Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 10:08:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081921.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_SRR3081921 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081921.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 10:08:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081921.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,673,672
Mapped reads	2,477,594 / 92.67%
Unmapped reads	196,078 / 7.33%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,225 / 0.61%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	115,071 / 4.3%
Duplication rate	3.74%
Clipped reads	899,202 / 33.63%

2.2. ACGT Content

Number/percentage of A's	48,349,671 / 28.51%
Number/percentage of C's	31,293,375 / 18.45%
Number/percentage of T's	53,890,640 / 31.78%
Number/percentage of G's	36,039,423 / 21.25%
Number/percentage of N's	22,212 / 0.01%
GC Percentage	39.7%

2.3. Coverage

Mean	0.0548

Standard Deviation	0.4533

2.4. Mapping Quality

Mean Mapping Quality	47.06

2.5. Mismatches and indels

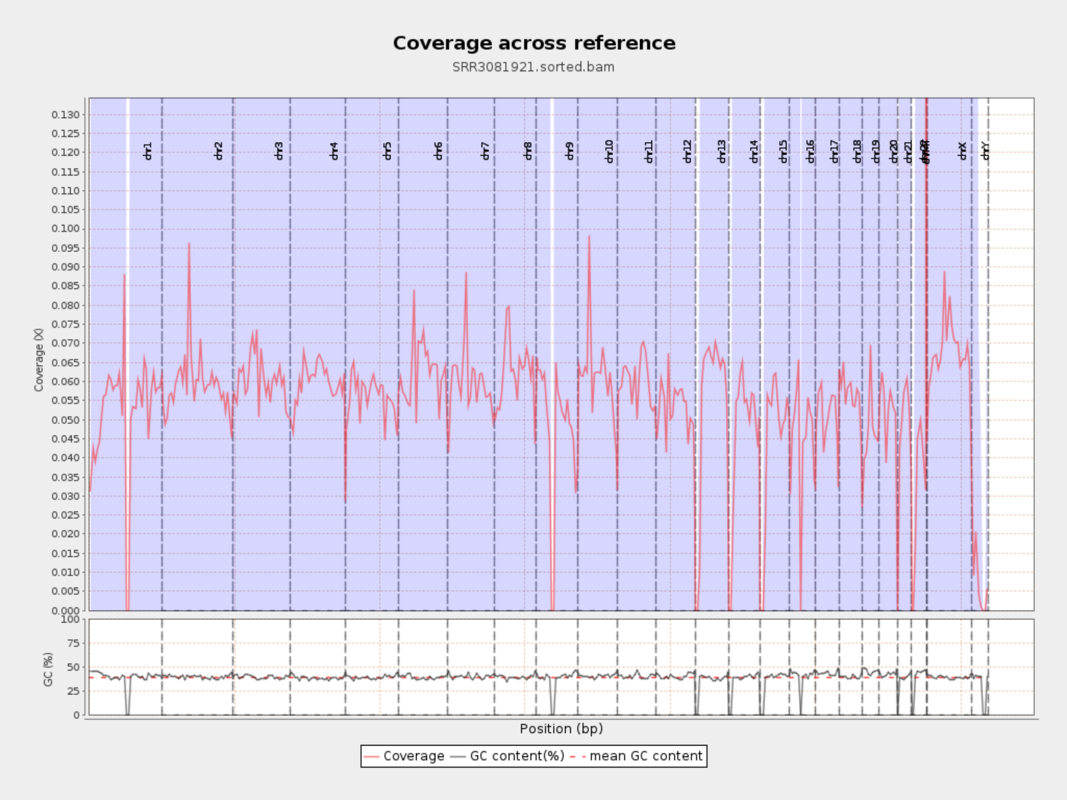
General error rate	0.75%
Mismatches	1,250,484
Insertions	12,150
Mapped reads with at least one insertion	0.49%
Deletions	34,680
Mapped reads with at least one deletion	1.39%
Homopolymer indels	48.33%

2.6. Chromosome stats

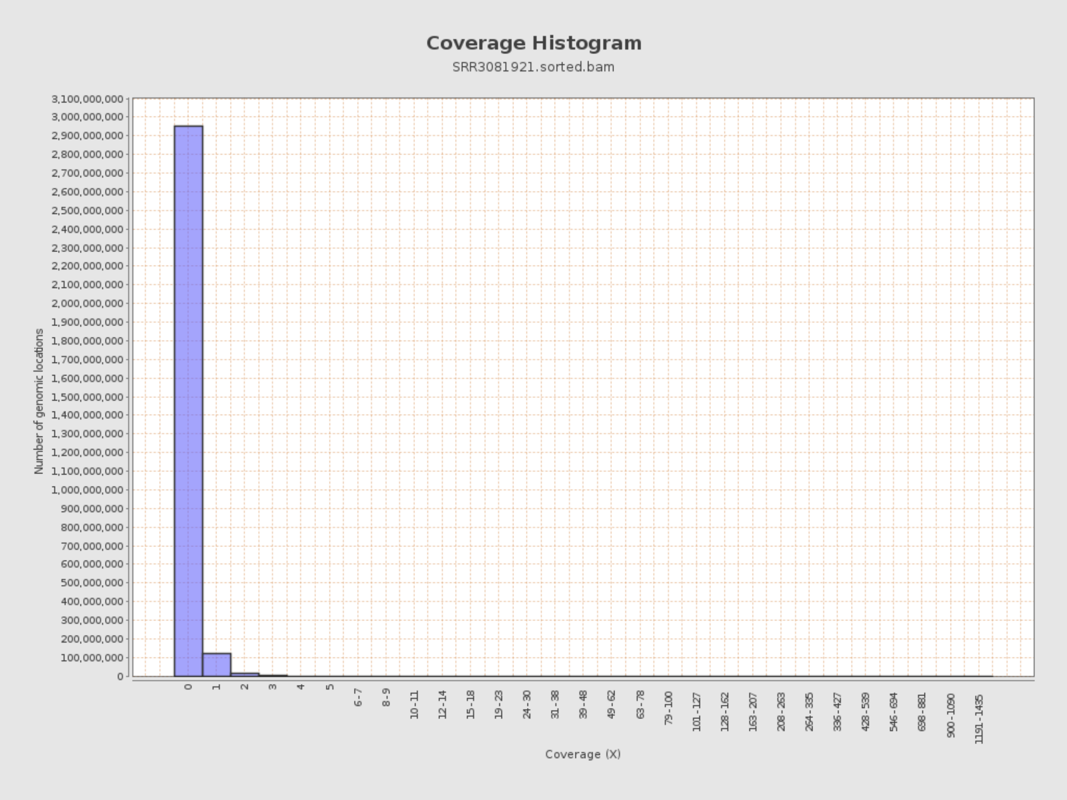
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12932407	0.0519	0.7756
chr2	243199373	14463295	0.0595	0.4516
chr3	198022430	11976928	0.0605	0.2842
chr4	191154276	11418930	0.0597	0.2931
chr5	180915260	10140812	0.0561	0.2723
chr6	171115067	10692872	0.0625	0.3381
chr7	159138663	9590168	0.0603	0.5777

chr8	146364022	9084435	0.0621	0.9165
chr9	141213431	6708857	0.0475	0.3691
chr10	135534747	8420435	0.0621	0.4722
chr11	135006516	8076112	0.0598	0.3577
chr12	133851895	7088750	0.053	0.2659
chr13	115169878	6192490	0.0538	0.266
chr14	107349540	4902638	0.0457	0.2554
chr15	102531392	4481058	0.0437	0.2406
chr16	90354753	4067002	0.045	0.2806
chr17	81195210	4107955	0.0506	0.2866
chr18	78077248	4446494	0.0569	0.6856
chr19	59128983	2784191	0.0471	0.5597
chr20	63025520	3302571	0.0524	0.2691
chr21	48129895	2223836	0.0462	0.2659
chr22	51304566	1535893	0.0299	0.1958
chrMT	16571	77910	4.7016	3.6997
chrX	155270560	10518410	0.0677	0.327
chrY	59373566	422675	0.0071	0.1523

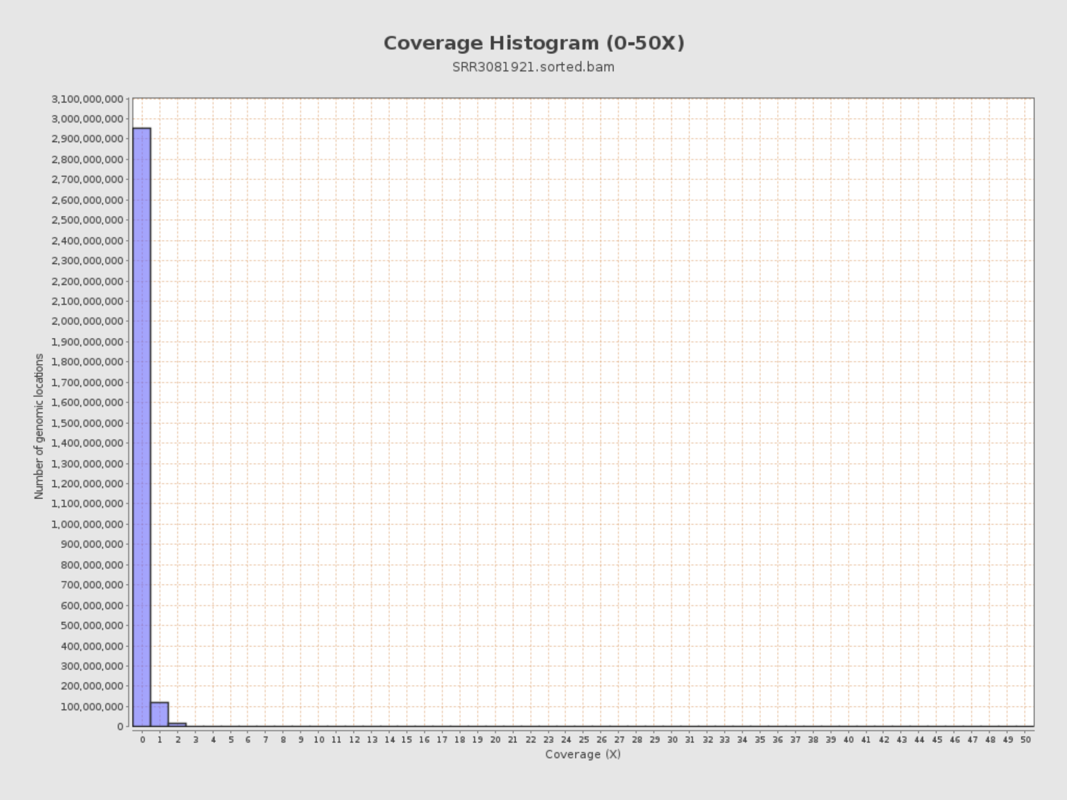
3. Results : Coverage across reference



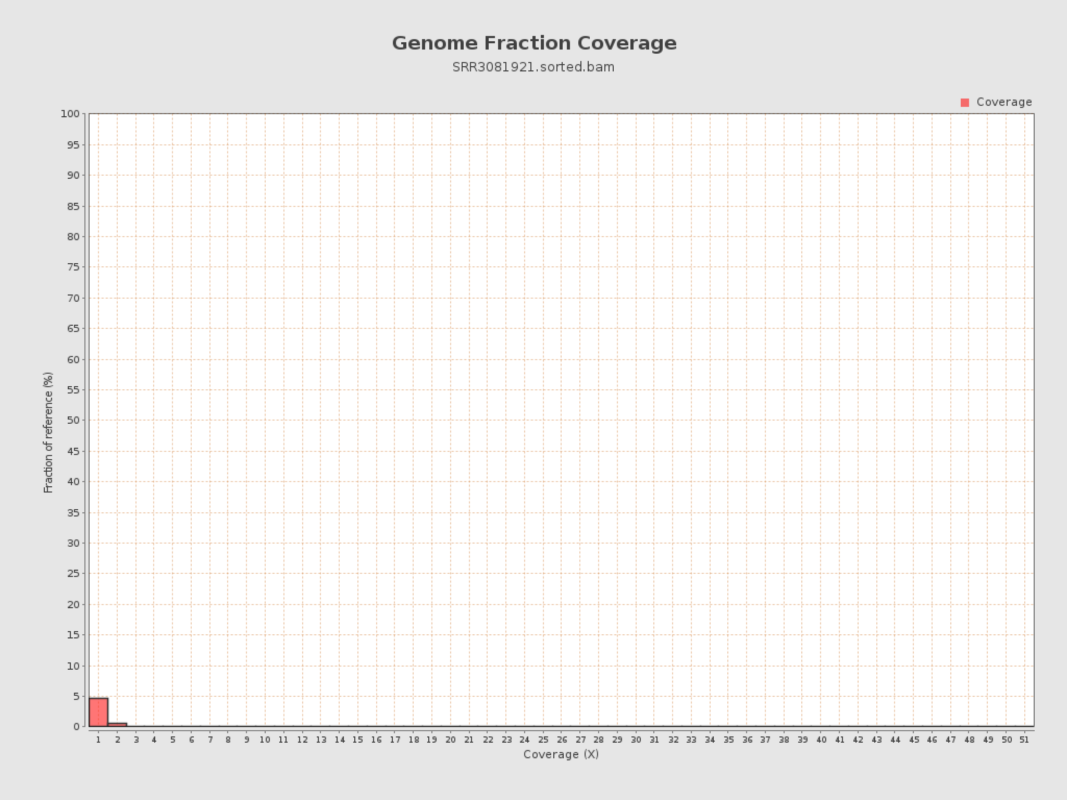
4. Results : Coverage Histogram



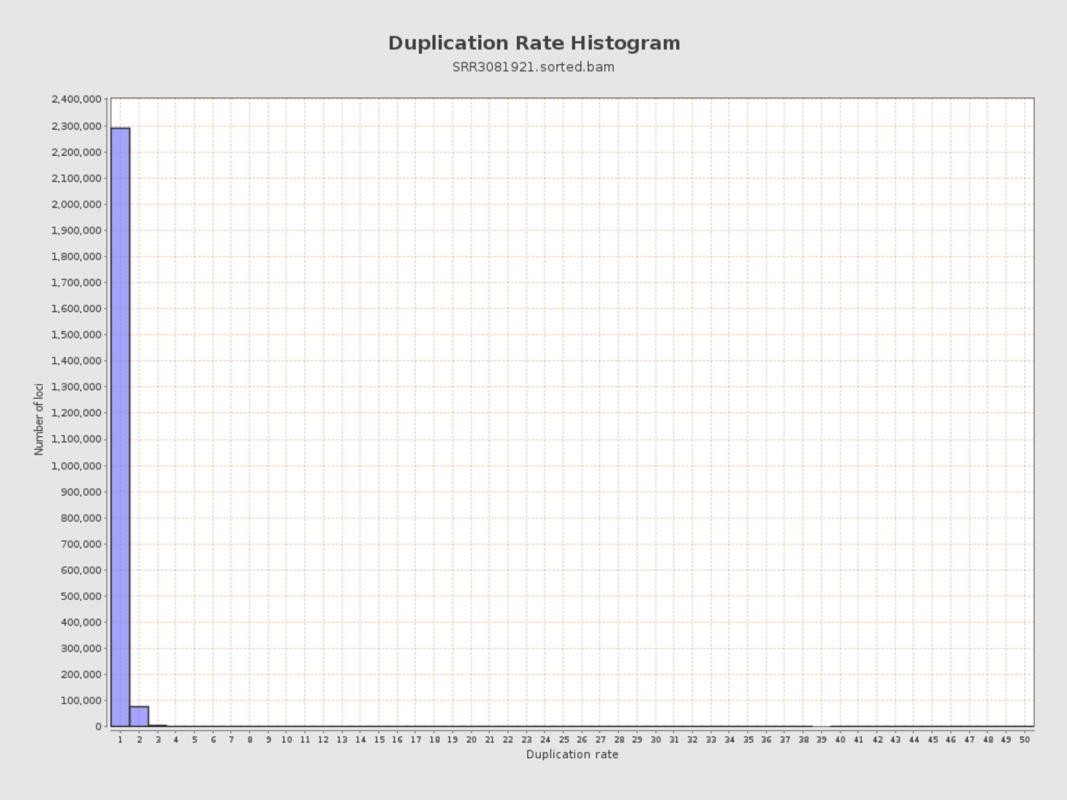
5. Results : Coverage Histogram (0-50X)



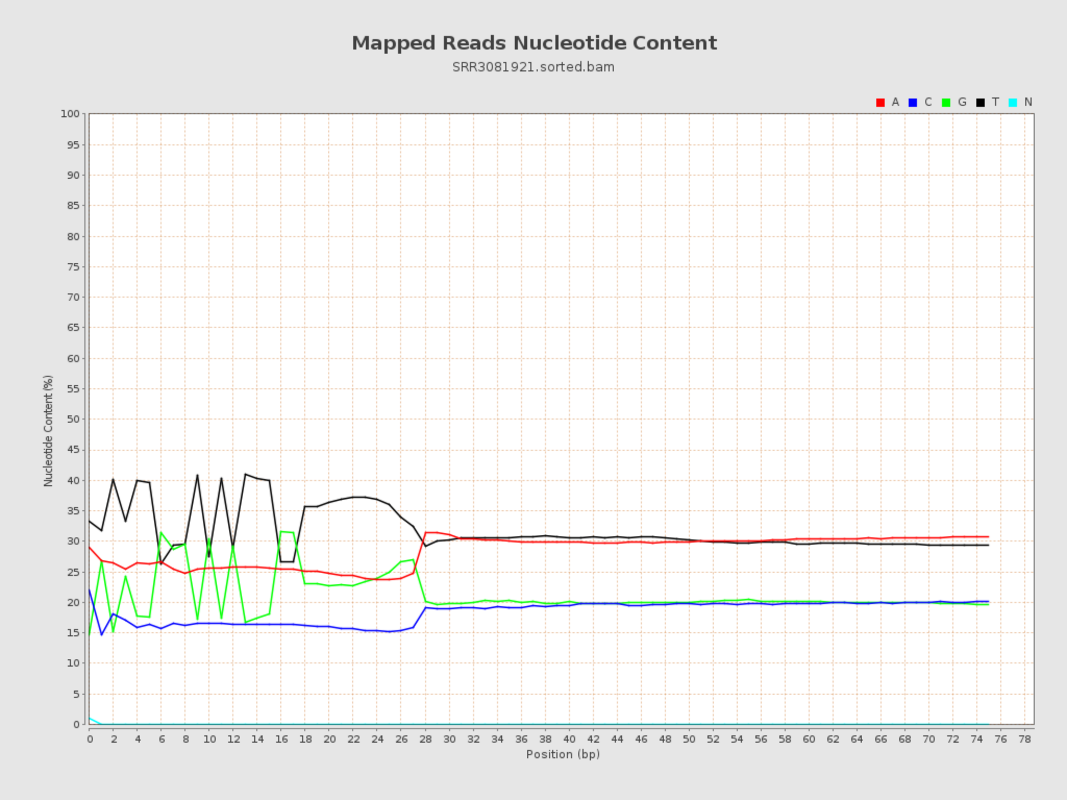
6. Results : Genome Fraction Coverage



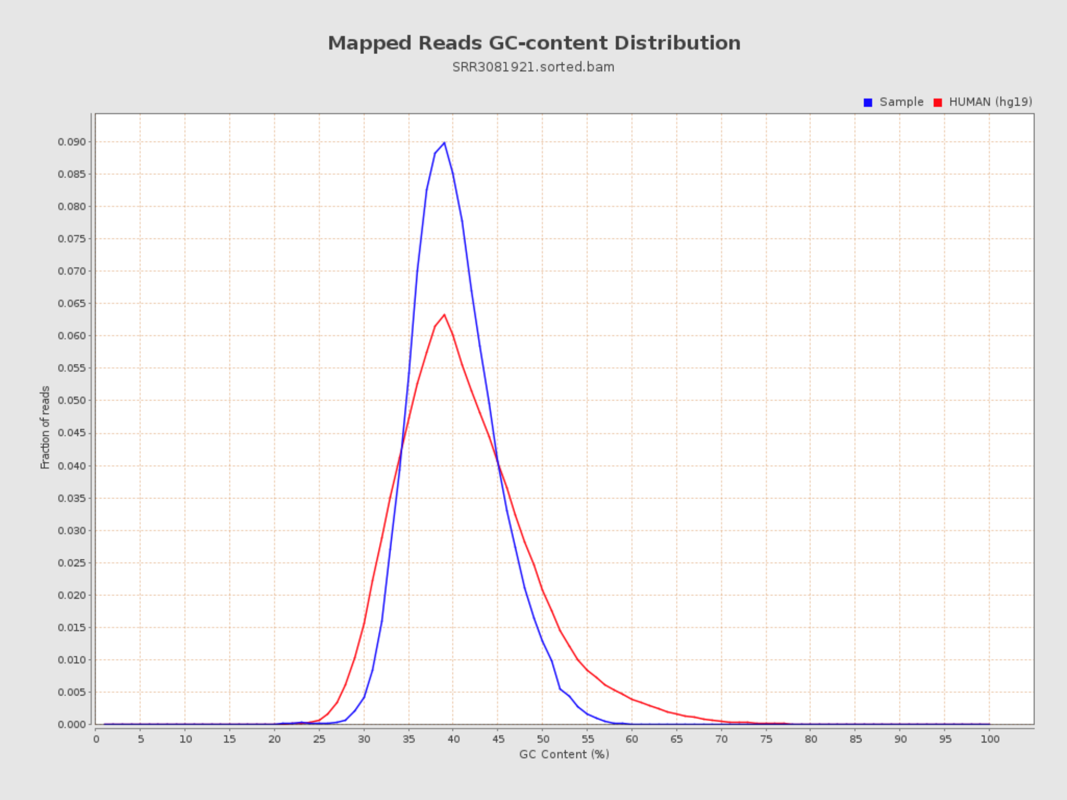
7. Results : Duplication Rate Histogram



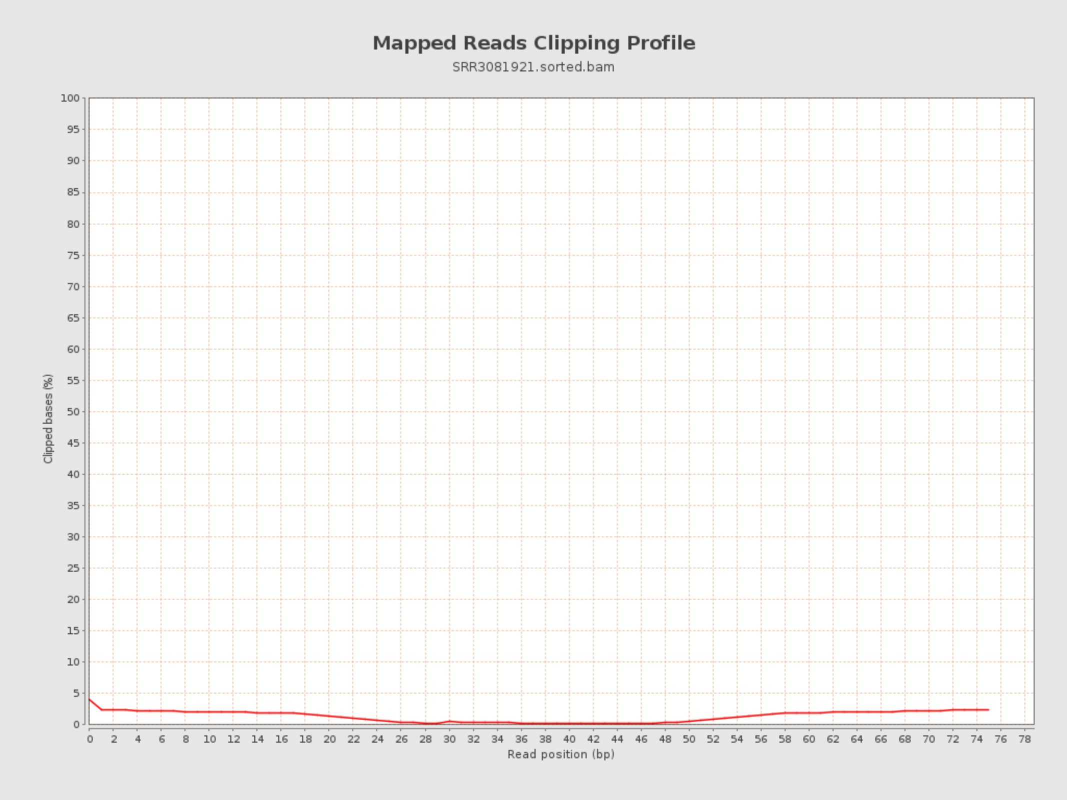
8. Results : Mapped Reads Nucleotide Content



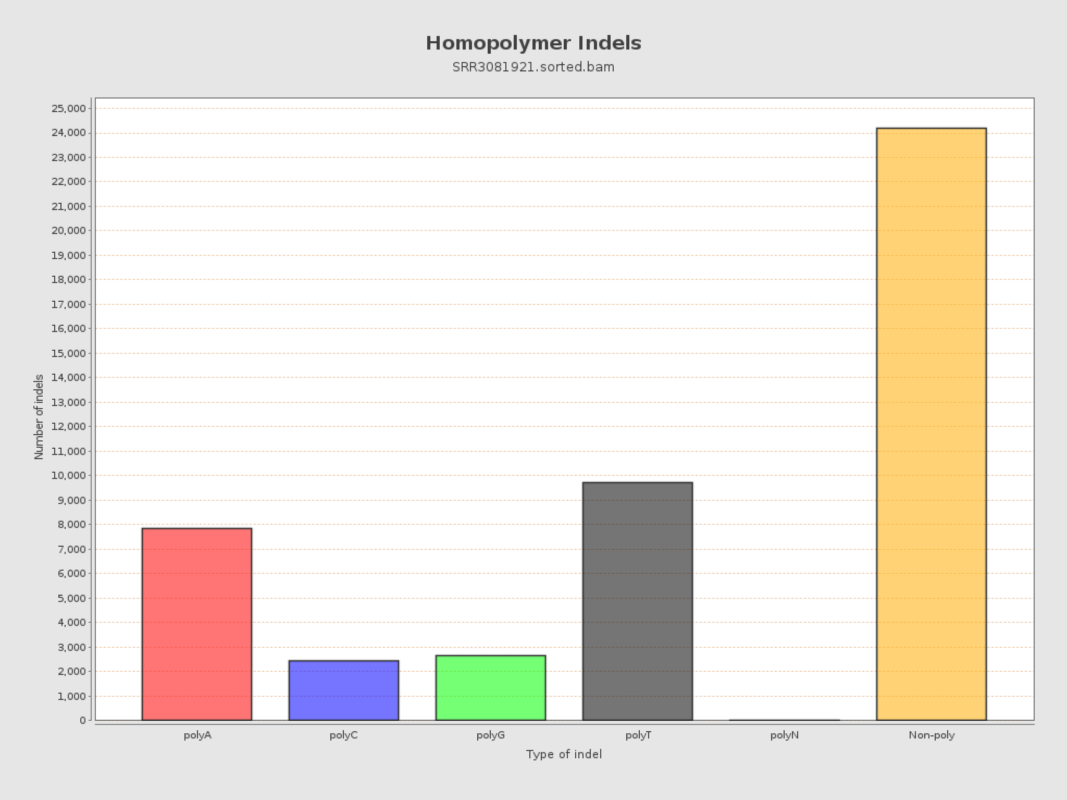
9. Results : Mapped Reads GC-content Distribution



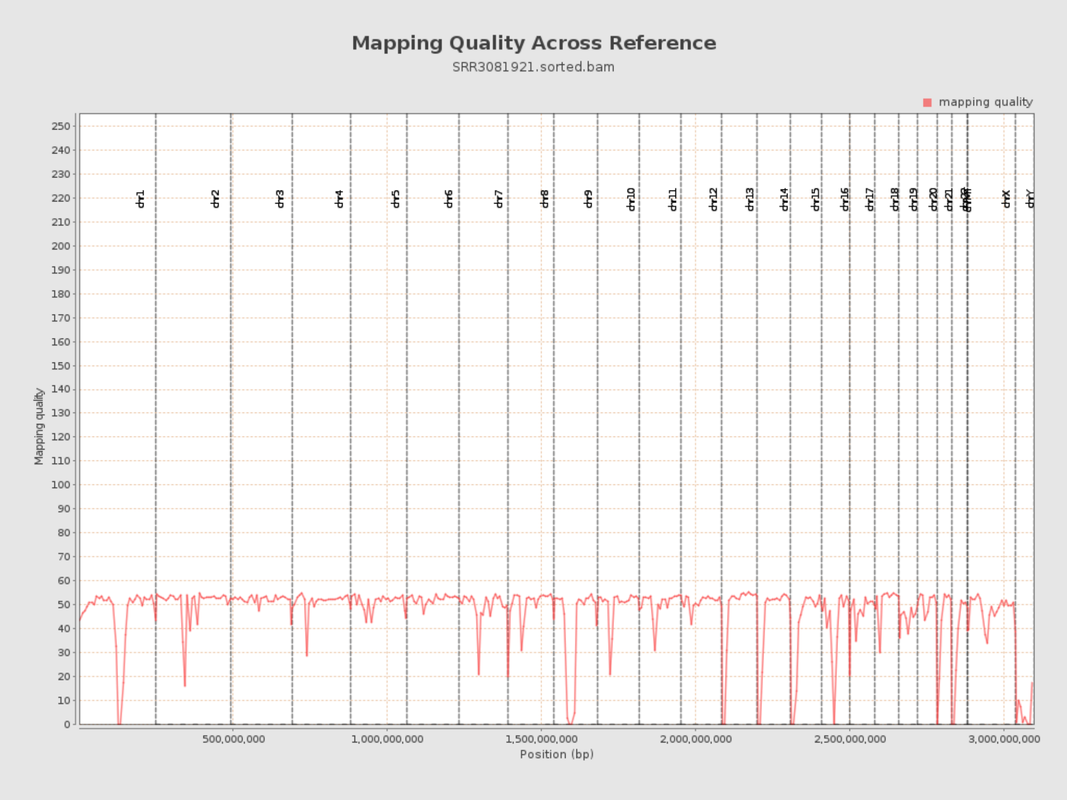
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram