Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 08:36:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081783.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_SRR3081783 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081783.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 08:36:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081783.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,012,558
Mapped reads	2,751,743 / 91.34%
Unmapped reads	260,815 / 8.66%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,711 / 0.59%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	119,924 / 3.98%
Duplication rate	2.97%
Clipped reads	1,134,632 / 37.66%

2.2. ACGT Content

Number/percentage of A's	51,128,506 / 27.53%
Number/percentage of C's	35,957,168 / 19.36%
Number/percentage of T's	56,545,705 / 30.44%
Number/percentage of G's	42,102,771 / 22.67%
Number/percentage of N's	2,003 / 0%
GC Percentage	42.03%

2.3. Coverage

Mean	0.06

Standard Deviation	0.5664

2.4. Mapping Quality

Mean Mapping Quality	44.08

2.5. Mismatches and indels

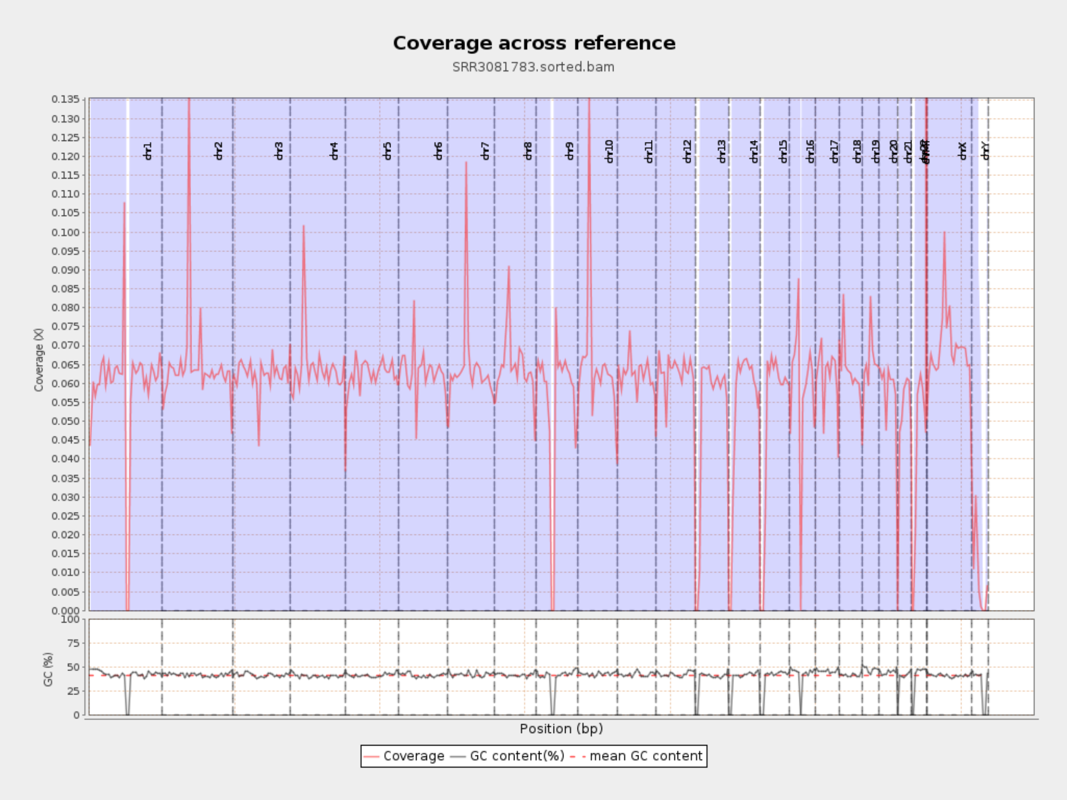
General error rate	0.87%
Mismatches	1,590,514
Insertions	14,248
Mapped reads with at least one insertion	0.51%
Deletions	42,524
Mapped reads with at least one deletion	1.53%
Homopolymer indels	45.66%

2.6. Chromosome stats

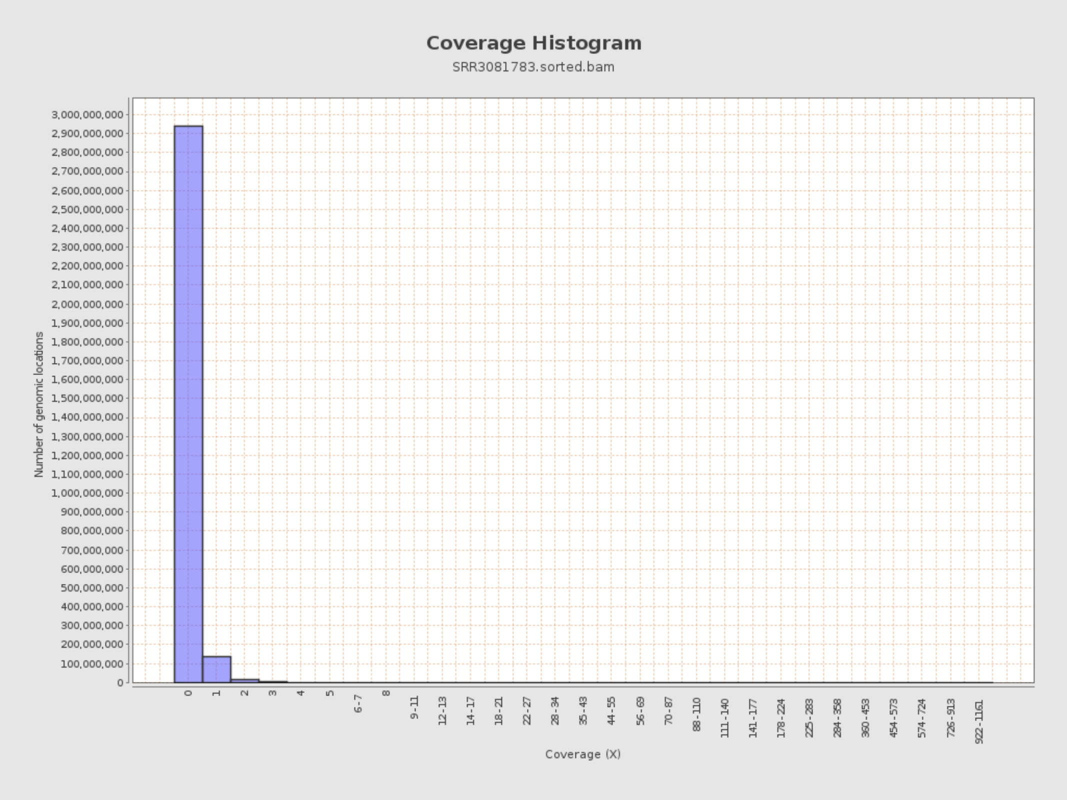
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14763257	0.0592	1.0295
chr2	243199373	15875050	0.0653	0.7415
chr3	198022430	12332002	0.0623	0.2895
chr4	191154276	12262474	0.0641	0.3588
chr5	180915260	11334056	0.0626	0.2887
chr6	171115067	10761431	0.0629	0.3647
chr7	159138663	10290135	0.0647	0.8323

chr8	146364022	9405934	0.0643	0.6232
chr9	141213431	7783493	0.0551	0.5312
chr10	135534747	8924267	0.0658	0.6735
chr11	135006516	8386388	0.0621	0.4696
chr12	133851895	8357781	0.0624	0.2924
chr13	115169878	5862810	0.0509	0.2566
chr14	107349540	5617413	0.0523	0.3082
chr15	102531392	5233369	0.051	0.2632
chr16	90354753	5305622	0.0587	0.3598
chr17	81195210	4993836	0.0615	0.3286
chr18	78077248	4998517	0.064	1.0358
chr19	59128983	3886648	0.0657	0.8006
chr20	63025520	3692192	0.0586	0.3006
chr21	48129895	2386577	0.0496	0.3051
chr22	51304566	2032218	0.0396	0.2264
chrMT	16571	20610	1.2437	1.3694
chrX	155270560	10761504	0.0693	0.3828
chrY	59373566	544699	0.0092	0.2527

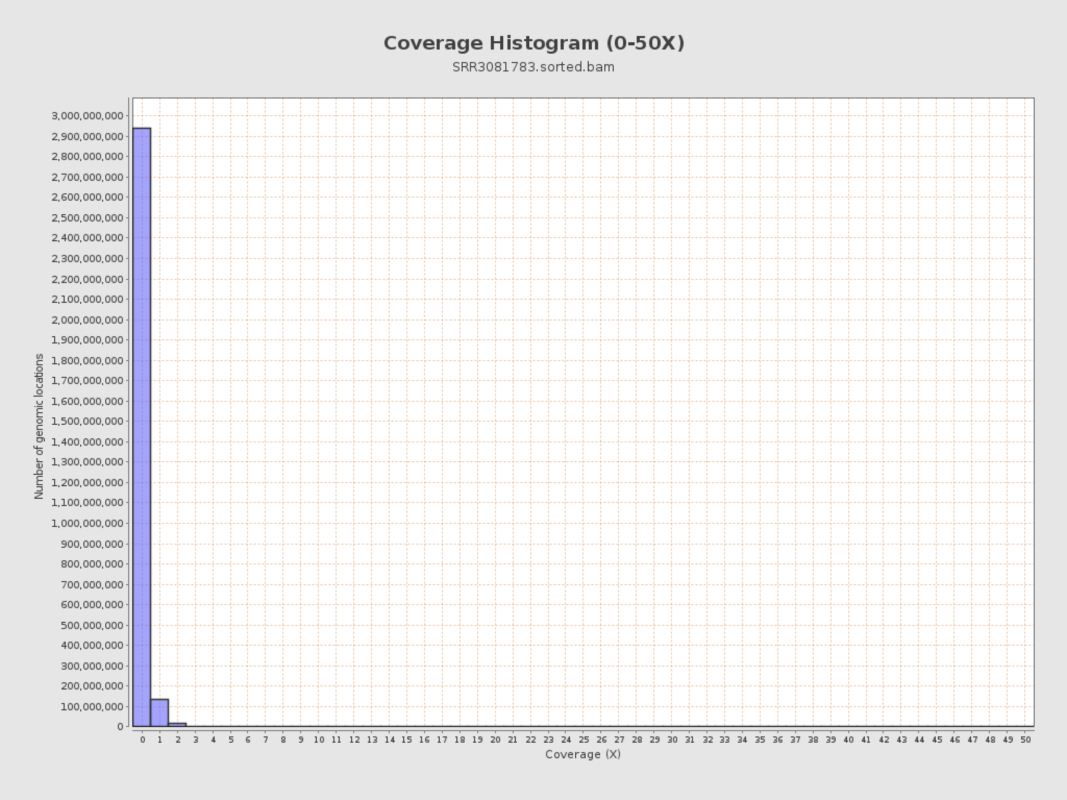
3. Results : Coverage across reference



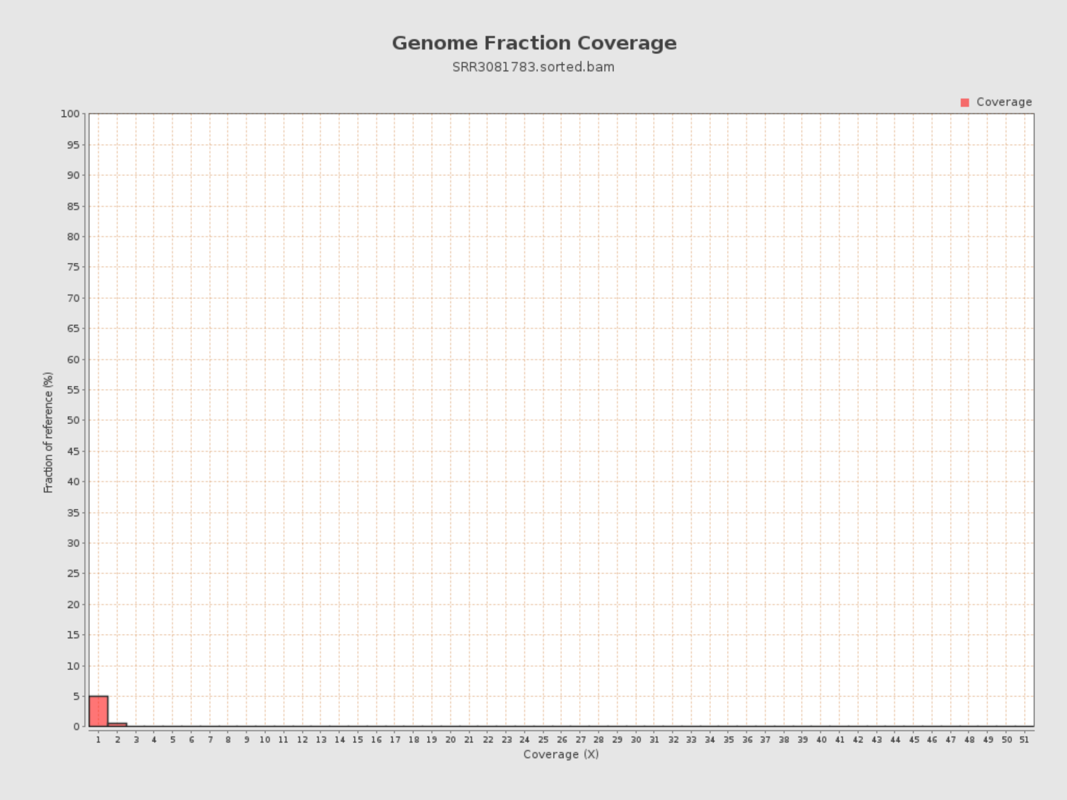
4. Results : Coverage Histogram



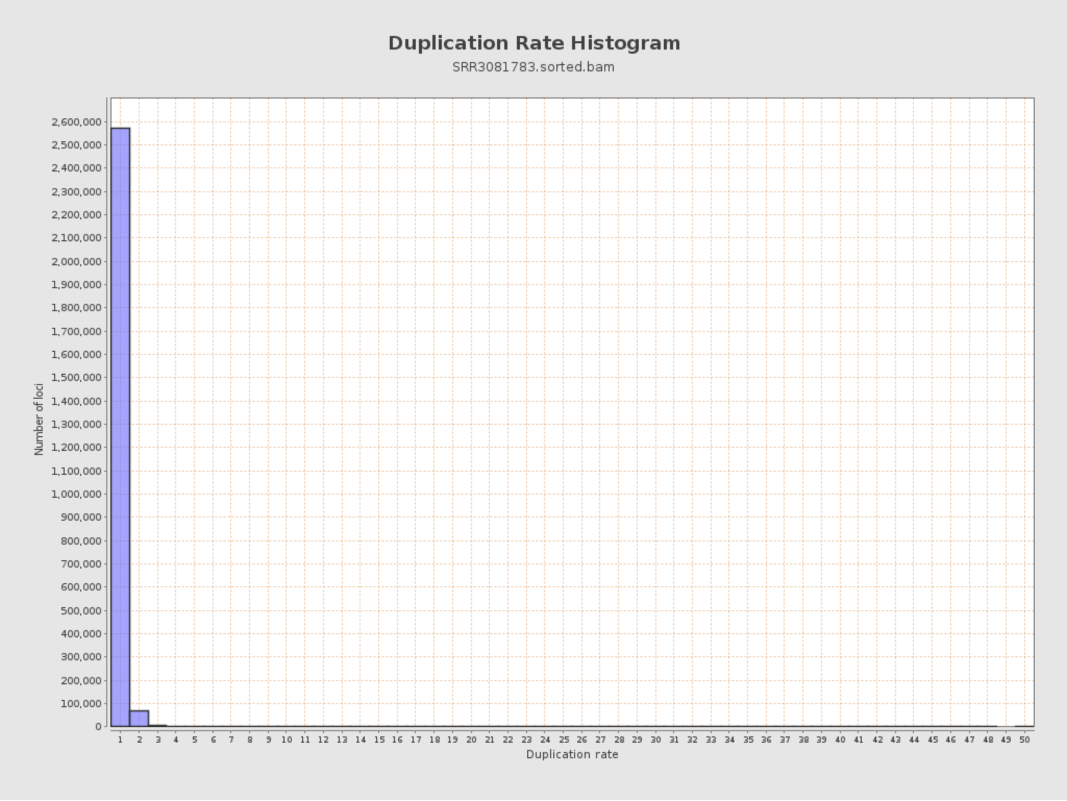
5. Results : Coverage Histogram (0-50X)



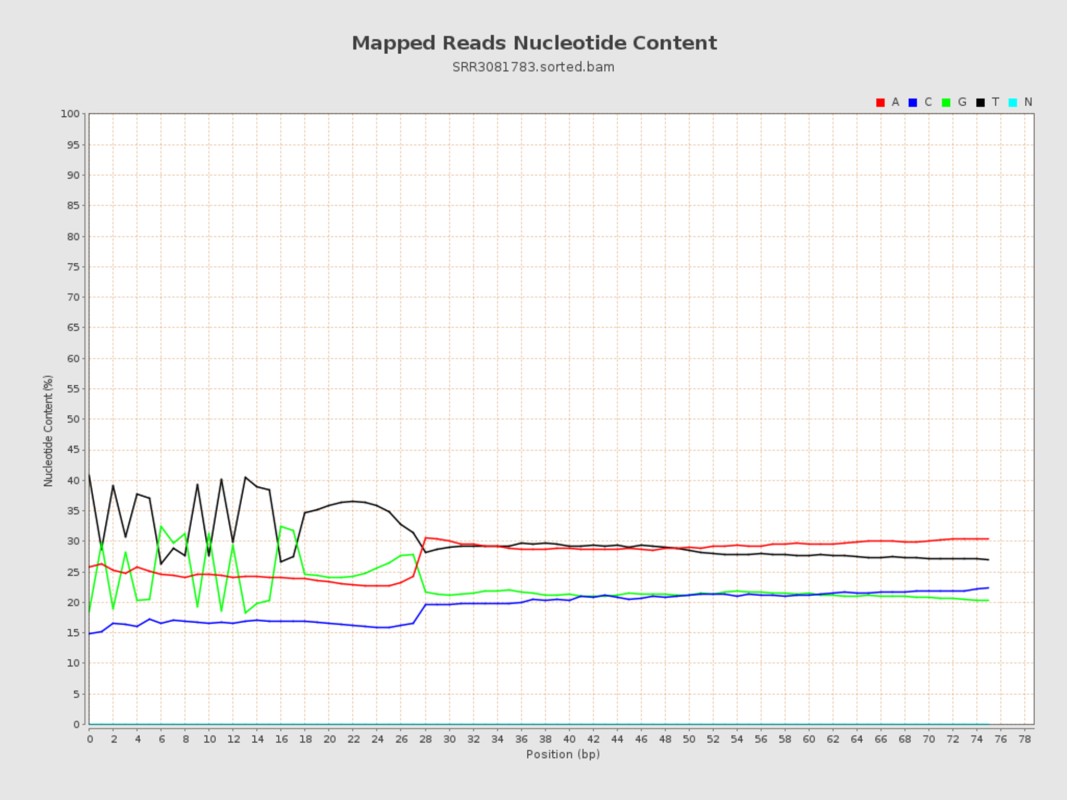
6. Results : Genome Fraction Coverage



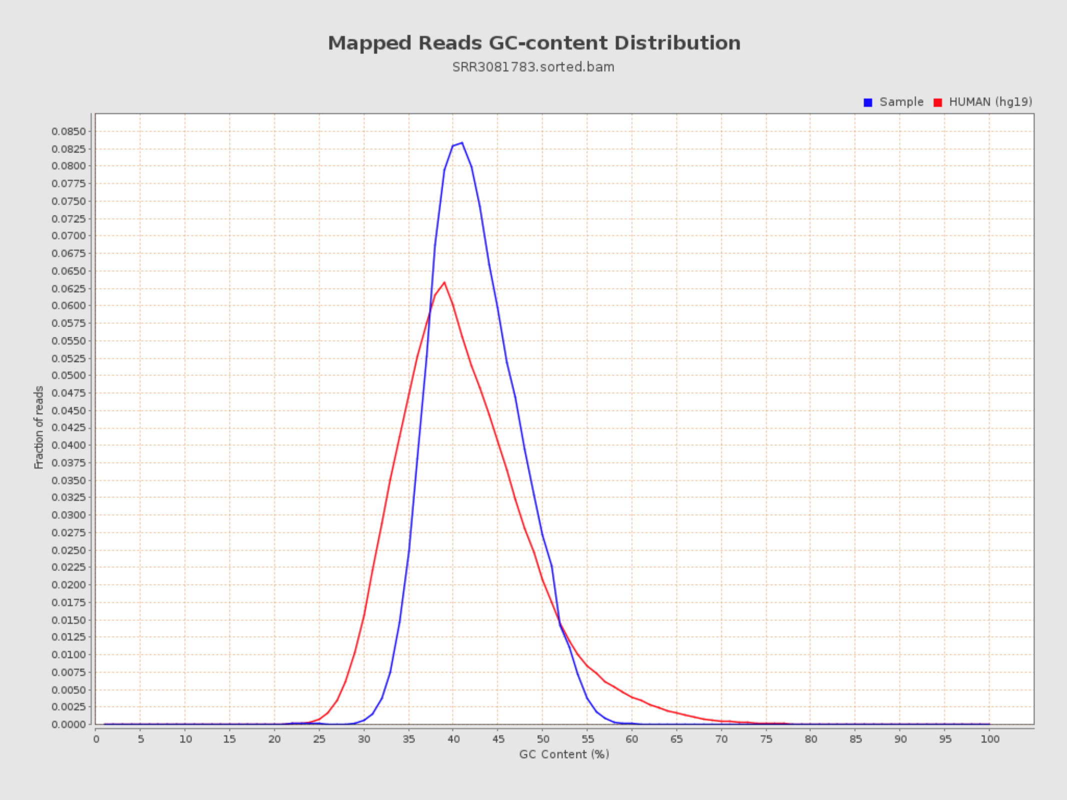
7. Results : Duplication Rate Histogram



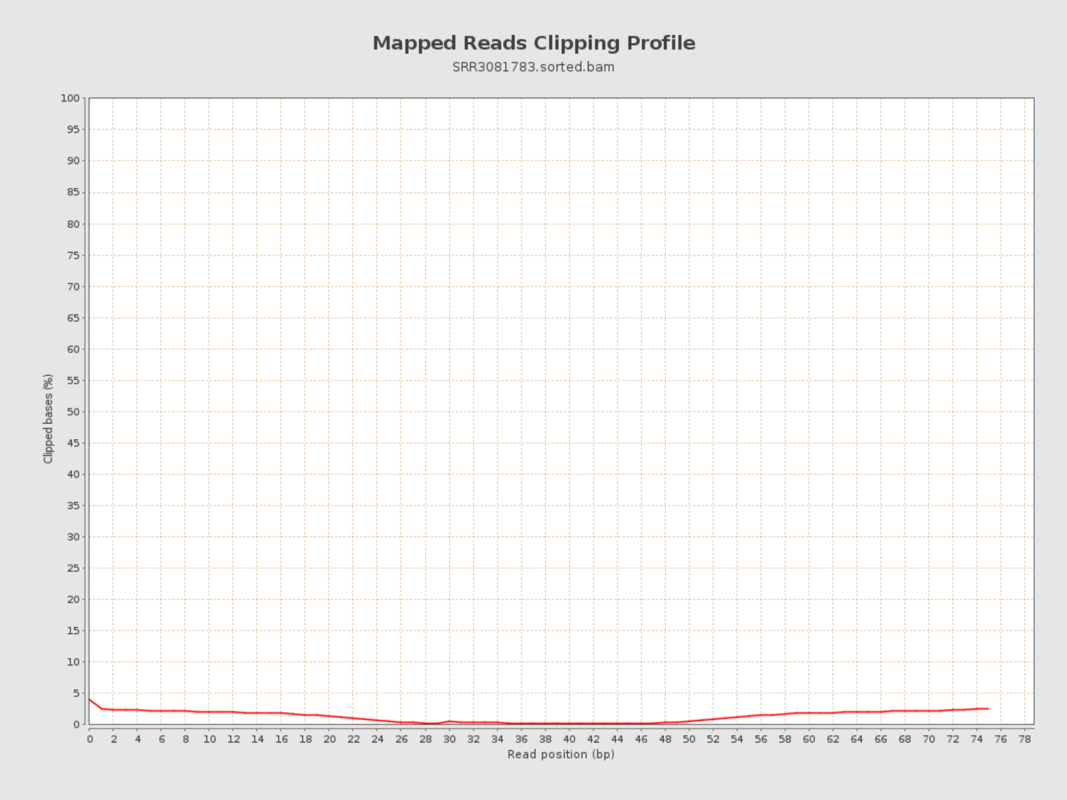
8. Results : Mapped Reads Nucleotide Content



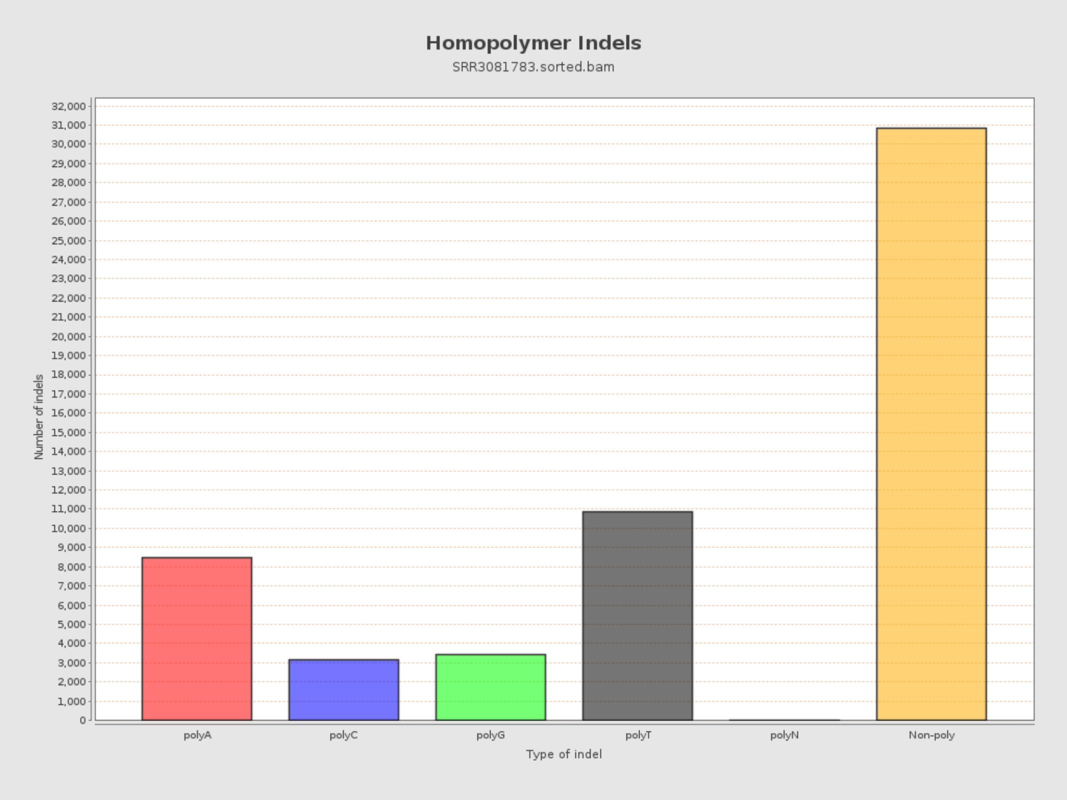
9. Results : Mapped Reads GC-content Distribution



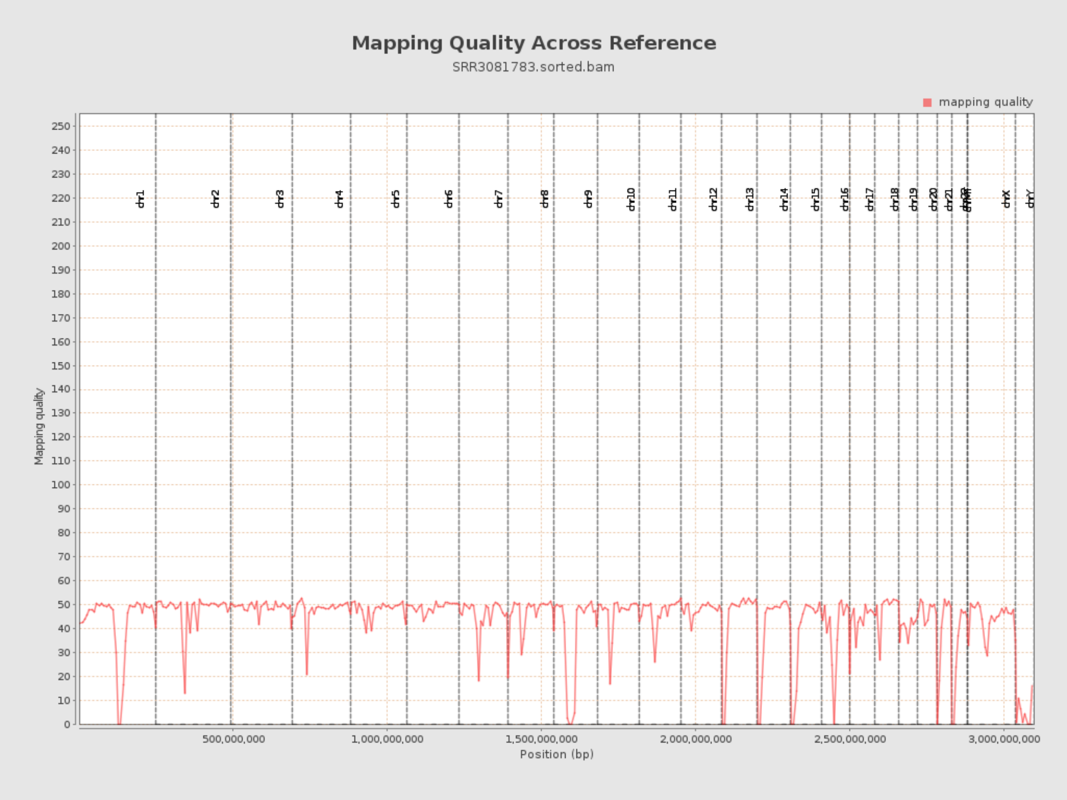
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram