Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 12:39:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081965.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_SRR3081965 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081965.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 12:39:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081965.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,336,536
Mapped reads	3,022,517 / 90.59%
Unmapped reads	314,019 / 9.41%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	31,043 / 0.93%
Read min/max/mean length	30 / 76 / 76.33
Duplicated reads (estimated)	175,287 / 5.25%
Duplication rate	4.78%
Clipped reads	1,377,960 / 41.3%

2.2. ACGT Content

Number/percentage of A's	56,980,900 / 28.26%
Number/percentage of C's	37,375,478 / 18.54%
Number/percentage of T's	63,549,660 / 31.52%
Number/percentage of G's	43,688,296 / 21.67%
Number/percentage of N's	24,673 / 0.01%
GC Percentage	40.21%

2.3. Coverage

Mean	0.0652

Standard Deviation	0.4688

2.4. Mapping Quality

Mean Mapping Quality	46.08

2.5. Mismatches and indels

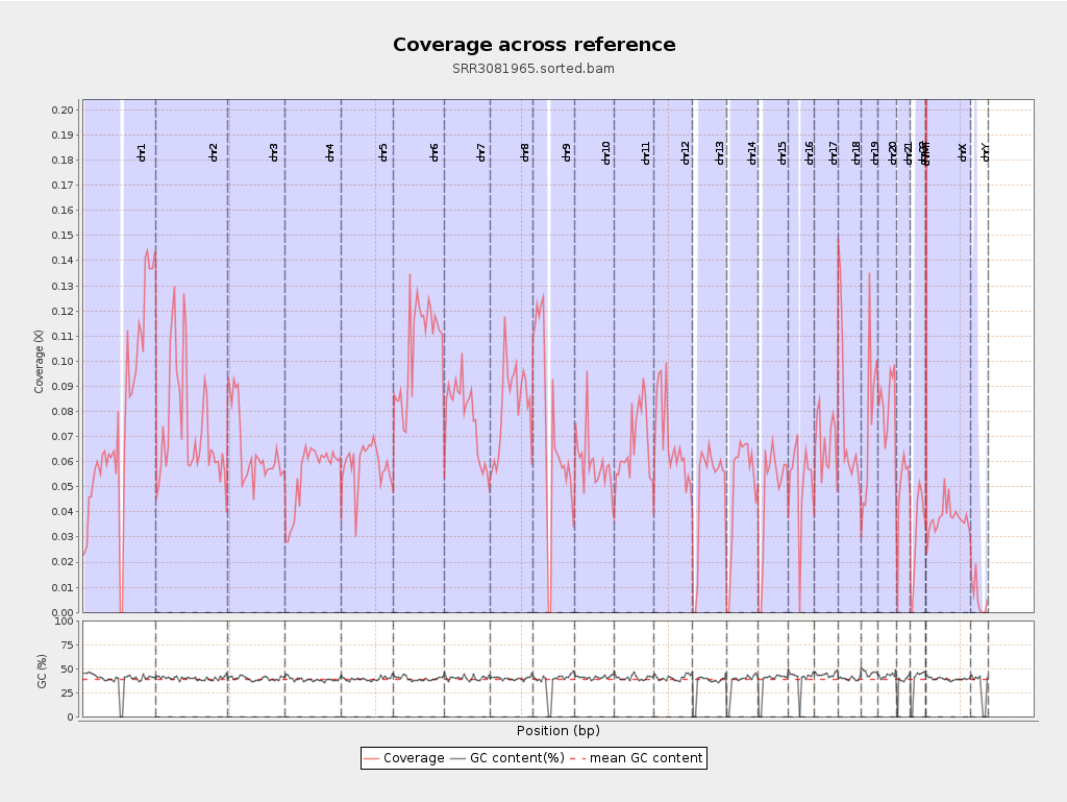
General error rate	0.78%
Mismatches	1,551,242
Insertions	14,081
Mapped reads with at least one insertion	0.46%
Deletions	40,987
Mapped reads with at least one deletion	1.34%
Homopolymer indels	48.08%

2.6. Chromosome stats

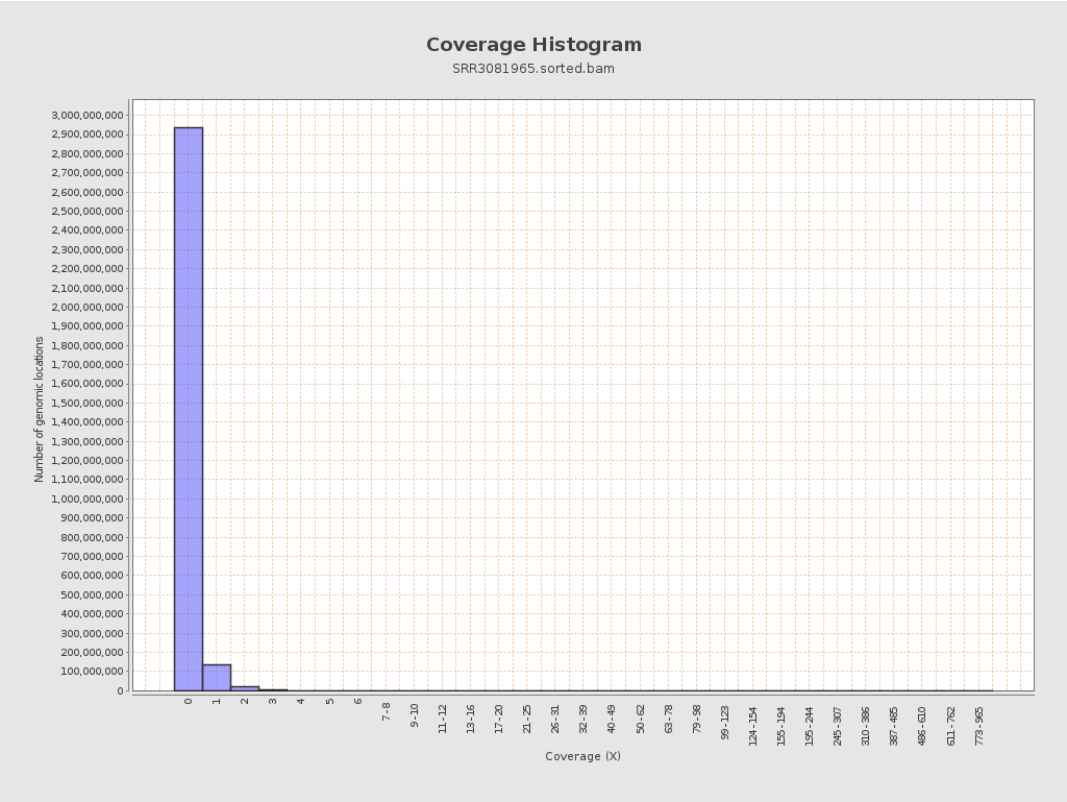
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	19155951	0.0769	0.7532
chr2	243199373	17966478	0.0739	0.6261
chr3	198022430	12810604	0.0647	0.3021
chr4	191154276	10545931	0.0552	0.2878
chr5	180915260	10560493	0.0584	0.2889
chr6	171115067	18071535	0.1056	0.4901
chr7	159138663	12212779	0.0767	0.5886

chr8	146364022	12077356	0.0825	0.7095
chr9	141213431	10082284	0.0714	0.4867
chr10	135534747	8089704	0.0597	0.4268
chr11	135006516	9023921	0.0668	0.3787
chr12	133851895	9060798	0.0677	0.3186
chr13	115169878	5679300	0.0493	0.268
chr14	107349540	5463615	0.0509	0.2912
chr15	102531392	4848282	0.0473	0.2654
chr16	90354753	4619047	0.0511	0.2946
chr17	81195210	5556156	0.0684	0.3384
chr18	78077248	5883094	0.0753	0.7407
chr19	59128983	4457871	0.0754	0.5999
chr20	63025520	5264446	0.0835	0.3508
chr21	48129895	2354696	0.0489	0.2796
chr22	51304566	1625758	0.0317	0.2081
chrMT	16571	110105	6.6444	4.5568
chrX	155270560	5817095	0.0375	0.2675
chrY	59373566	353386	0.006	0.1267

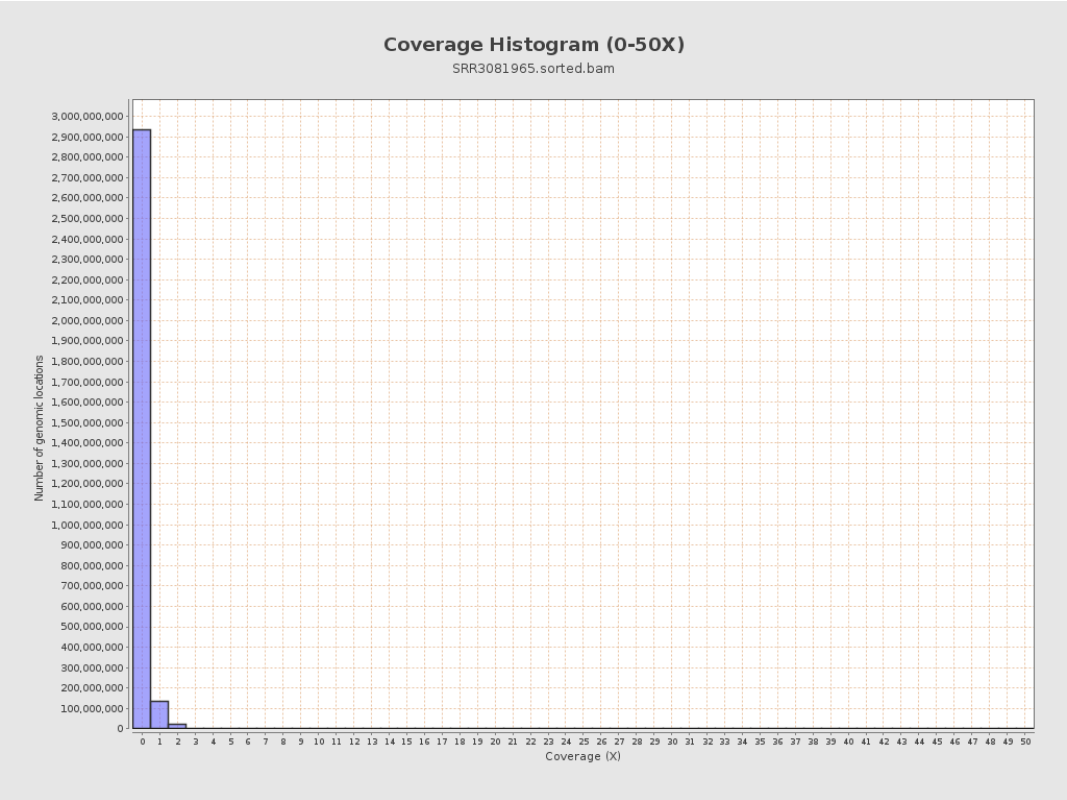
3. Results : Coverage across reference



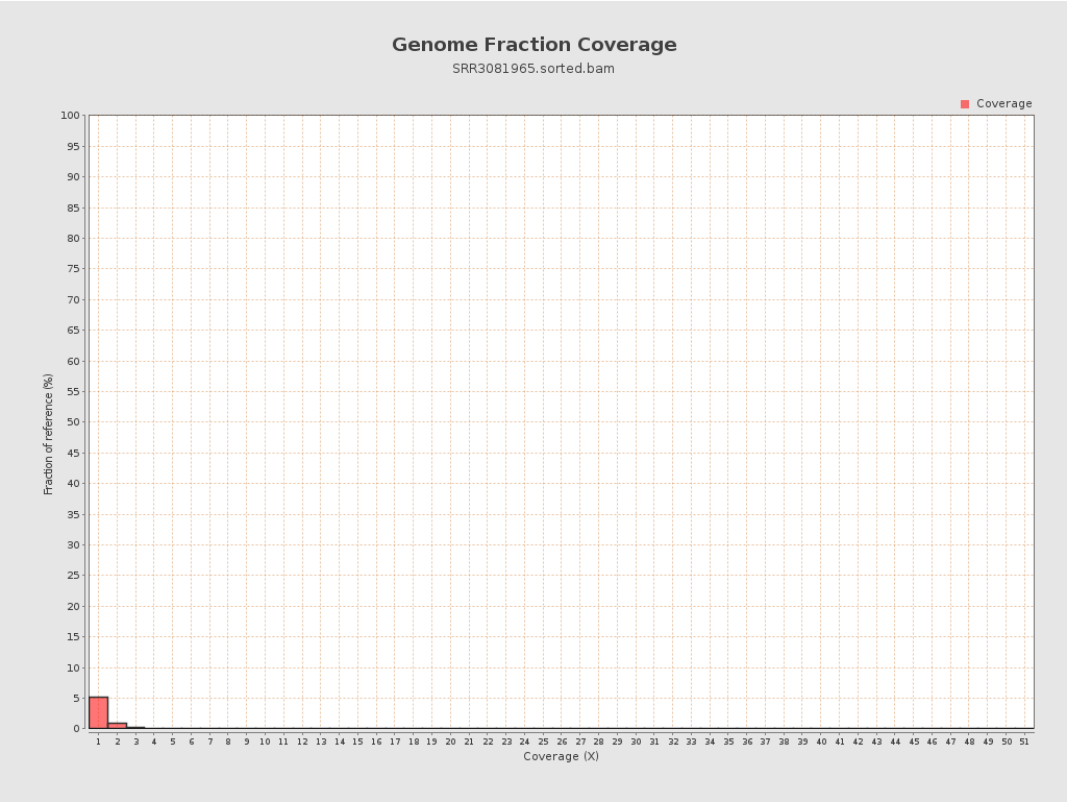
4. Results : Coverage Histogram



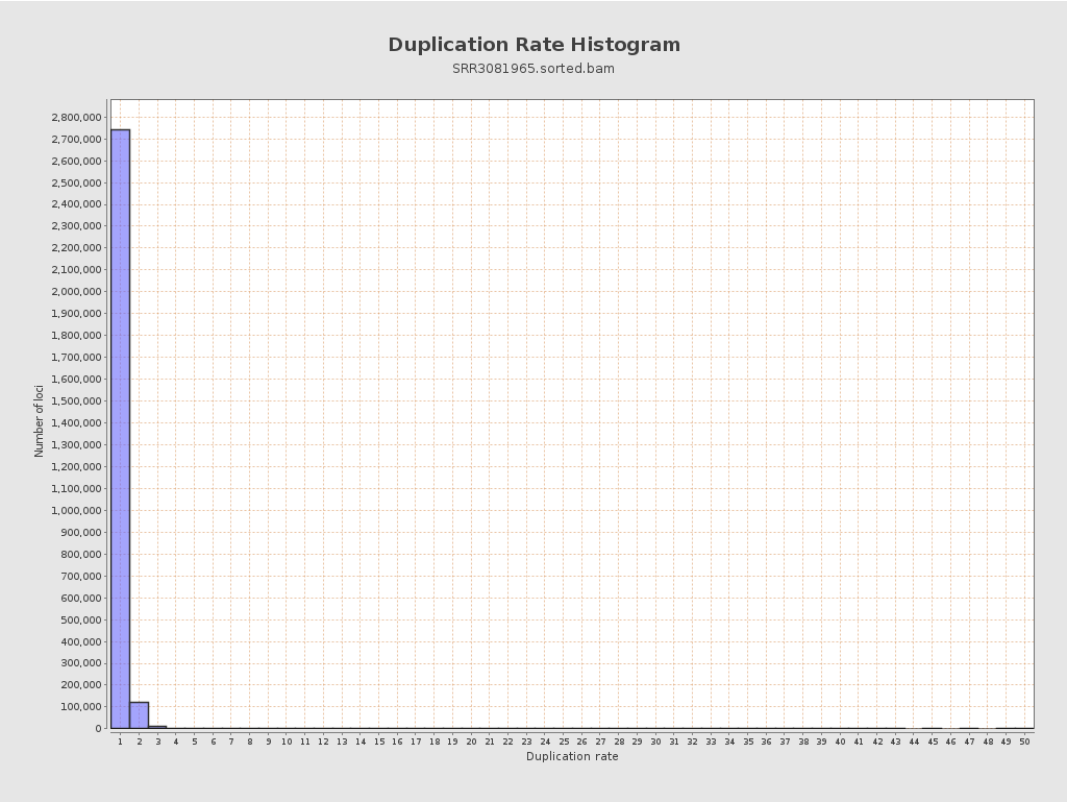
5. Results : Coverage Histogram (0-50X)



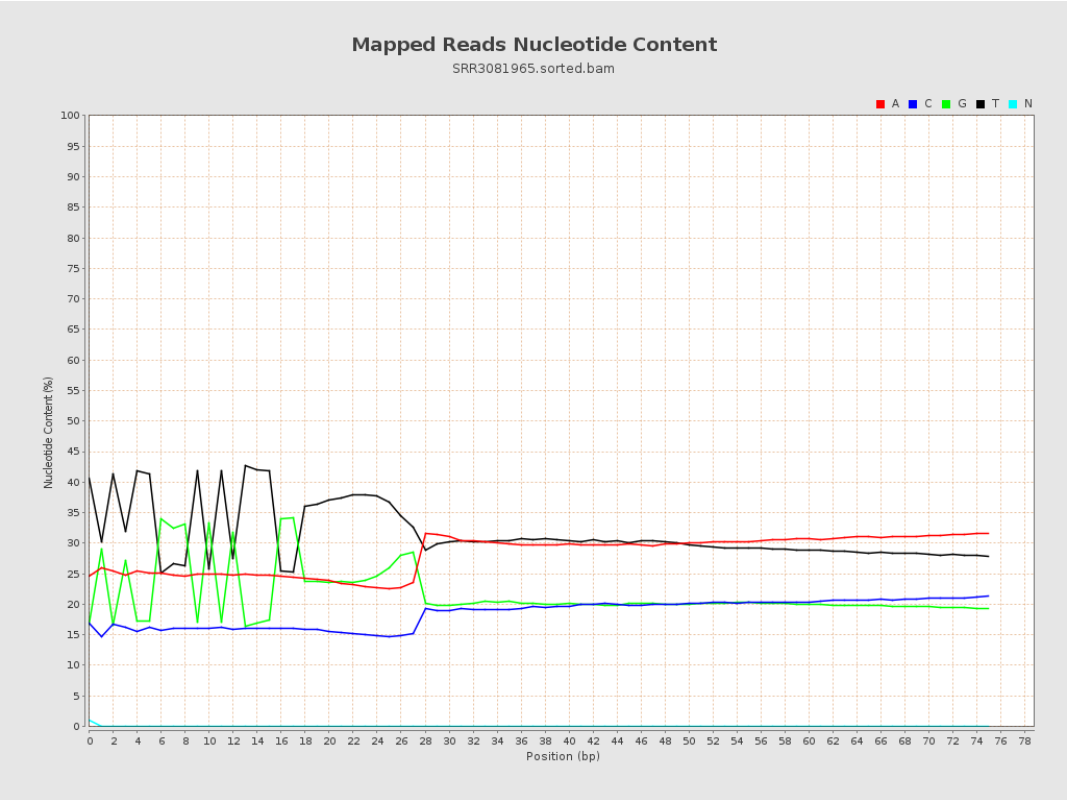
6. Results : Genome Fraction Coverage



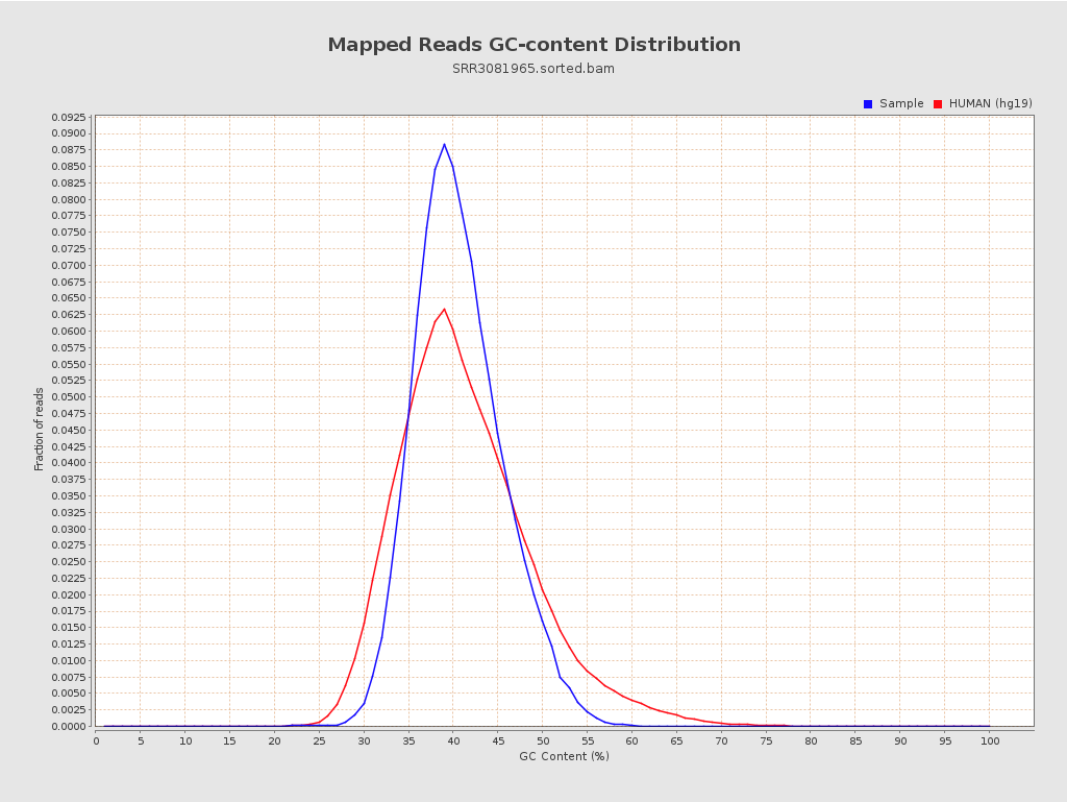
7. Results : Duplication Rate Histogram



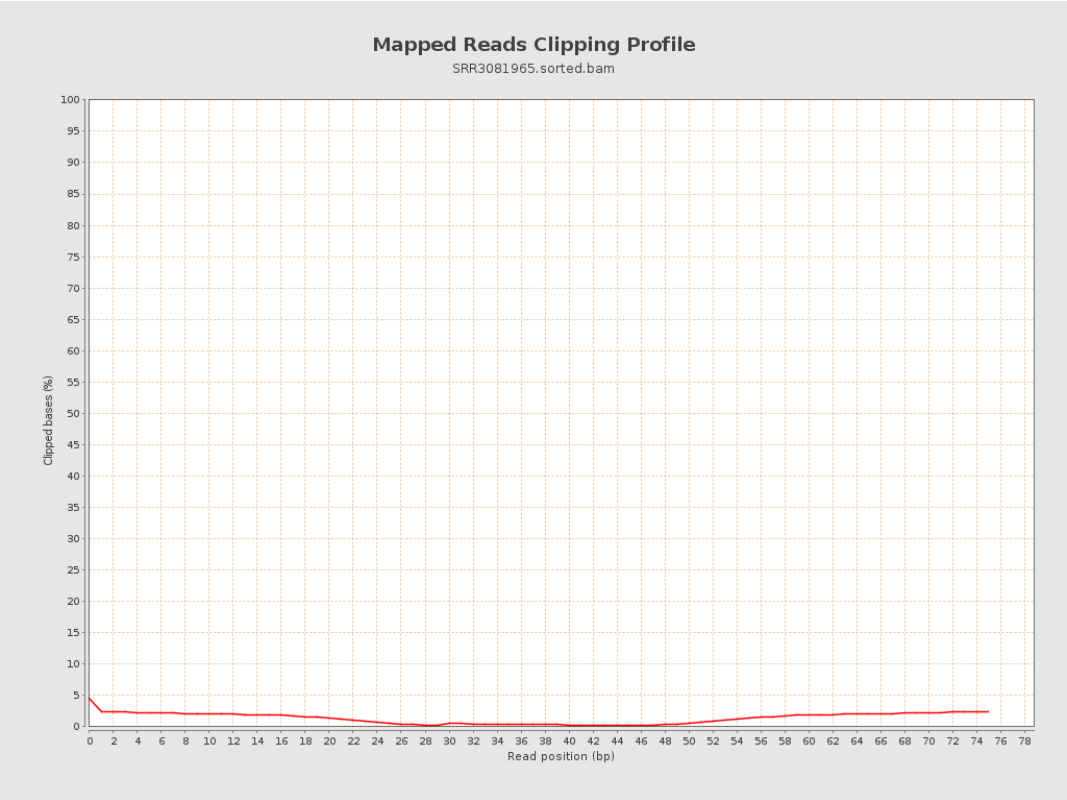
8. Results : Mapped Reads Nucleotide Content



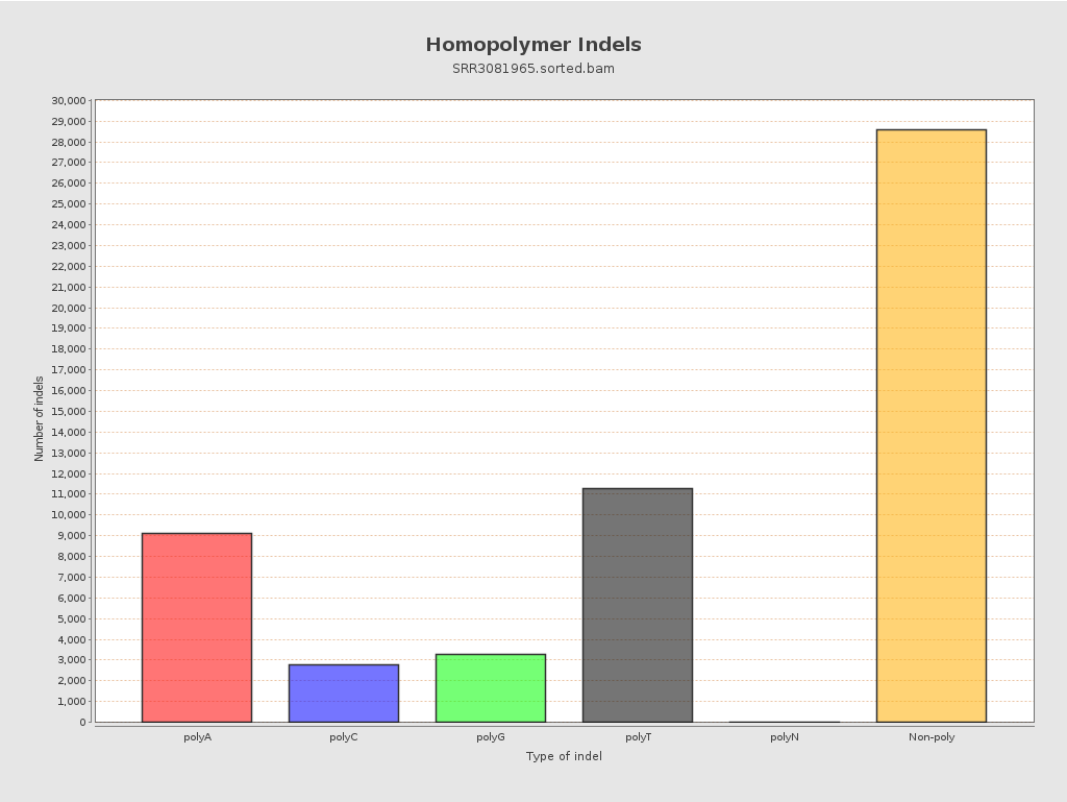
9. Results : Mapped Reads GC-content Distribution



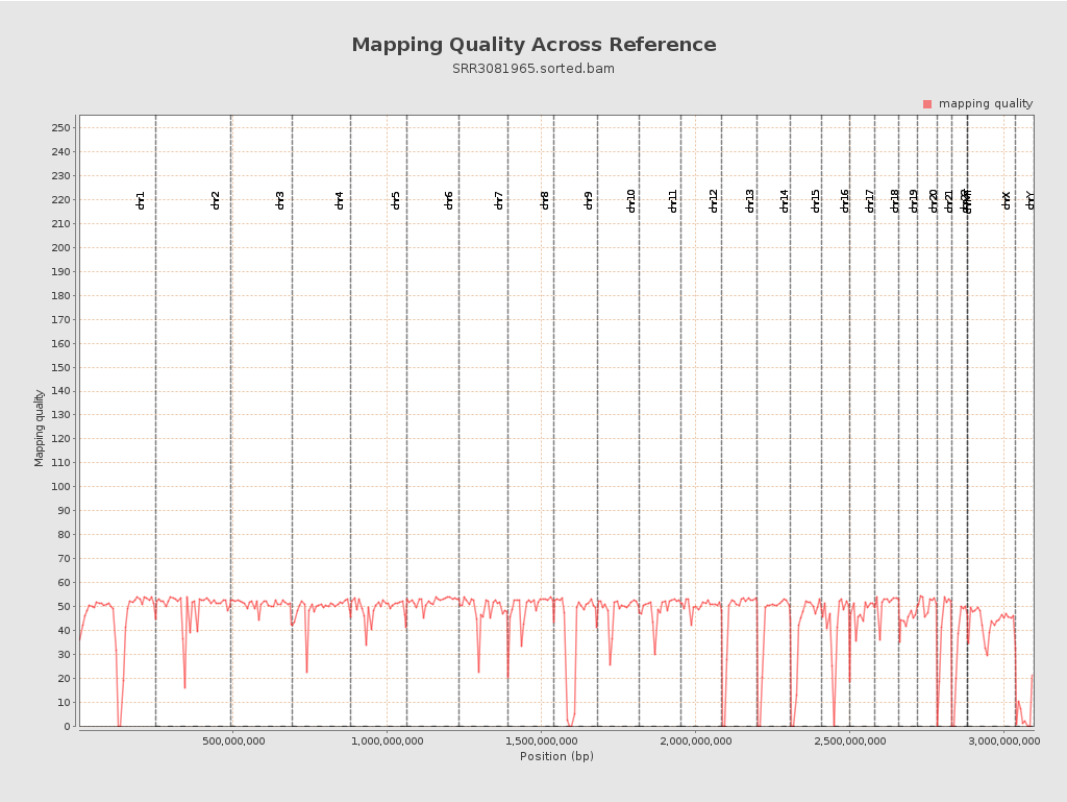
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram