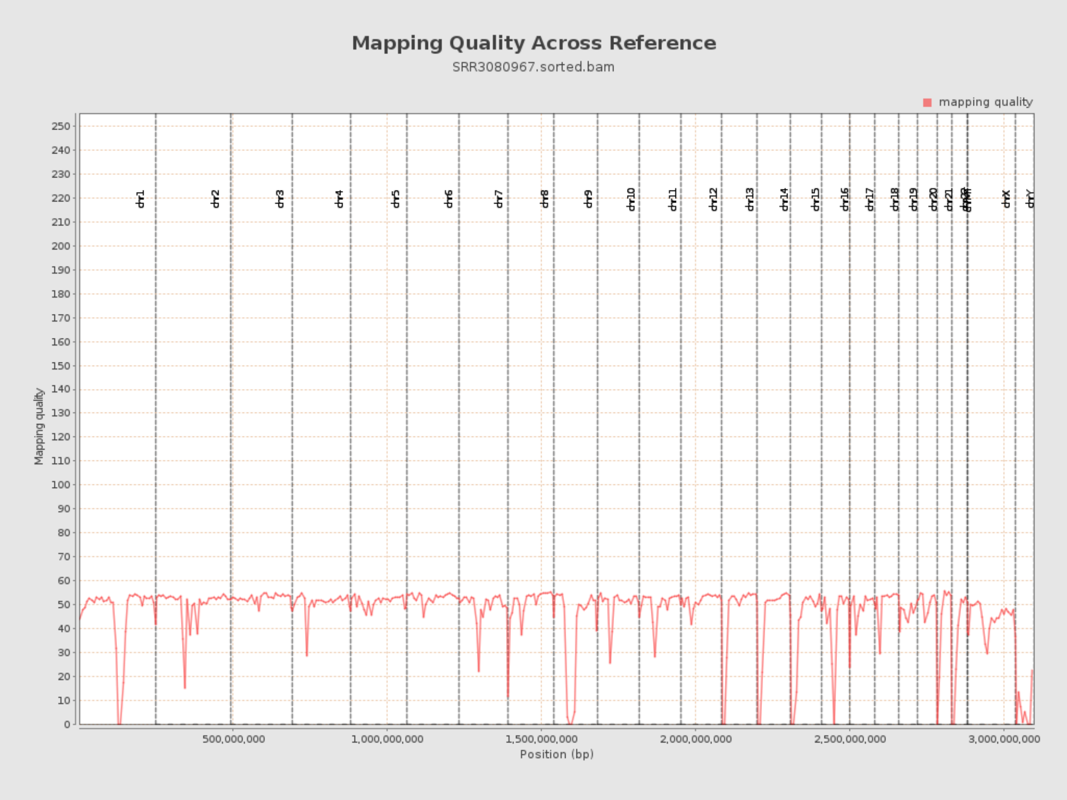
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram