Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 08:47:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081883.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_SRR3081883 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081883.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 08:47:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081883.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,421,657
Mapped reads	2,221,574 / 91.74%
Unmapped reads	200,083 / 8.26%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,515 / 0.64%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	85,903 / 3.55%
Duplication rate	2.92%
Clipped reads	898,163 / 37.09%

2.2. ACGT Content

Number/percentage of A's	41,542,687 / 27.65%
Number/percentage of C's	28,825,369 / 19.19%
Number/percentage of T's	46,107,210 / 30.69%
Number/percentage of G's	33,761,215 / 22.47%
Number/percentage of N's	1,745 / 0%
GC Percentage	41.66%

2.3. Coverage

Mean	0.0485

Standard Deviation	0.4082

2.4. Mapping Quality

Mean Mapping Quality	45.25

2.5. Mismatches and indels

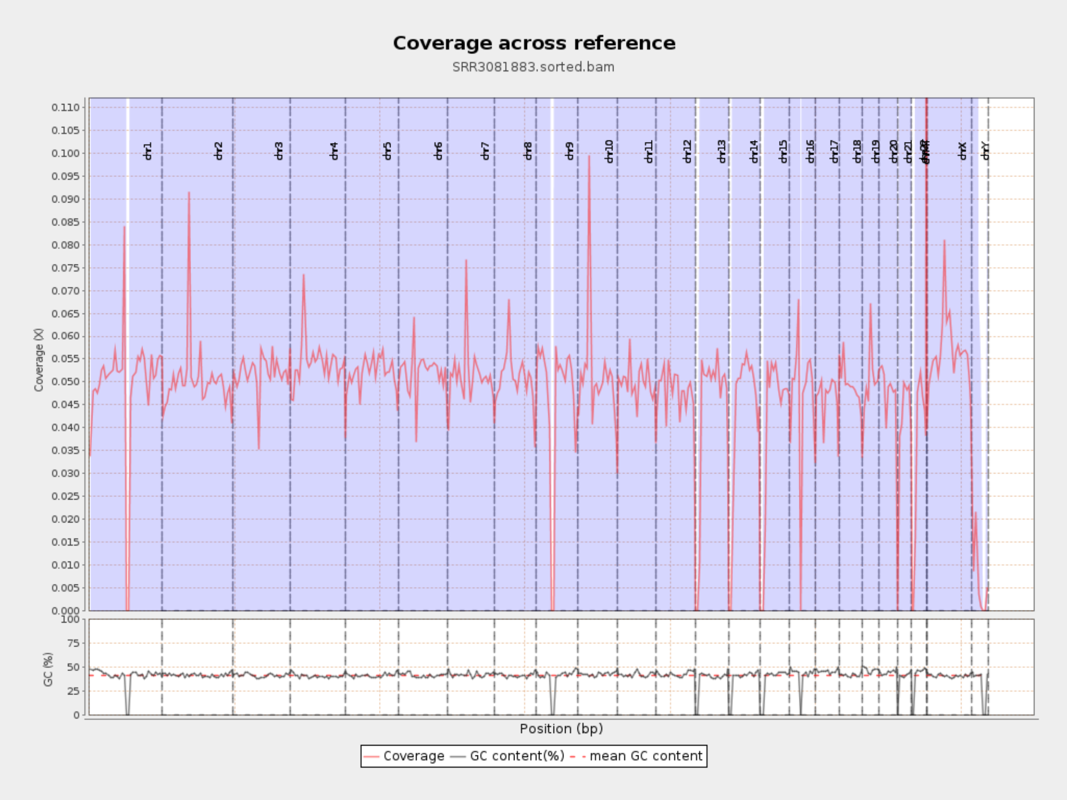
General error rate	0.81%
Mismatches	1,197,927
Insertions	10,657
Mapped reads with at least one insertion	0.48%
Deletions	30,027
Mapped reads with at least one deletion	1.34%
Homopolymer indels	46.4%

2.6. Chromosome stats

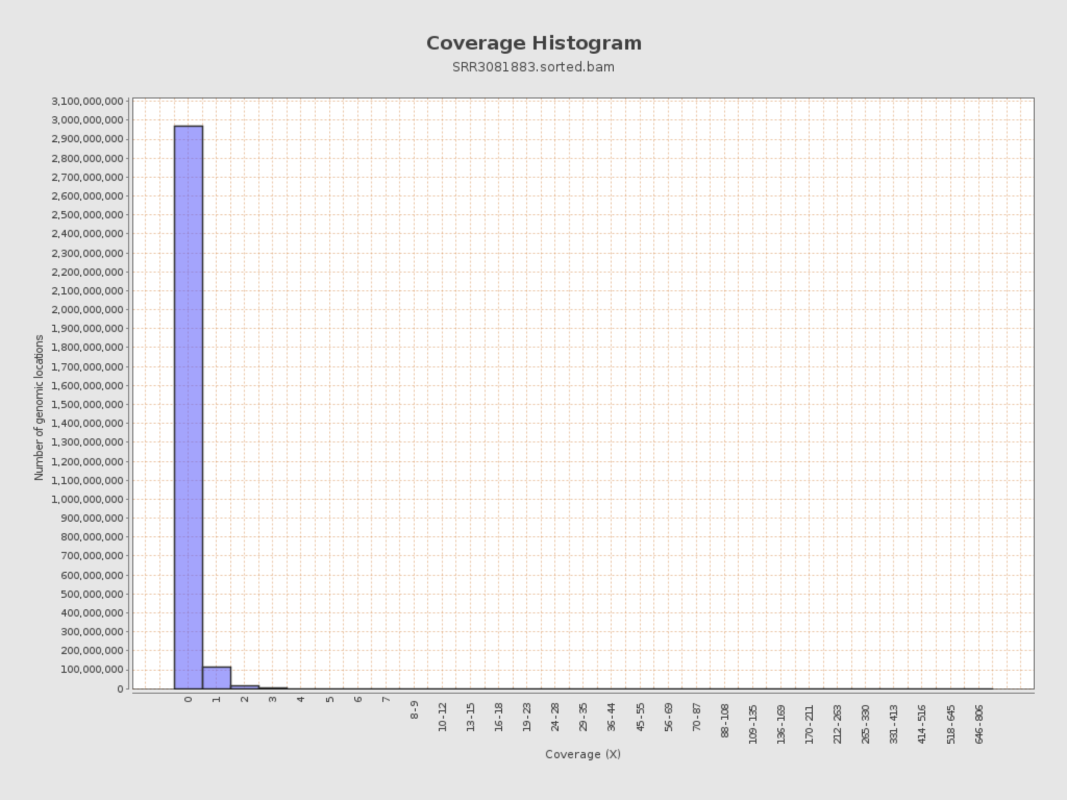
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12277769	0.0493	0.7608
chr2	243199373	12312594	0.0506	0.4685
chr3	198022430	10288183	0.052	0.2625
chr4	191154276	10363408	0.0542	0.2863
chr5	180915260	9445625	0.0522	0.2569
chr6	171115067	8912091	0.0521	0.2936
chr7	159138663	8251063	0.0518	0.4717

chr8	146364022	7458946	0.051	0.5195
chr9	141213431	6518197	0.0462	0.3669
chr10	135534747	7025955	0.0518	0.5062
chr11	135006516	6696985	0.0496	0.3276
chr12	133851895	6410729	0.0479	0.2506
chr13	115169878	4940125	0.0429	0.2318
chr14	107349540	4534768	0.0422	0.2452
chr15	102531392	4175332	0.0407	0.2305
chr16	90354753	4217350	0.0467	0.2928
chr17	81195210	3766377	0.0464	0.2614
chr18	78077248	3876369	0.0496	0.6608
chr19	59128983	2978135	0.0504	0.5786
chr20	63025520	3016361	0.0479	0.255
chr21	48129895	1942849	0.0404	0.2491
chr22	51304566	1673846	0.0326	0.2024
chrMT	16571	6843	0.413	0.7787
chrX	155270560	8791418	0.0566	0.3019
chrY	59373566	410492	0.0069	0.171

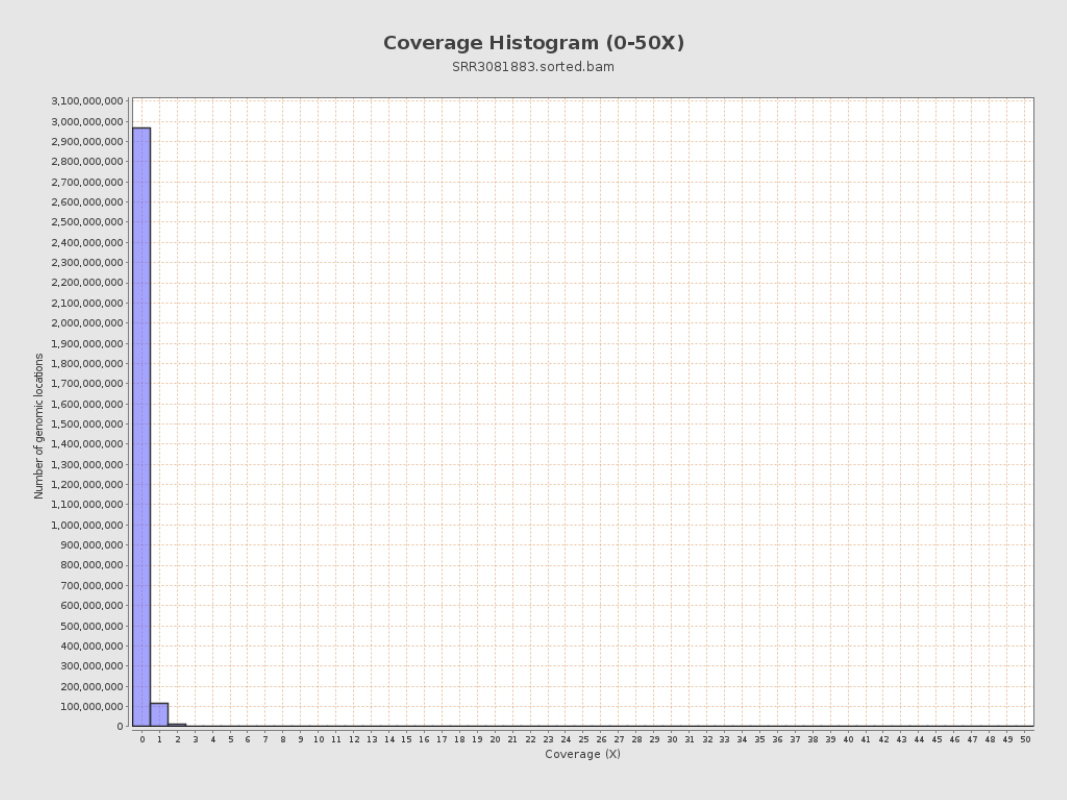
3. Results : Coverage across reference



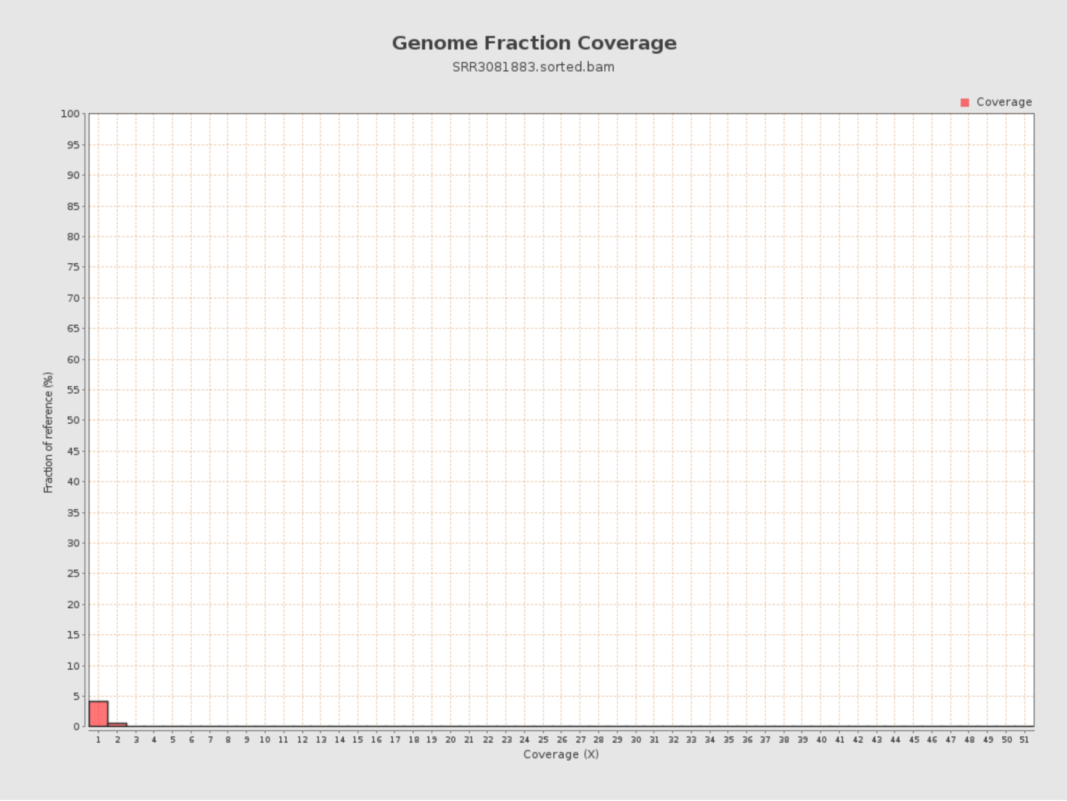
4. Results : Coverage Histogram



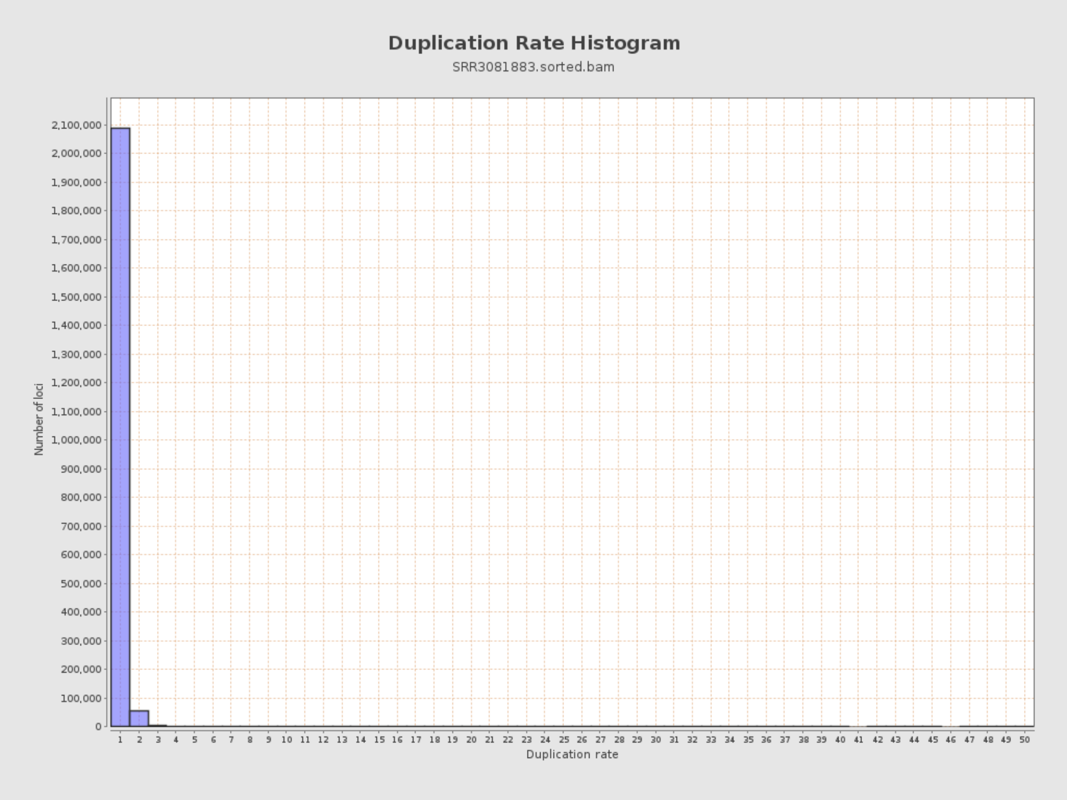
5. Results : Coverage Histogram (0-50X)



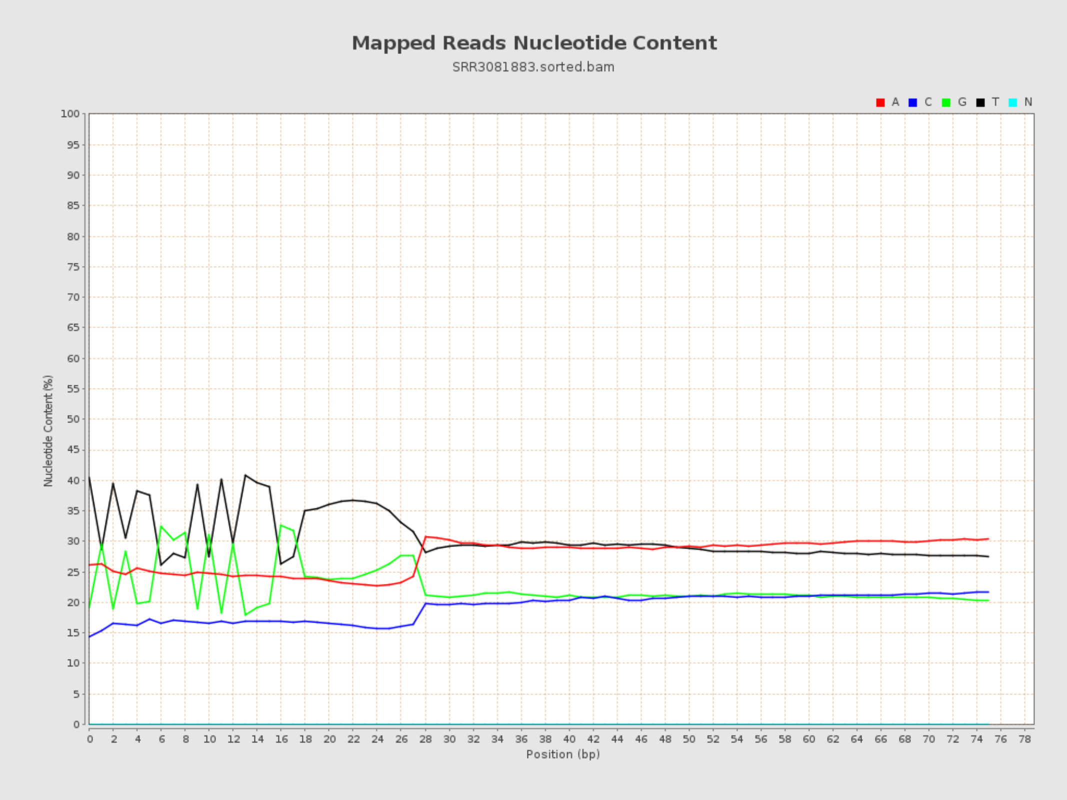
6. Results : Genome Fraction Coverage



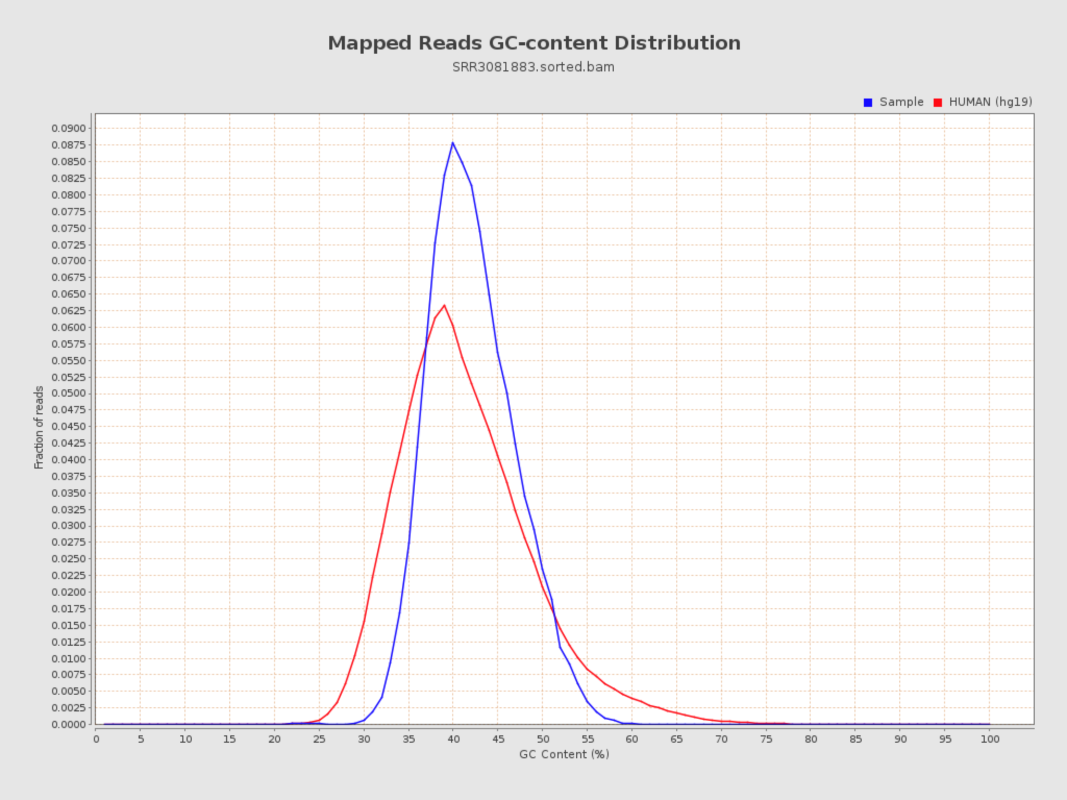
7. Results : Duplication Rate Histogram



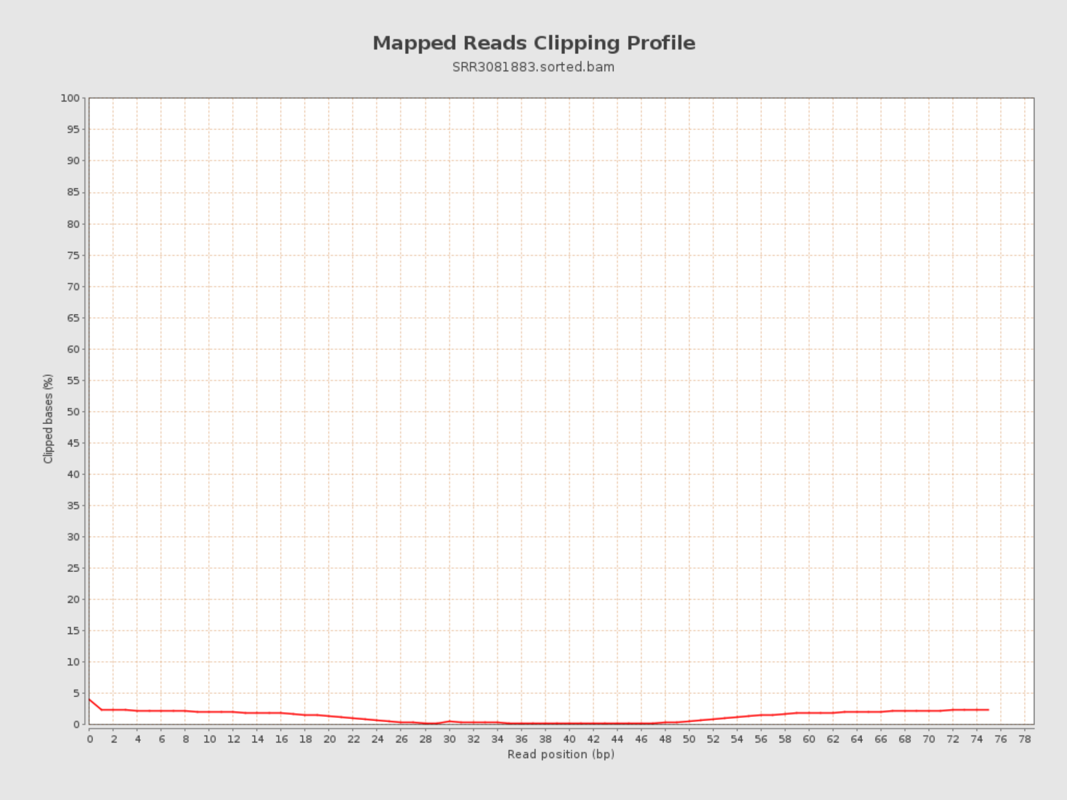
8. Results : Mapped Reads Nucleotide Content



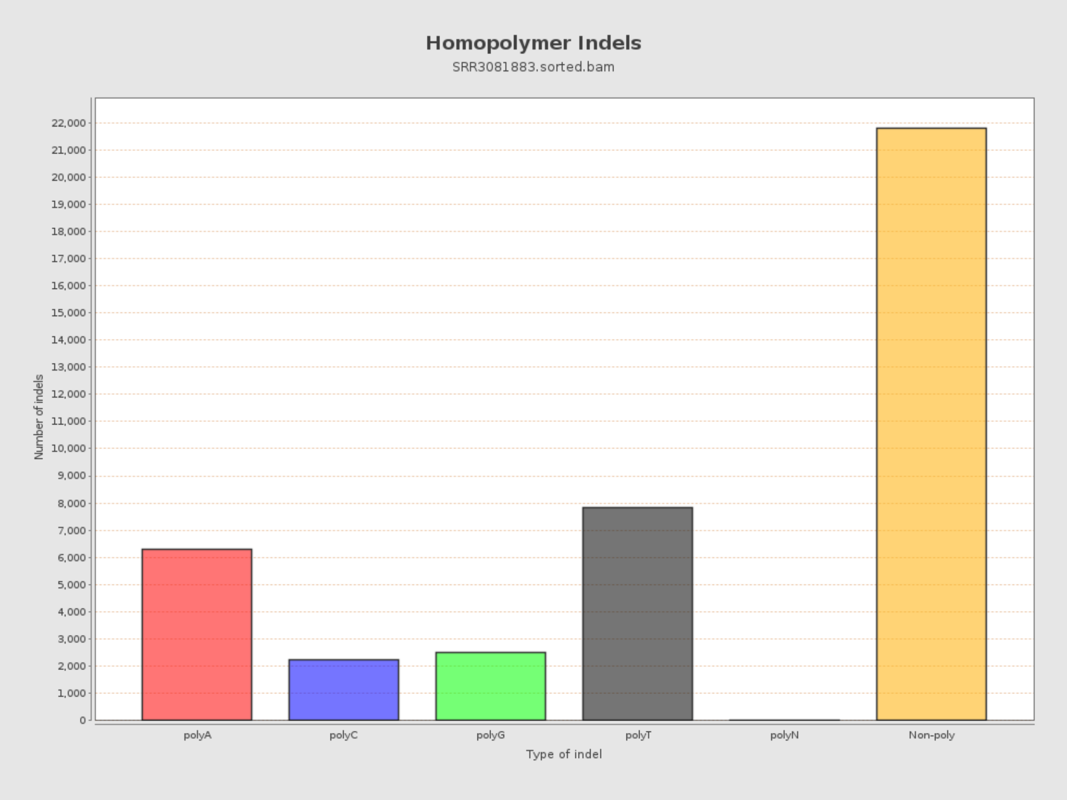
9. Results : Mapped Reads GC-content Distribution



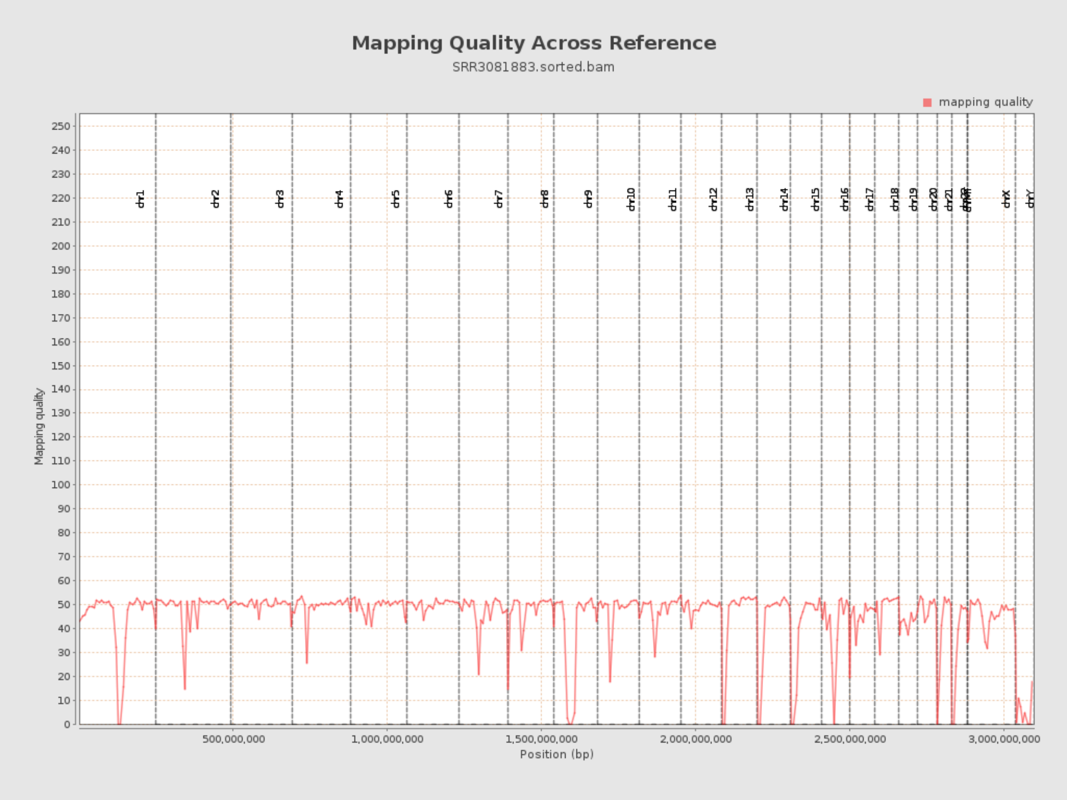
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram