Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 03:40:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081228.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_SRR3081228 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081228.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 03:40:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081228.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,086,921
Mapped reads	1,833,343 / 87.85%
Unmapped reads	253,578 / 12.15%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	22,717 / 1.09%
Read min/max/mean length	30 / 76 / 76.38
Duplicated reads (estimated)	79,853 / 3.83%
Duplication rate	3.65%
Clipped reads	969,940 / 46.48%

2.2. ACGT Content

Number/percentage of A's	33,987,736 / 28.48%
Number/percentage of C's	22,993,981 / 19.26%
Number/percentage of T's	36,617,356 / 30.68%
Number/percentage of G's	25,742,449 / 21.57%
Number/percentage of N's	15,092 / 0.01%
GC Percentage	40.83%

2.3. Coverage

Mean	0.0386

Standard Deviation	0.2967

2.4. Mapping Quality

Mean Mapping Quality	45.22

2.5. Mismatches and indels

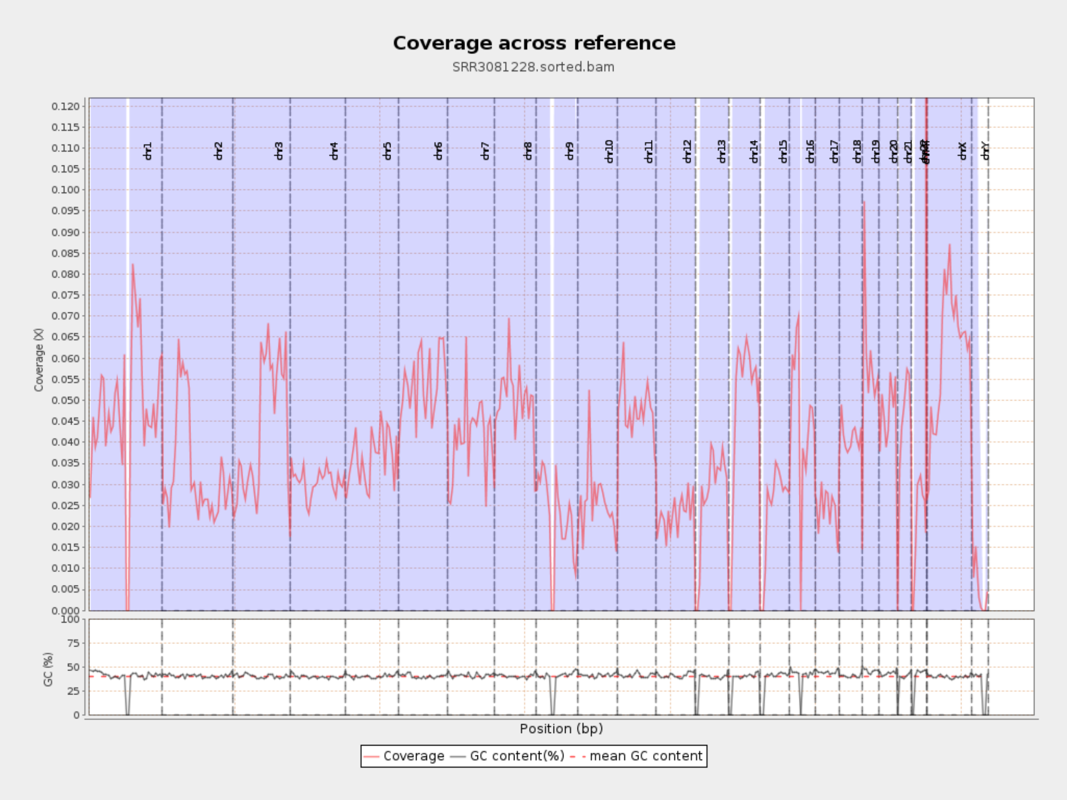
General error rate	0.88%
Mismatches	1,032,583
Insertions	8,969
Mapped reads with at least one insertion	0.49%
Deletions	27,184
Mapped reads with at least one deletion	1.47%
Homopolymer indels	47.95%

2.6. Chromosome stats

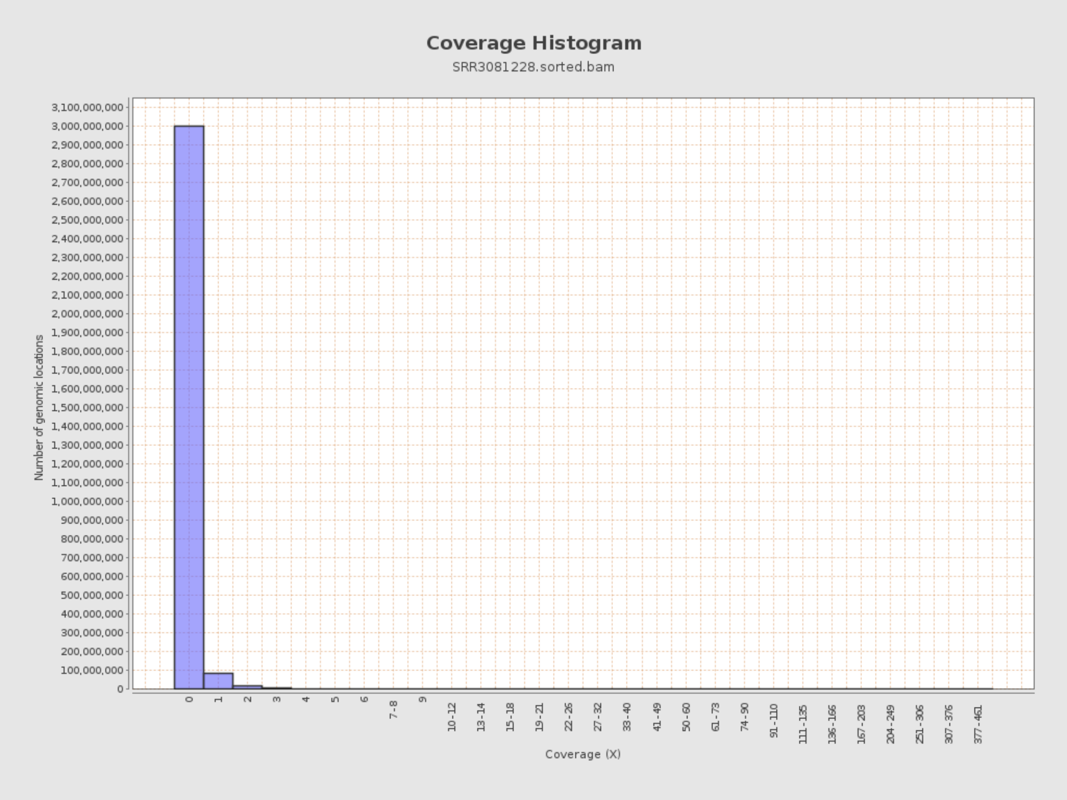
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11786034	0.0473	0.4521
chr2	243199373	8048198	0.0331	0.3079
chr3	198022430	8575458	0.0433	0.2481
chr4	191154276	5890581	0.0308	0.2118
chr5	180915260	6608620	0.0365	0.225
chr6	171115067	9172631	0.0536	0.3
chr7	159138663	6537736	0.0411	0.4329

chr8	146364022	7362115	0.0503	0.3609
chr9	141213431	3094065	0.0219	0.2175
chr10	135534747	3516504	0.0259	0.2878
chr11	135006516	6396697	0.0474	0.3157
chr12	133851895	3039179	0.0227	0.1814
chr13	115169878	3105554	0.027	0.1935
chr14	107349540	5188535	0.0483	0.2638
chr15	102531392	2438057	0.0238	0.1861
chr16	90354753	4138784	0.0458	0.26
chr17	81195210	1921247	0.0237	0.1932
chr18	78077248	3222212	0.0413	0.3626
chr19	59128983	3506786	0.0593	0.3961
chr20	63025520	2937419	0.0466	0.2556
chr21	48129895	2061320	0.0428	0.2505
chr22	51304566	1033926	0.0202	0.164
chrMT	16571	49082	2.9619	2.7609
chrX	155270560	9437107	0.0608	0.3065
chrY	59373566	333753	0.0056	0.1085

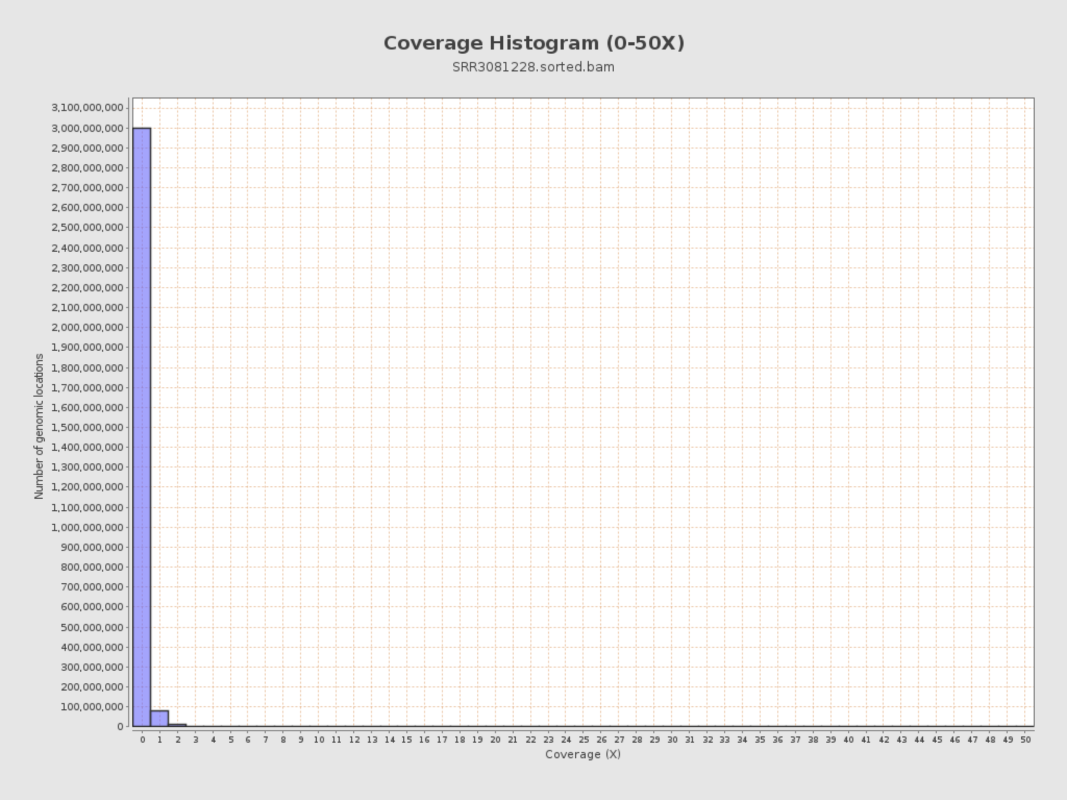
3. Results : Coverage across reference



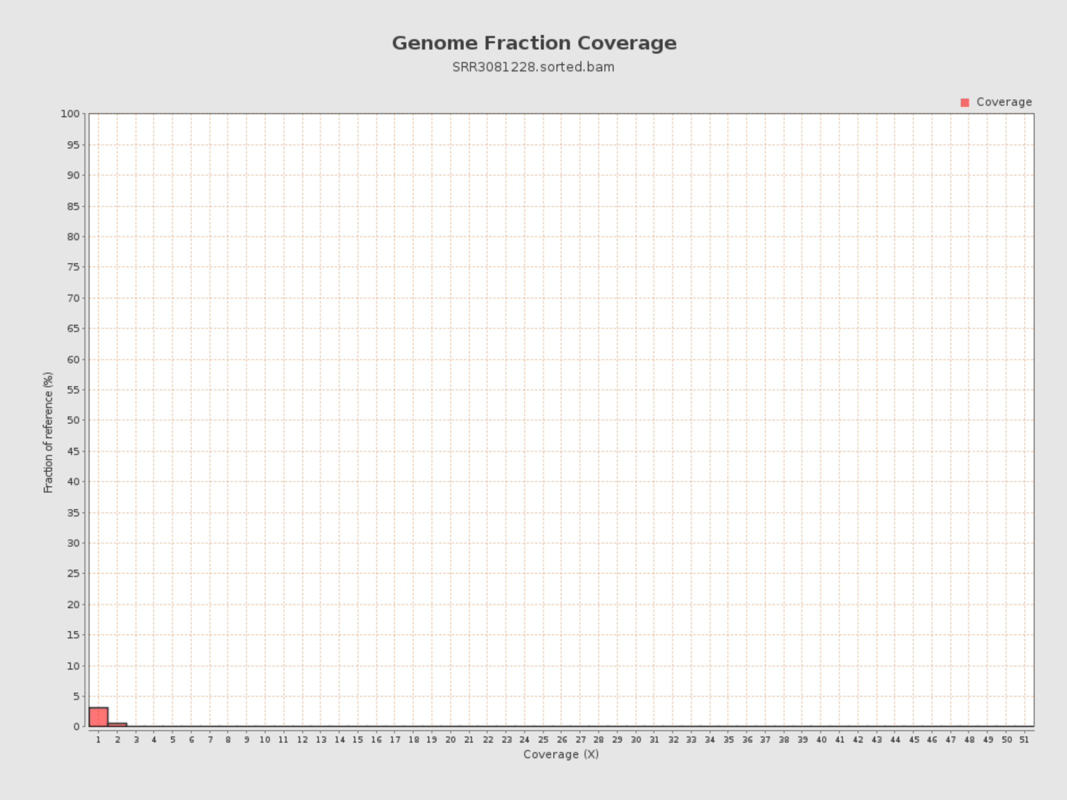
4. Results : Coverage Histogram



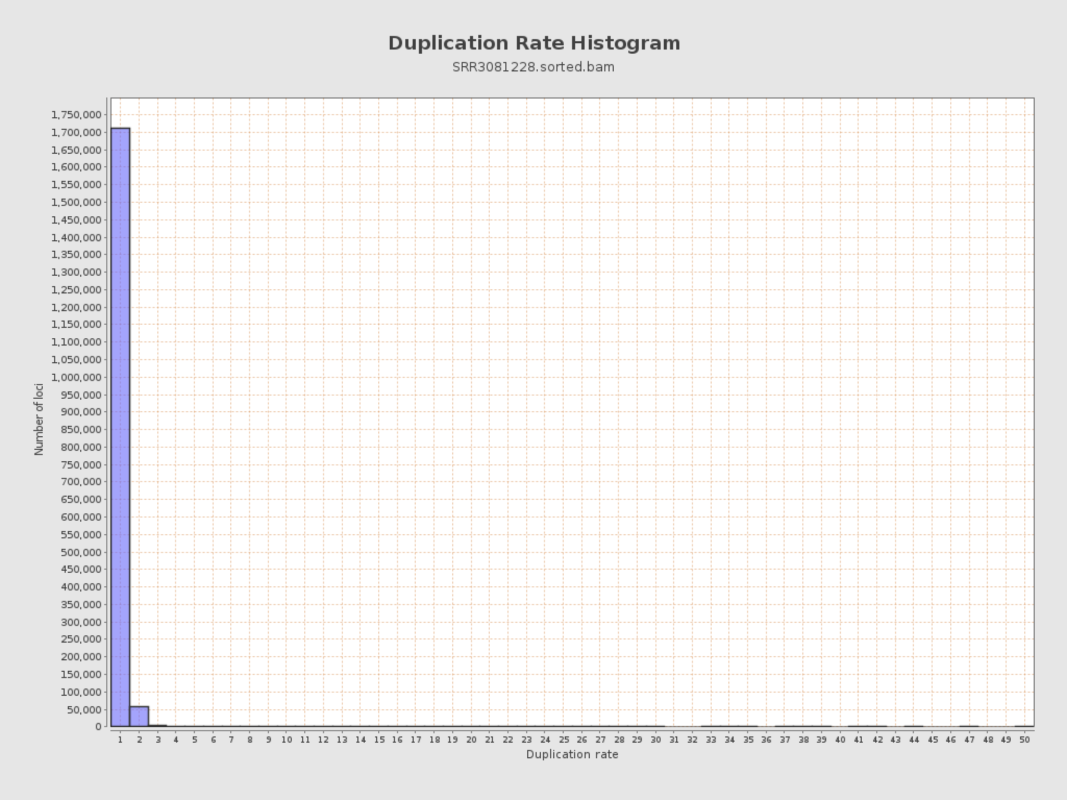
5. Results : Coverage Histogram (0-50X)



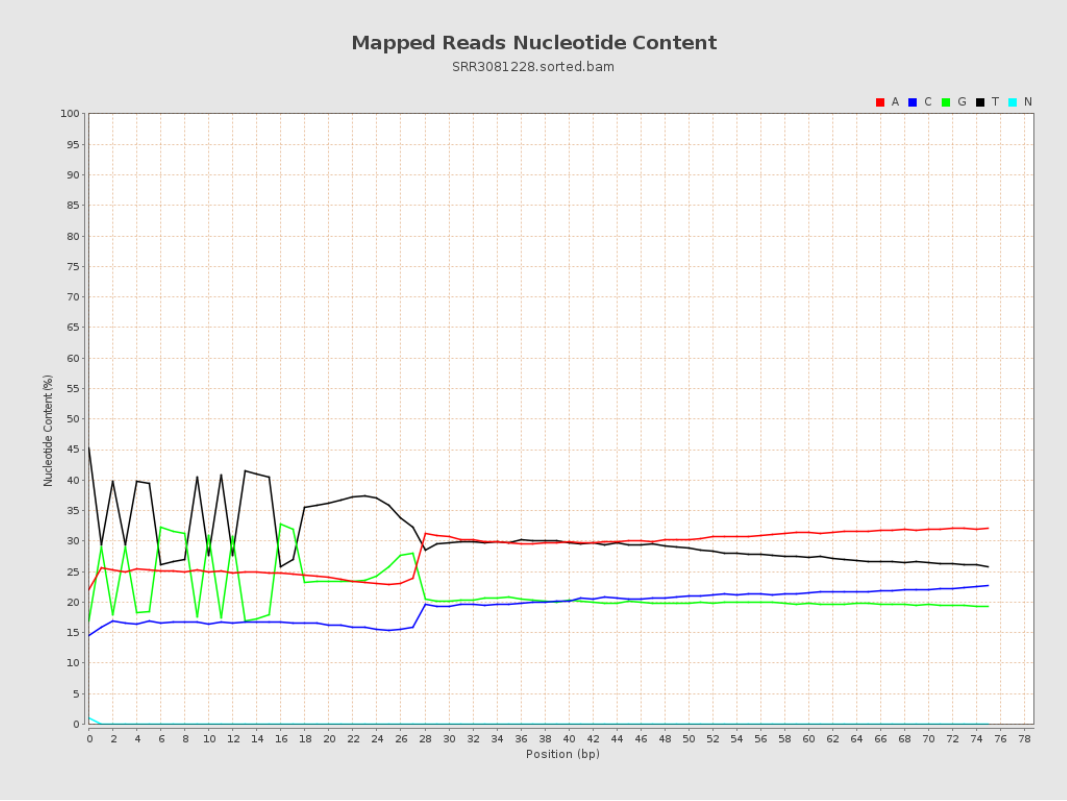
6. Results : Genome Fraction Coverage



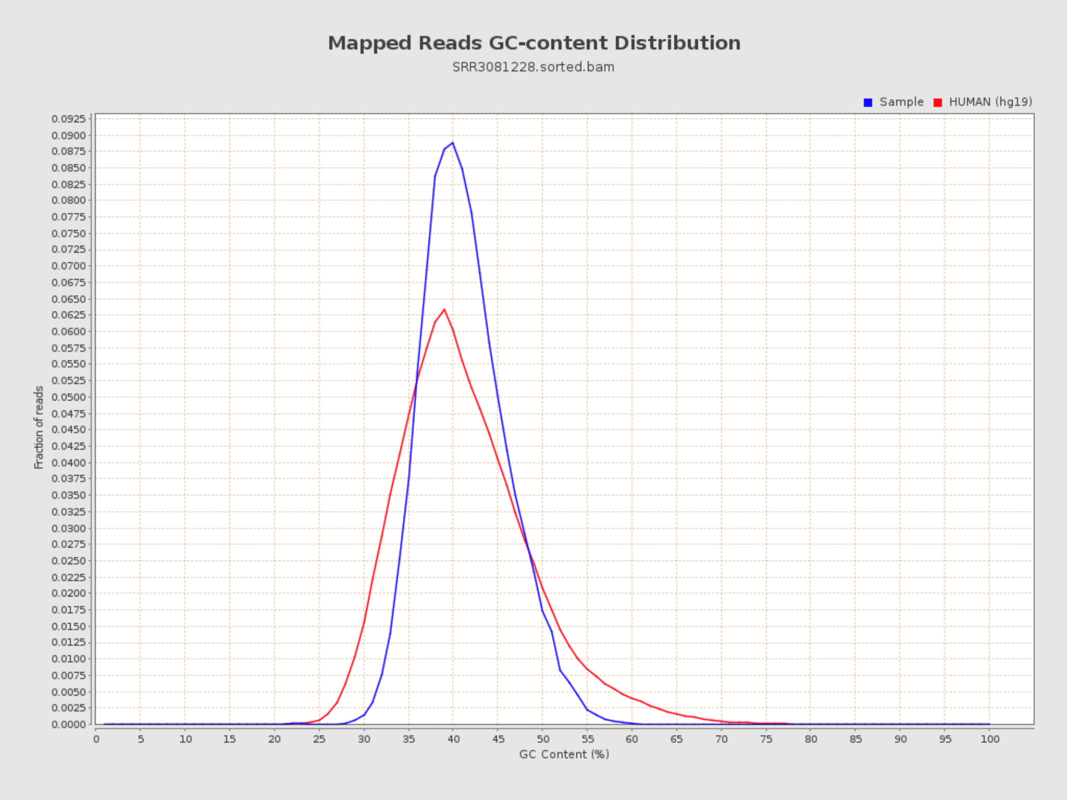
7. Results : Duplication Rate Histogram



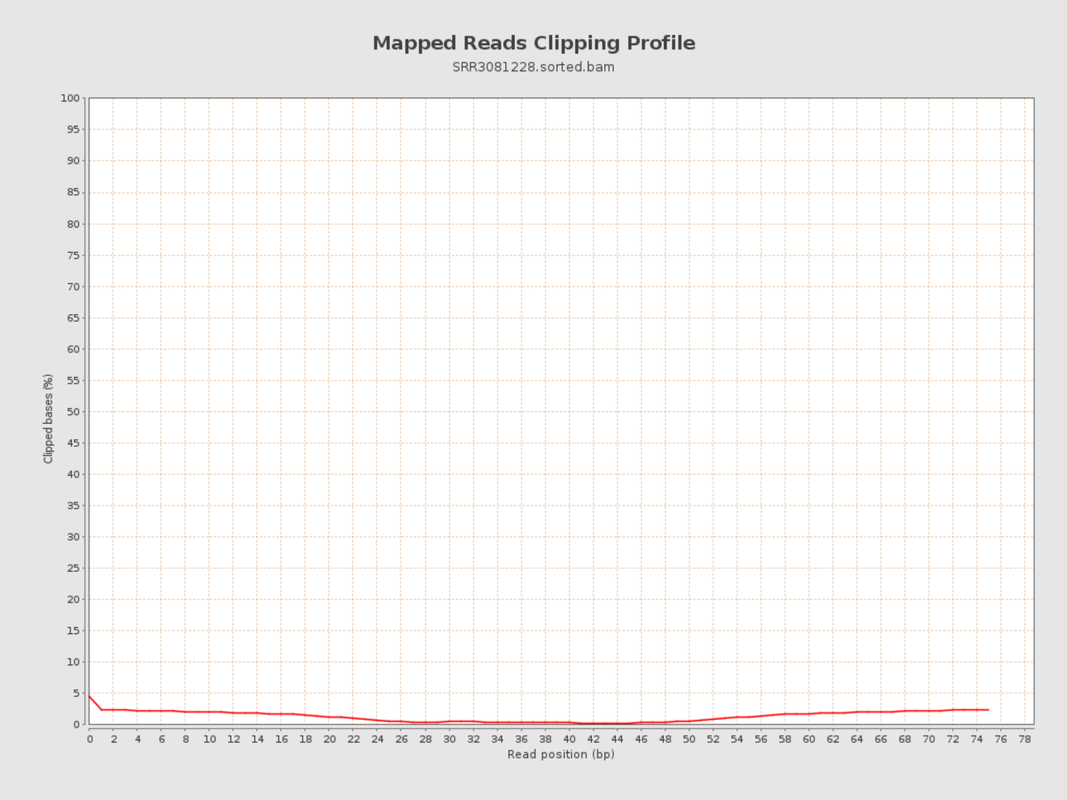
8. Results : Mapped Reads Nucleotide Content



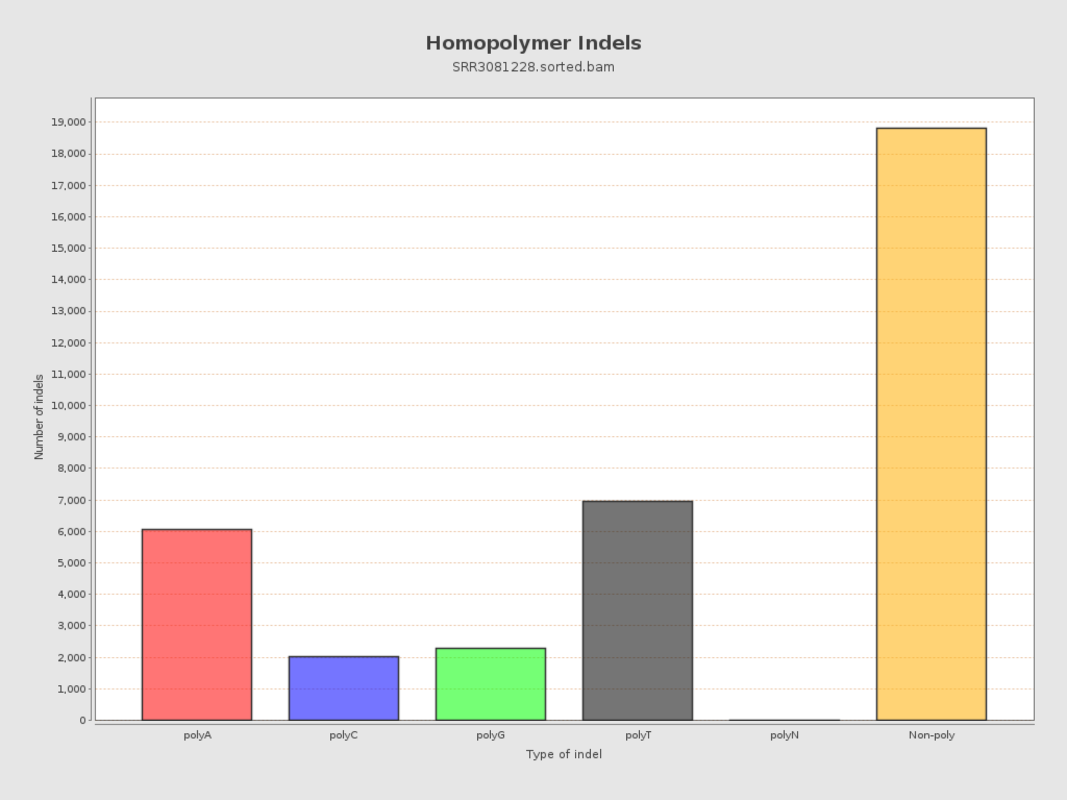
9. Results : Mapped Reads GC-content Distribution



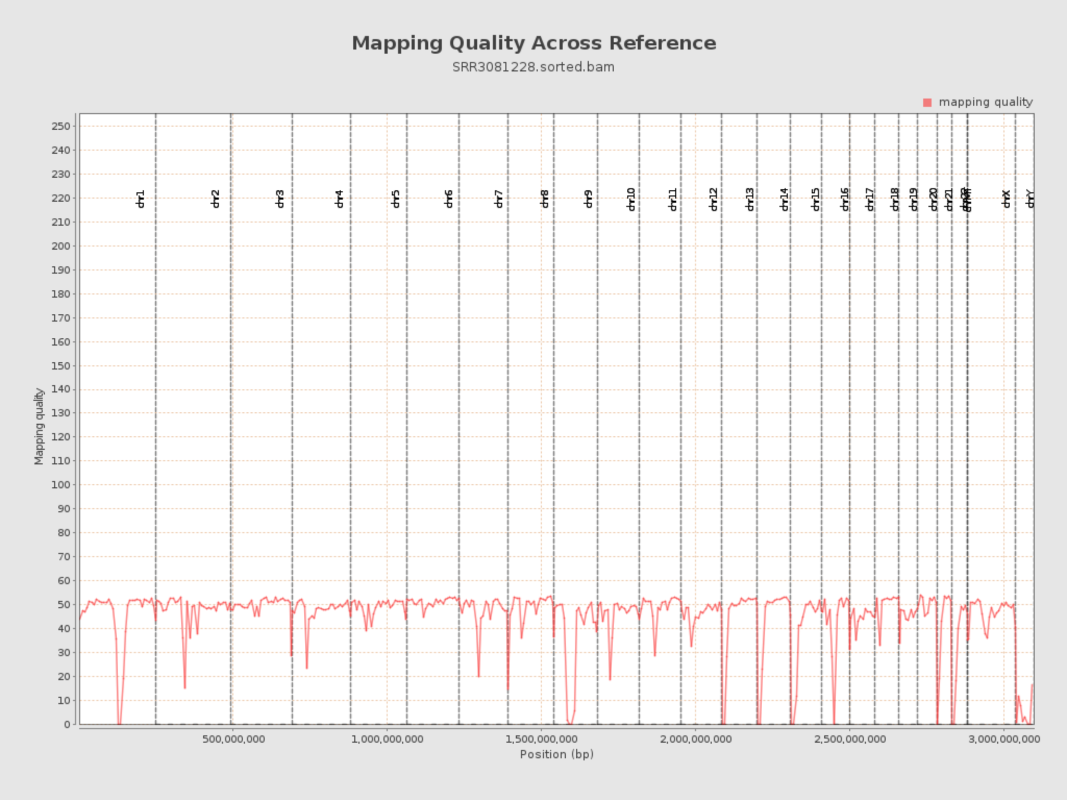
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram