Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 17:02:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081028.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_SRR3081028 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081028.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 17:01:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081028.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,826,137
Mapped reads	2,111,606 / 74.72%
Unmapped reads	714,531 / 25.28%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,573 / 0.37%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	71,917 / 2.54%
Duplication rate	2.84%
Clipped reads	1,342,607 / 47.51%

2.2. ACGT Content

Number/percentage of A's	37,315,901 / 28.84%
Number/percentage of C's	26,064,513 / 20.14%
Number/percentage of T's	37,614,150 / 29.07%
Number/percentage of G's	28,398,771 / 21.95%
Number/percentage of N's	1,605 / 0%
GC Percentage	42.09%

2.3. Coverage

Mean	0.0418

Standard Deviation	0.2854

2.4. Mapping Quality

Mean Mapping Quality	45.21

2.5. Mismatches and indels

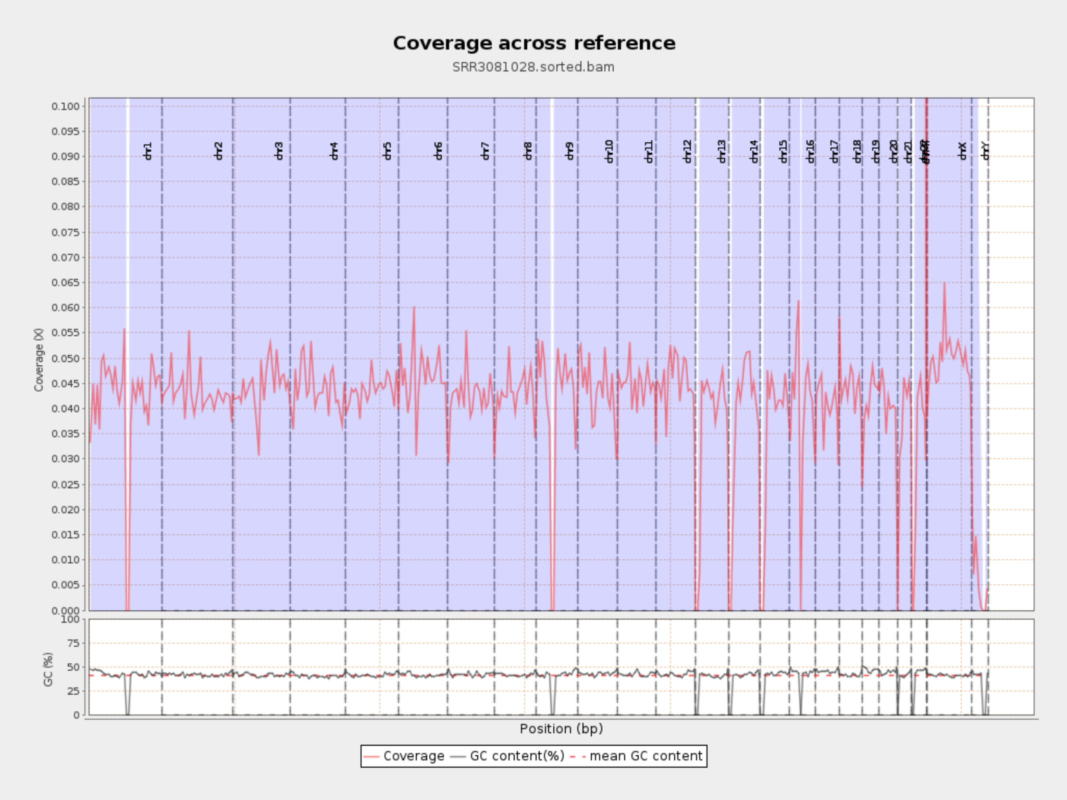
General error rate	0.74%
Mismatches	943,298
Insertions	8,482
Mapped reads with at least one insertion	0.4%
Deletions	24,735
Mapped reads with at least one deletion	1.16%
Homopolymer indels	45.56%

2.6. Chromosome stats

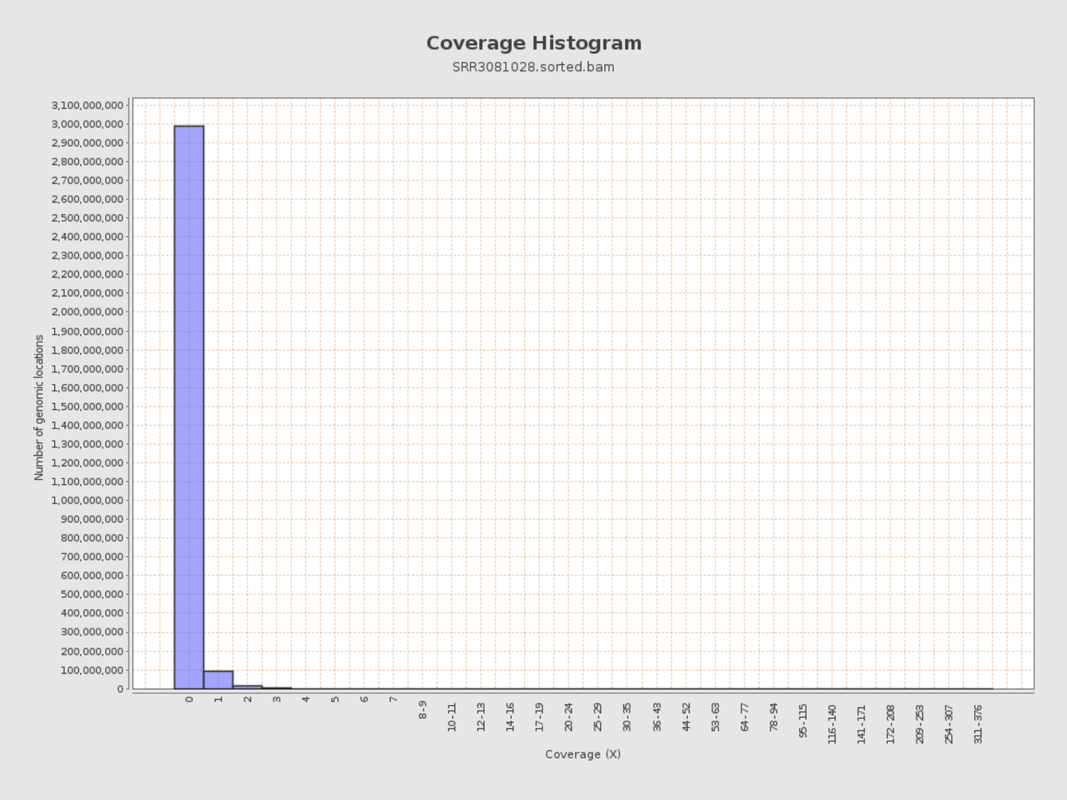
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10338142	0.0415	0.3827
chr2	243199373	10533498	0.0433	0.3118
chr3	198022430	8799584	0.0444	0.2431
chr4	191154276	8396585	0.0439	0.252
chr5	180915260	7919800	0.0438	0.2406
chr6	171115067	7916847	0.0463	0.2871
chr7	159138663	6798968	0.0427	0.3427

chr8	146364022	6310635	0.0431	0.3039
chr9	141213431	5787009	0.041	0.2876
chr10	135534747	5975090	0.0441	0.2787
chr11	135006516	6040119	0.0447	0.2868
chr12	133851895	6119895	0.0457	0.2472
chr13	115169878	4112637	0.0357	0.2172
chr14	107349540	3995533	0.0372	0.2317
chr15	102531392	3584188	0.035	0.228
chr16	90354753	3672295	0.0406	0.2481
chr17	81195210	3296808	0.0406	0.2478
chr18	78077248	3484011	0.0446	0.4516
chr19	59128983	2478373	0.0419	0.3191
chr20	63025520	2568328	0.0408	0.2363
chr21	48129895	1734821	0.036	0.2266
chr22	51304566	1472127	0.0287	0.1931
chrMT	16571	26372	1.5915	1.4596
chrX	155270560	7752862	0.0499	0.2791
chrY	59373566	322718	0.0054	0.1103

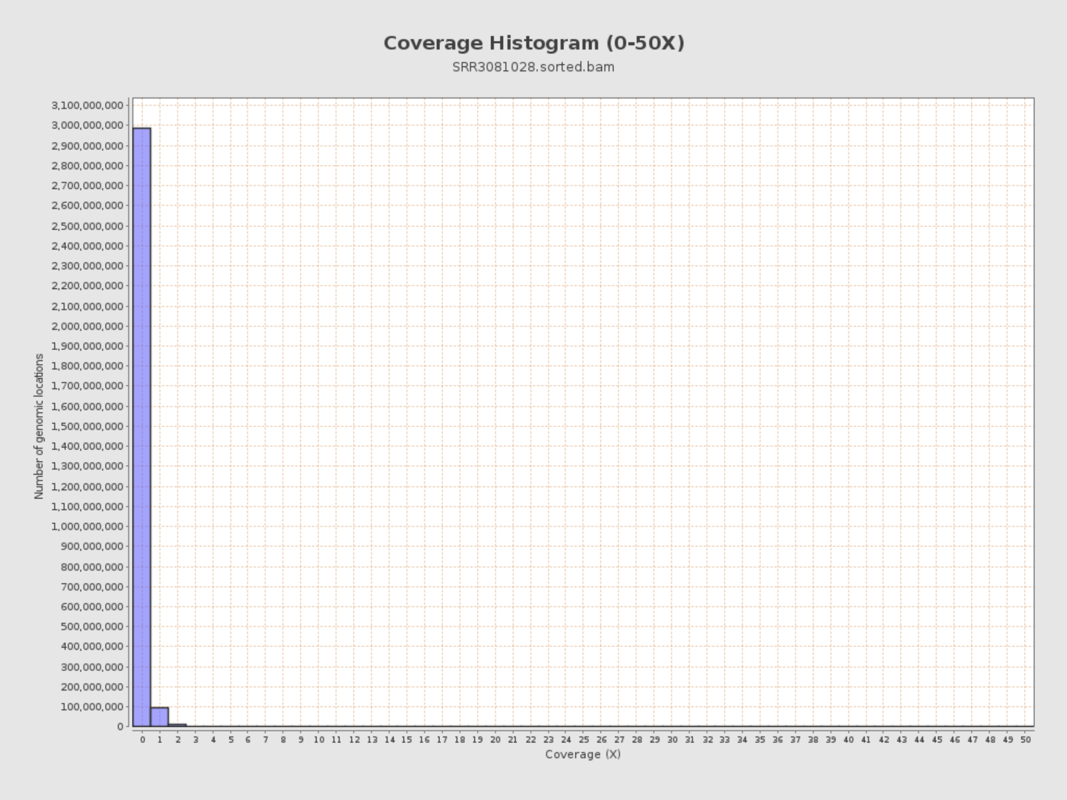
3. Results : Coverage across reference



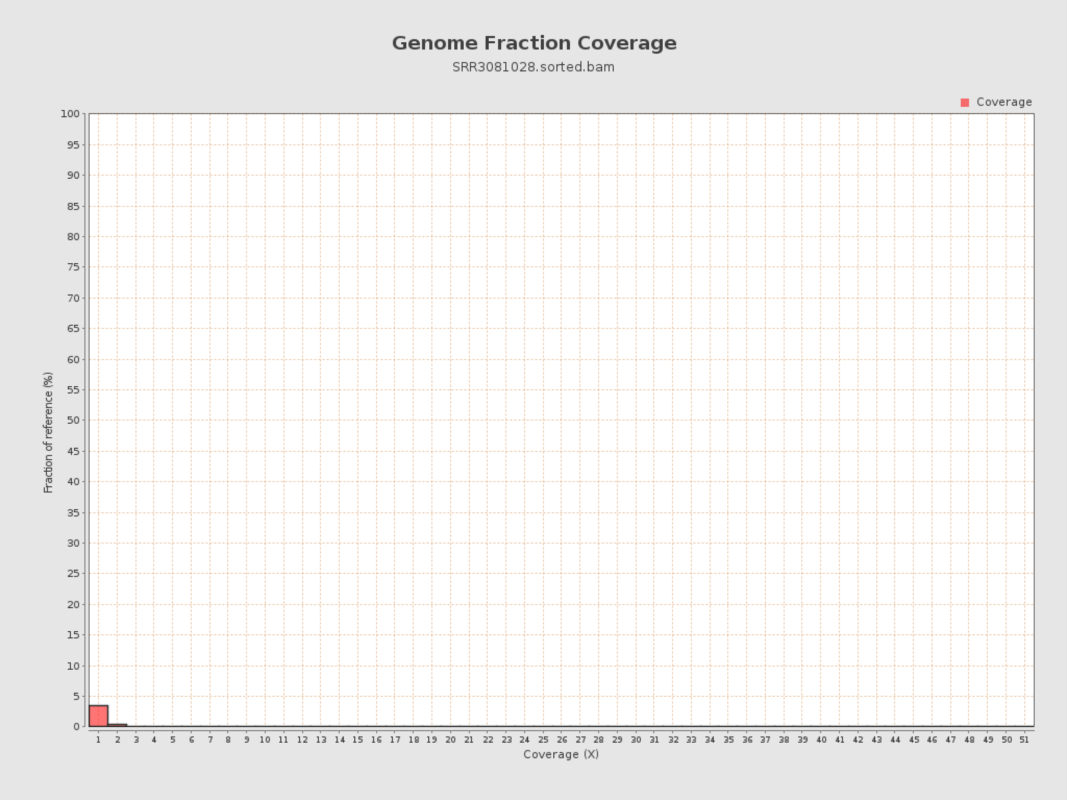
4. Results : Coverage Histogram



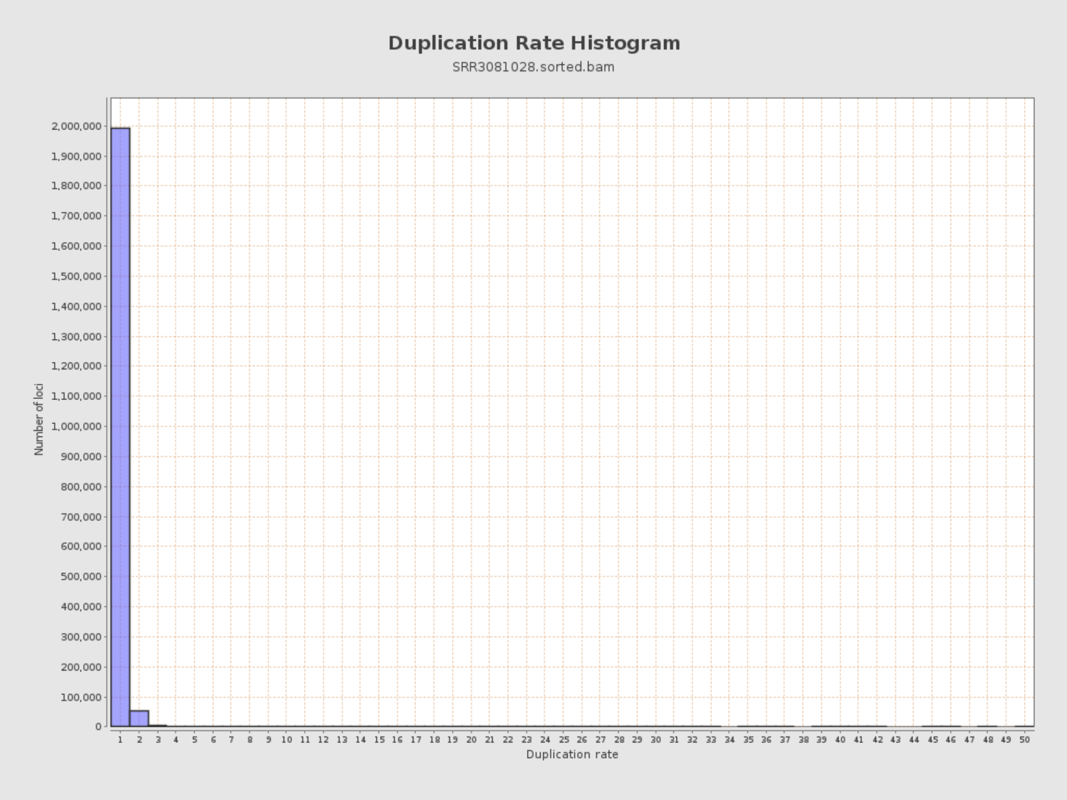
5. Results : Coverage Histogram (0-50X)



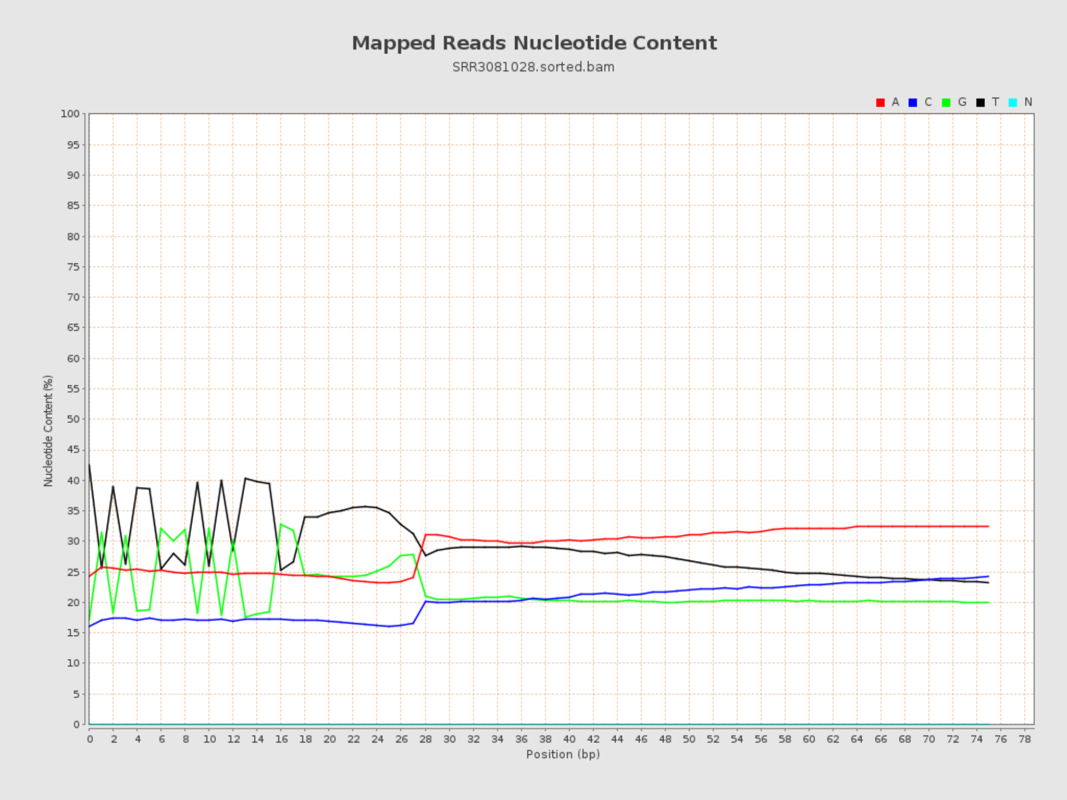
6. Results : Genome Fraction Coverage



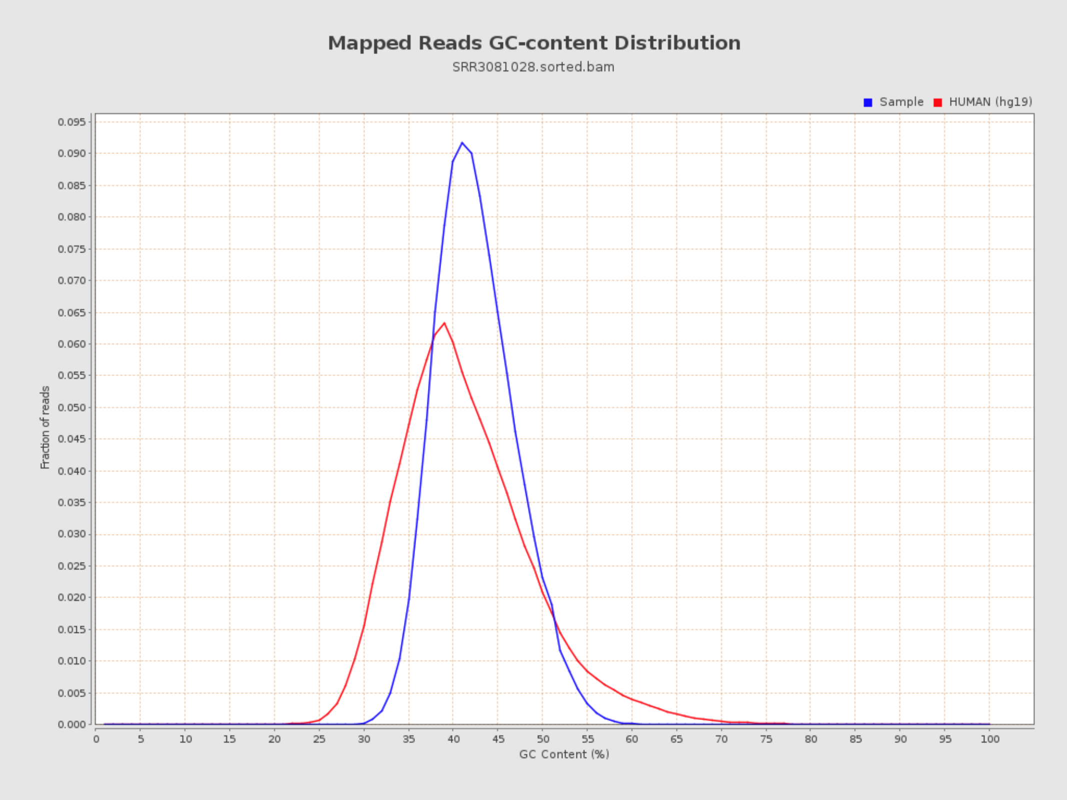
7. Results : Duplication Rate Histogram



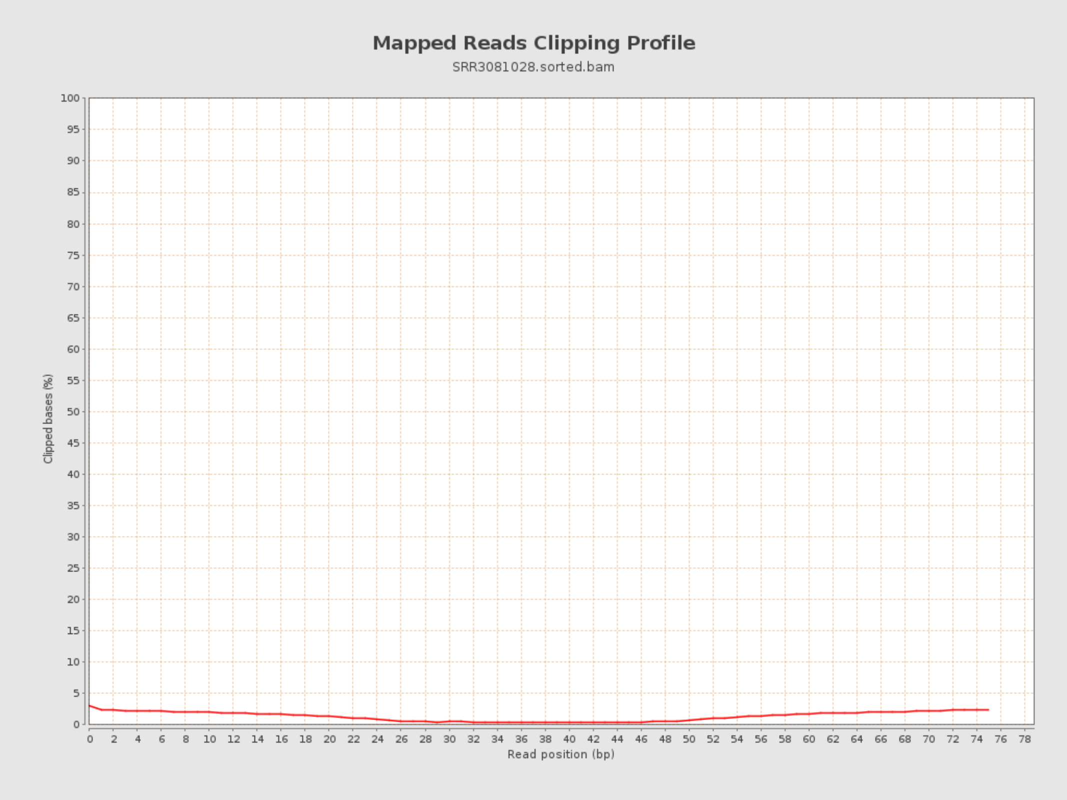
8. Results : Mapped Reads Nucleotide Content



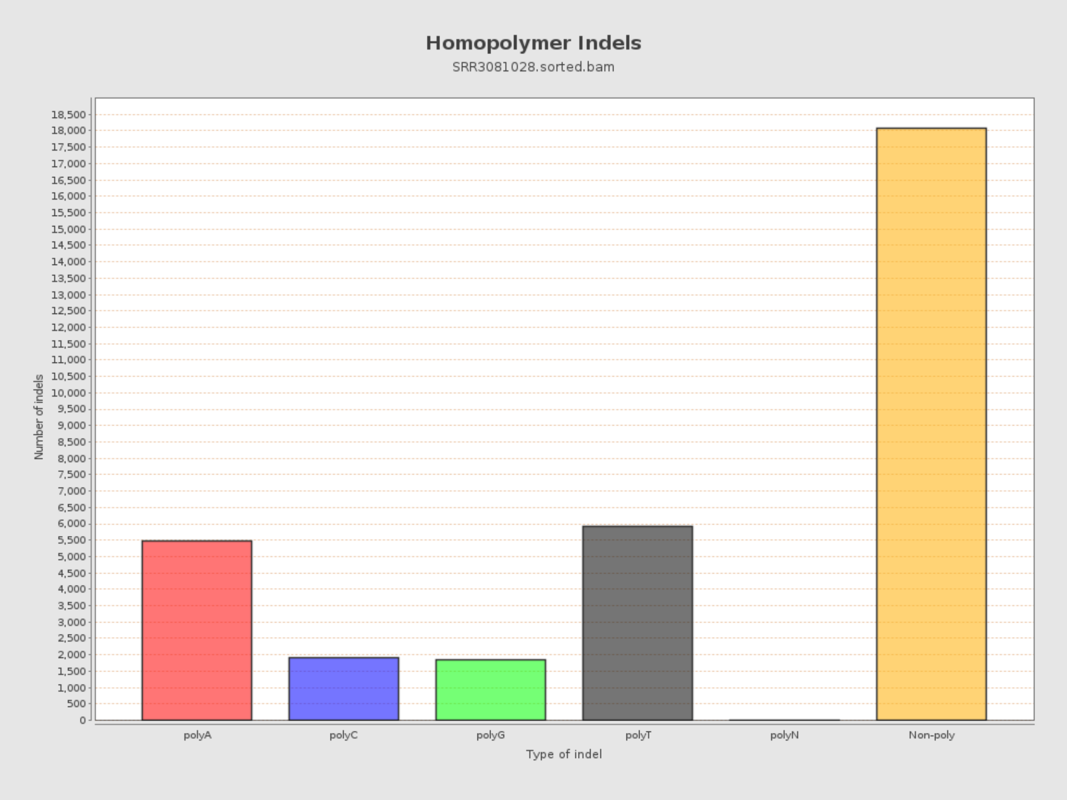
9. Results : Mapped Reads GC-content Distribution



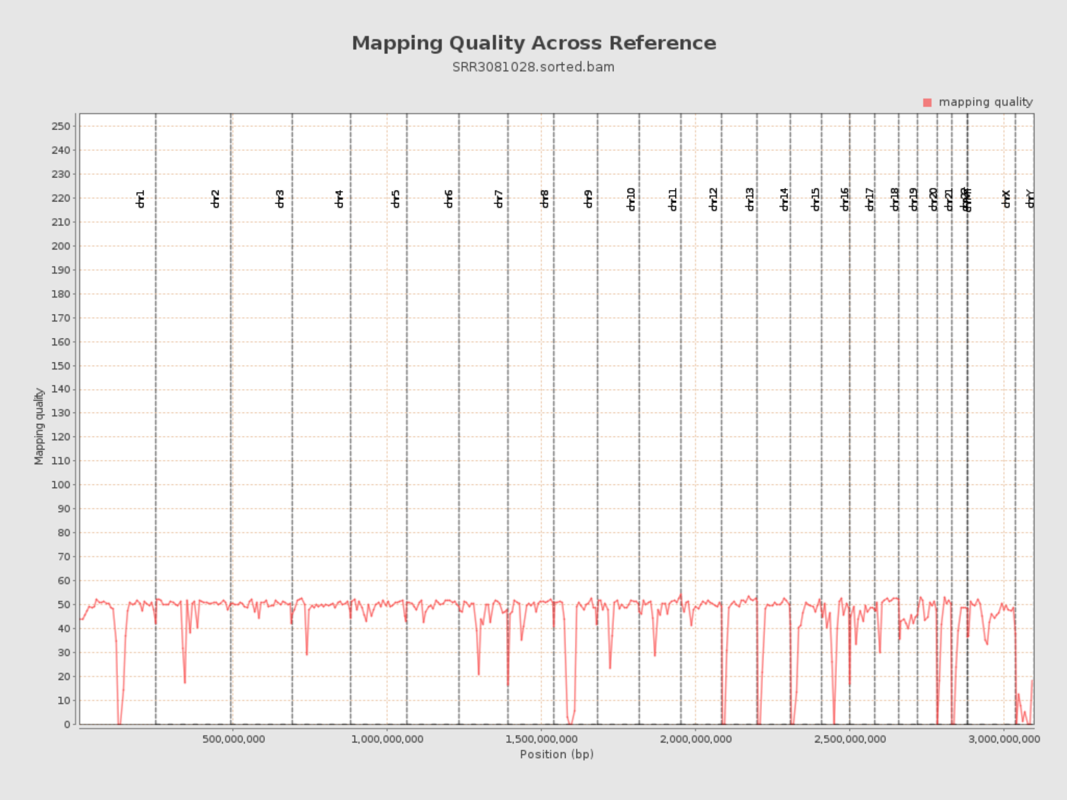
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram