Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 05:56:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081257.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_SRR3081257 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081257.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 05:56:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081257.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,022,475
Mapped reads	2,565,086 / 84.87%
Unmapped reads	457,389 / 15.13%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,767 / 0.65%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	106,486 / 3.52%
Duplication rate	3.22%
Clipped reads	1,091,008 / 36.1%

2.2. ACGT Content

Number/percentage of A's	47,329,697 / 27.51%
Number/percentage of C's	31,116,072 / 18.09%
Number/percentage of T's	55,353,128 / 32.18%
Number/percentage of G's	38,176,802 / 22.19%
Number/percentage of N's	42,982 / 0.02%
GC Percentage	40.28%

2.3. Coverage

Mean	0.0556

Standard Deviation	0.4816

2.4. Mapping Quality

Mean Mapping Quality	46.48

2.5. Mismatches and indels

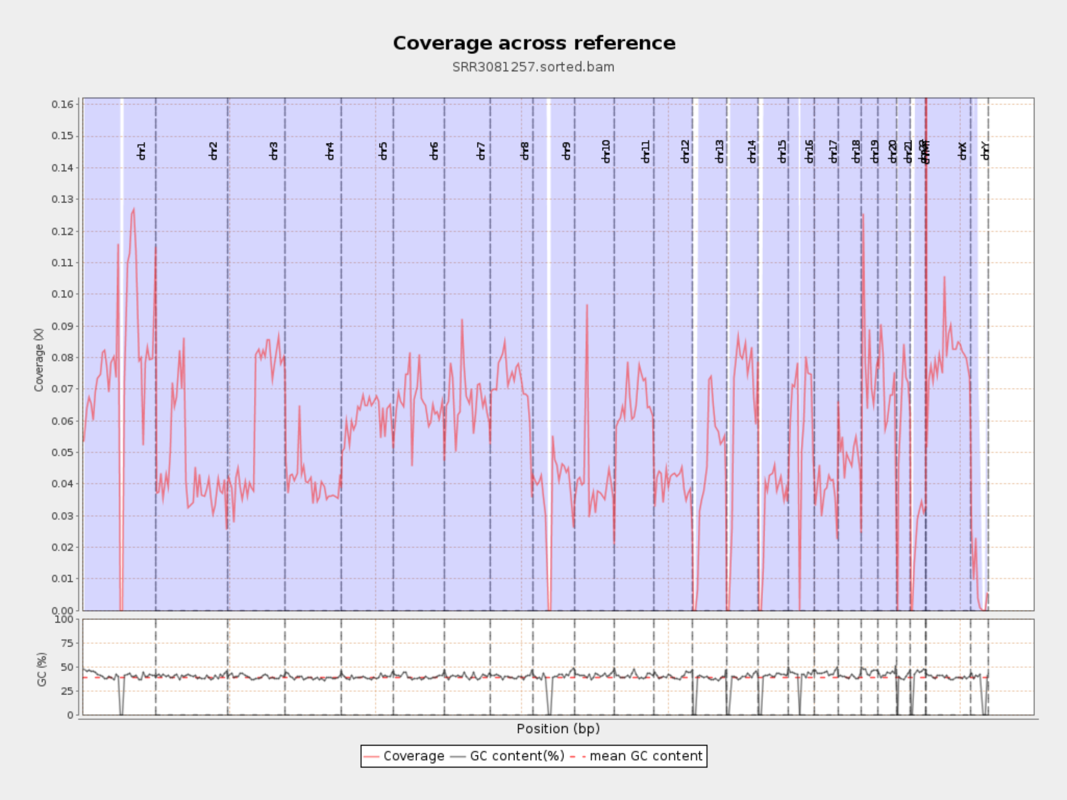
General error rate	0.87%
Mismatches	1,477,743
Insertions	14,184
Mapped reads with at least one insertion	0.55%
Deletions	45,430
Mapped reads with at least one deletion	1.75%
Homopolymer indels	49.77%

2.6. Chromosome stats

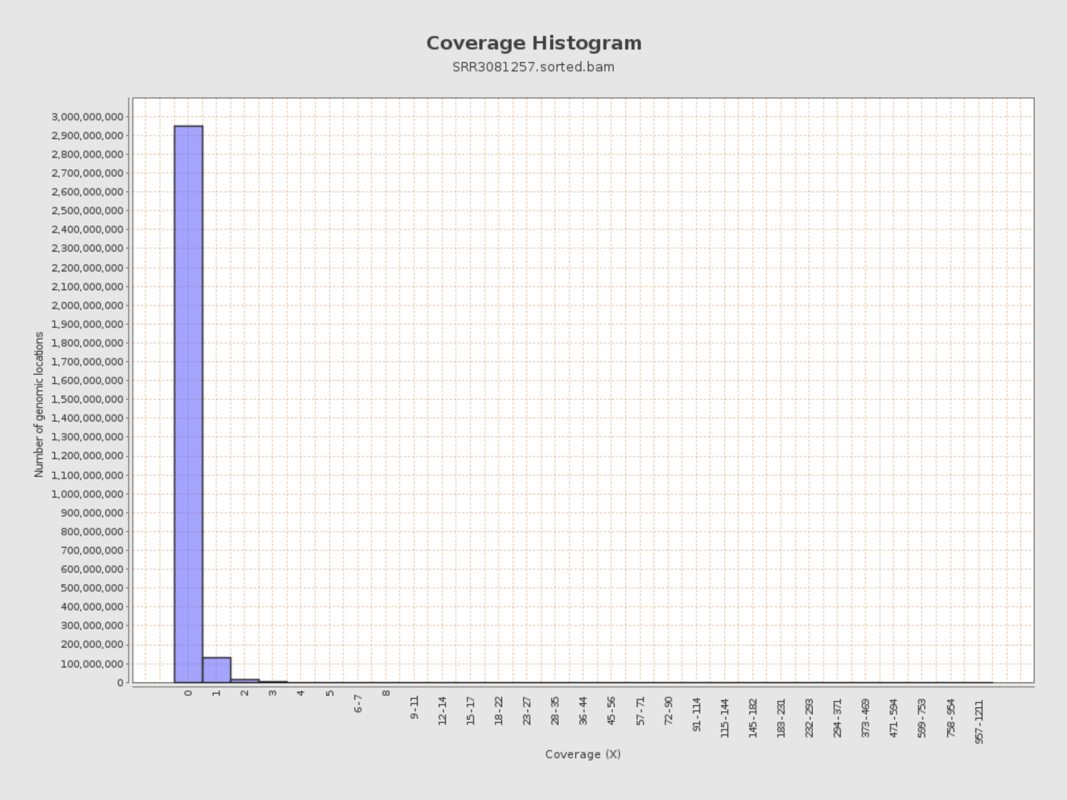
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	19394441	0.0778	1.0745
chr2	243199373	10932661	0.045	0.4194
chr3	198022430	12004923	0.0606	0.2877
chr4	191154276	7736405	0.0405	0.2478
chr5	180915260	11021927	0.0609	0.2792
chr6	171115067	11263725	0.0658	0.3572
chr7	159138663	10615555	0.0667	0.5261

chr8	146364022	10454552	0.0714	0.6574
chr9	141213431	5235843	0.0371	0.3507
chr10	135534747	5567147	0.0411	0.5188
chr11	135006516	8809528	0.0653	0.4663
chr12	133851895	5394126	0.0403	0.2308
chr13	115169878	5078174	0.0441	0.2344
chr14	107349540	6836207	0.0637	0.2997
chr15	102531392	3330603	0.0325	0.2019
chr16	90354753	5381513	0.0596	0.2978
chr17	81195210	3073657	0.0379	0.276
chr18	78077248	3902305	0.05	0.5858
chr19	59128983	4638701	0.0785	0.7271
chr20	63025520	4452096	0.0706	0.3064
chr21	48129895	2922857	0.0607	0.2986
chr22	51304566	1160175	0.0226	0.1659
chrMT	16571	13272	0.8009	0.9693
chrX	155270560	12407269	0.0799	0.3544
chrY	59373566	467333	0.0079	0.1554

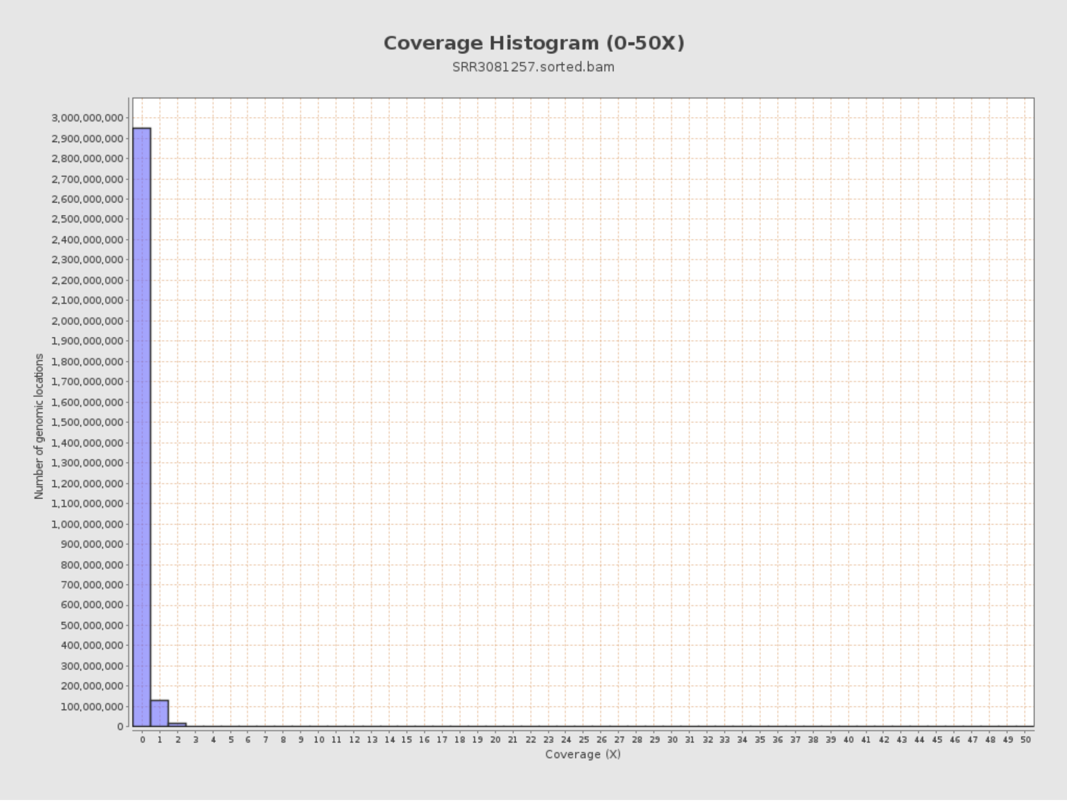
3. Results : Coverage across reference



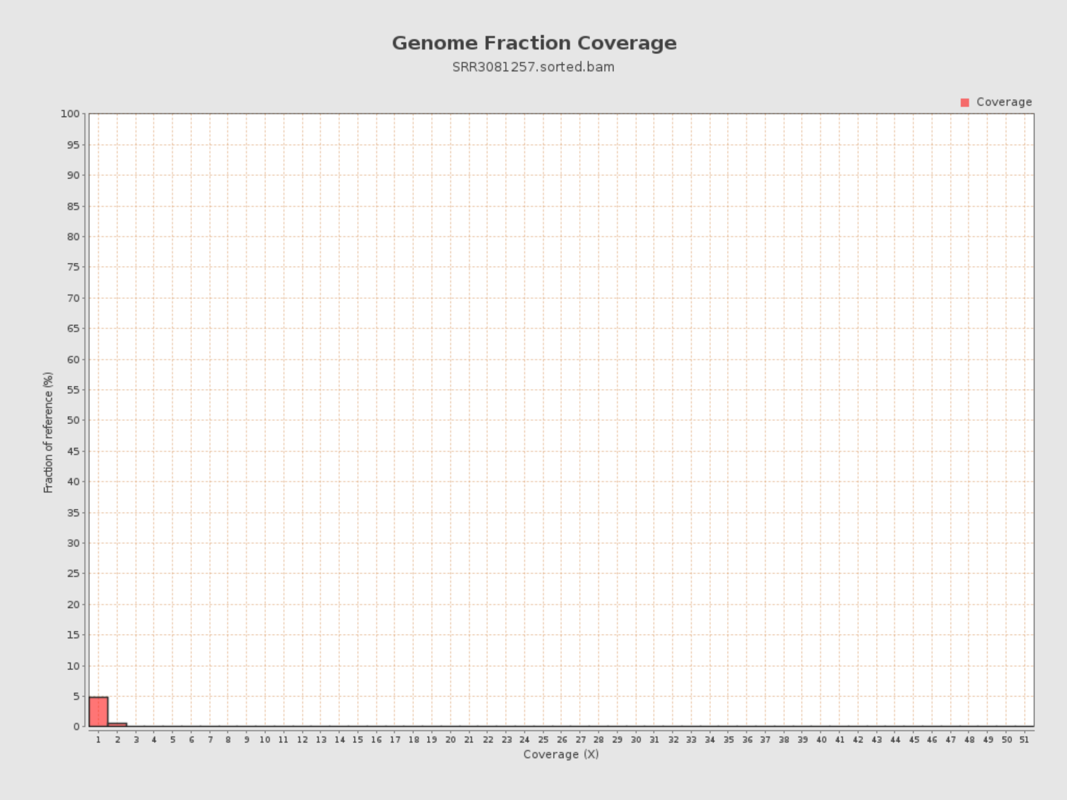
4. Results : Coverage Histogram



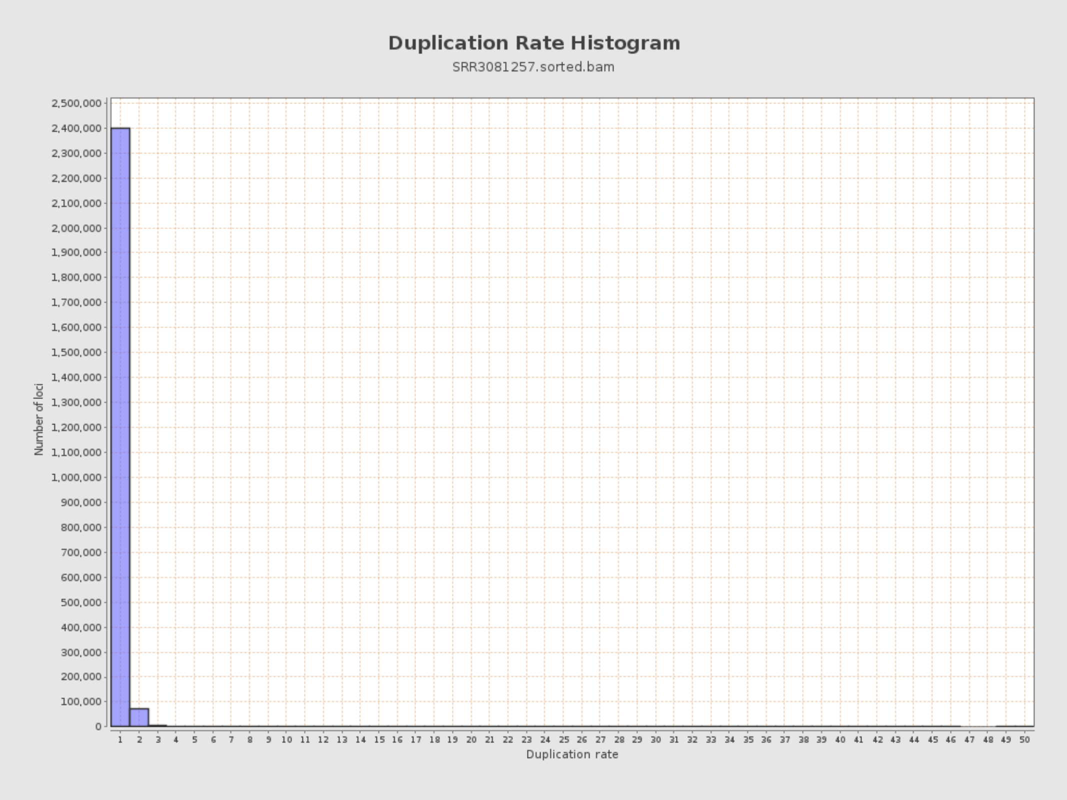
5. Results : Coverage Histogram (0-50X)



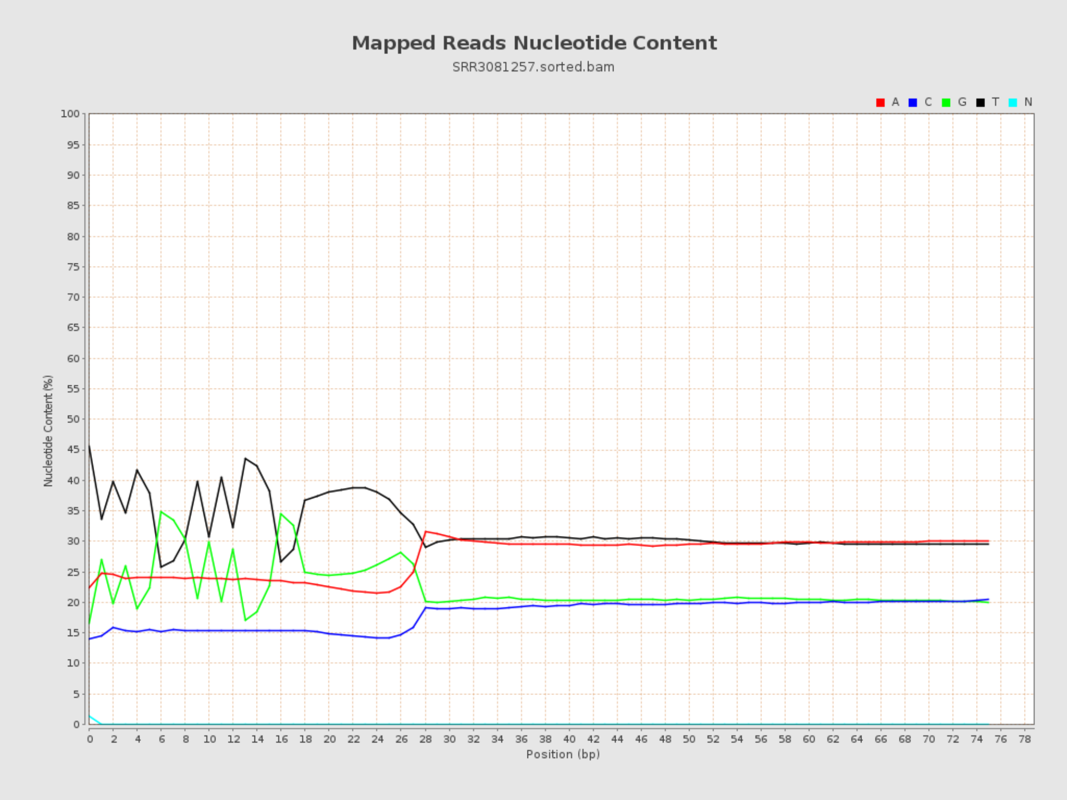
6. Results : Genome Fraction Coverage



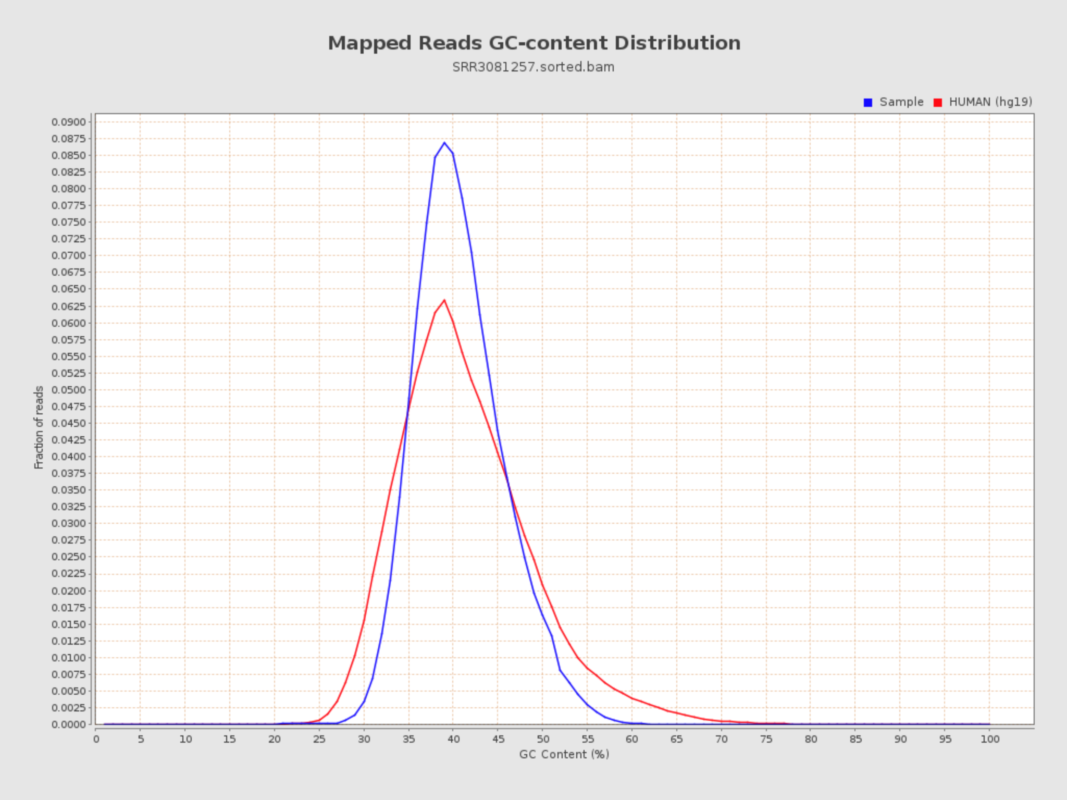
7. Results : Duplication Rate Histogram



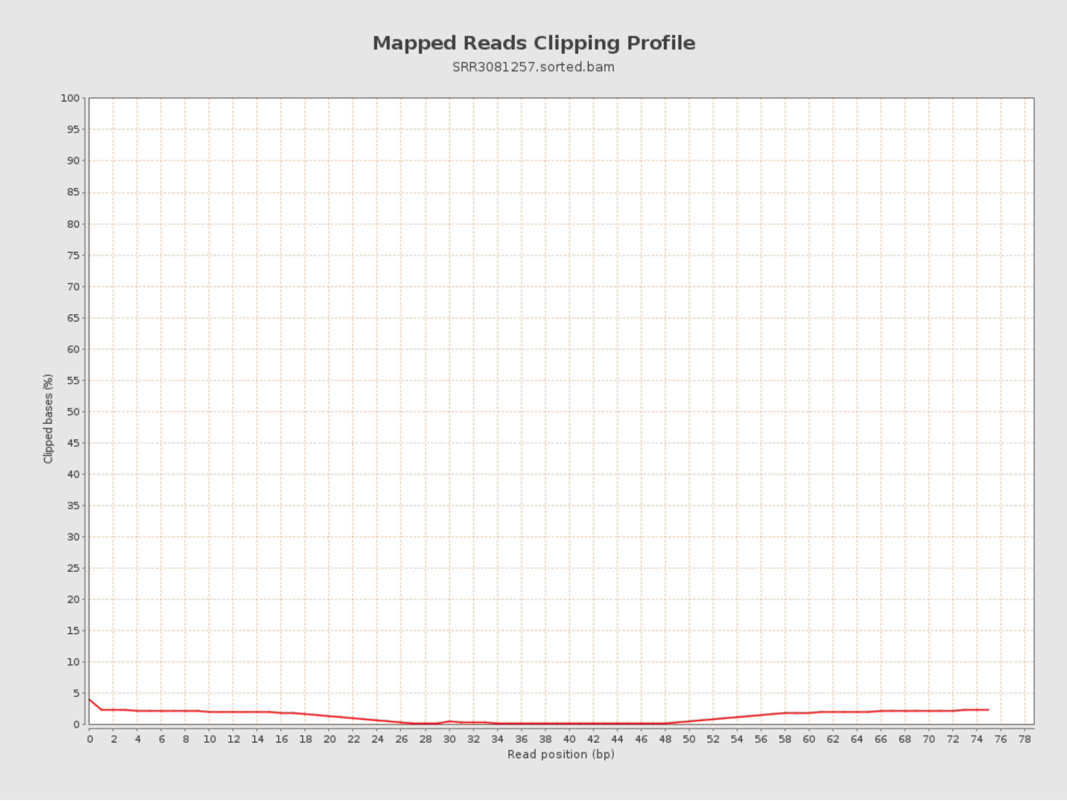
8. Results : Mapped Reads Nucleotide Content



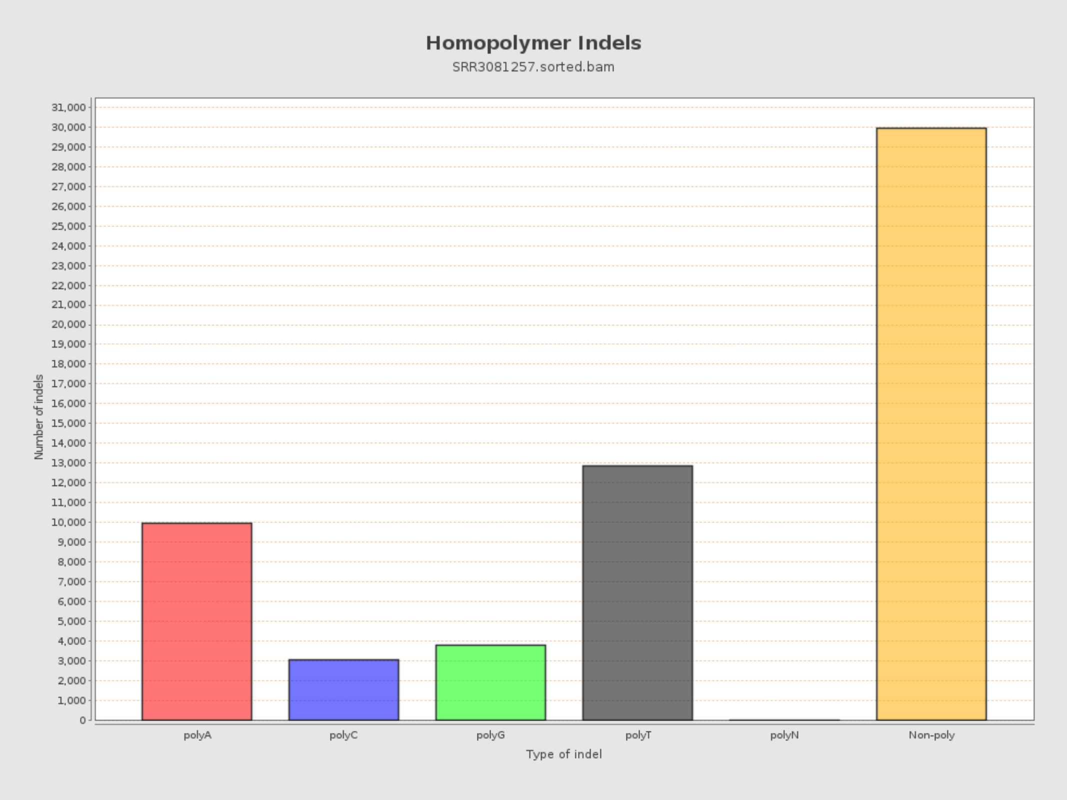
9. Results : Mapped Reads GC-content Distribution



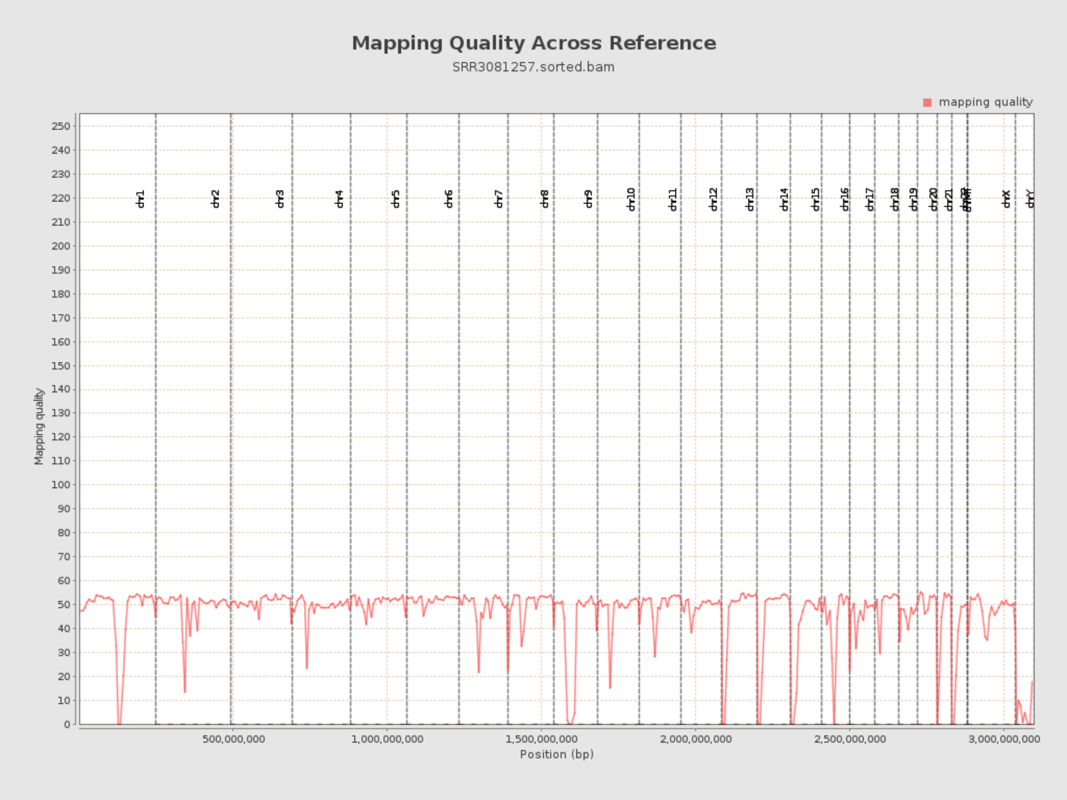
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram