Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 03:09:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081218.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_SRR3081218 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081218.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 03:09:15 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081218.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,182,951
Mapped reads	2,823,935 / 88.72%
Unmapped reads	359,016 / 11.28%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	30,464 / 0.96%
Read min/max/mean length	30 / 76 / 76.33
Duplicated reads (estimated)	140,198 / 4.4%
Duplication rate	3.97%
Clipped reads	1,503,760 / 47.24%

2.2. ACGT Content

Number/percentage of A's	52,038,781 / 28.38%
Number/percentage of C's	35,090,046 / 19.13%
Number/percentage of T's	56,490,168 / 30.8%
Number/percentage of G's	39,755,293 / 21.68%
Number/percentage of N's	12,298 / 0.01%
GC Percentage	40.81%

2.3. Coverage

Mean	0.0593

Standard Deviation	0.4527

2.4. Mapping Quality

Mean Mapping Quality	45.19

2.5. Mismatches and indels

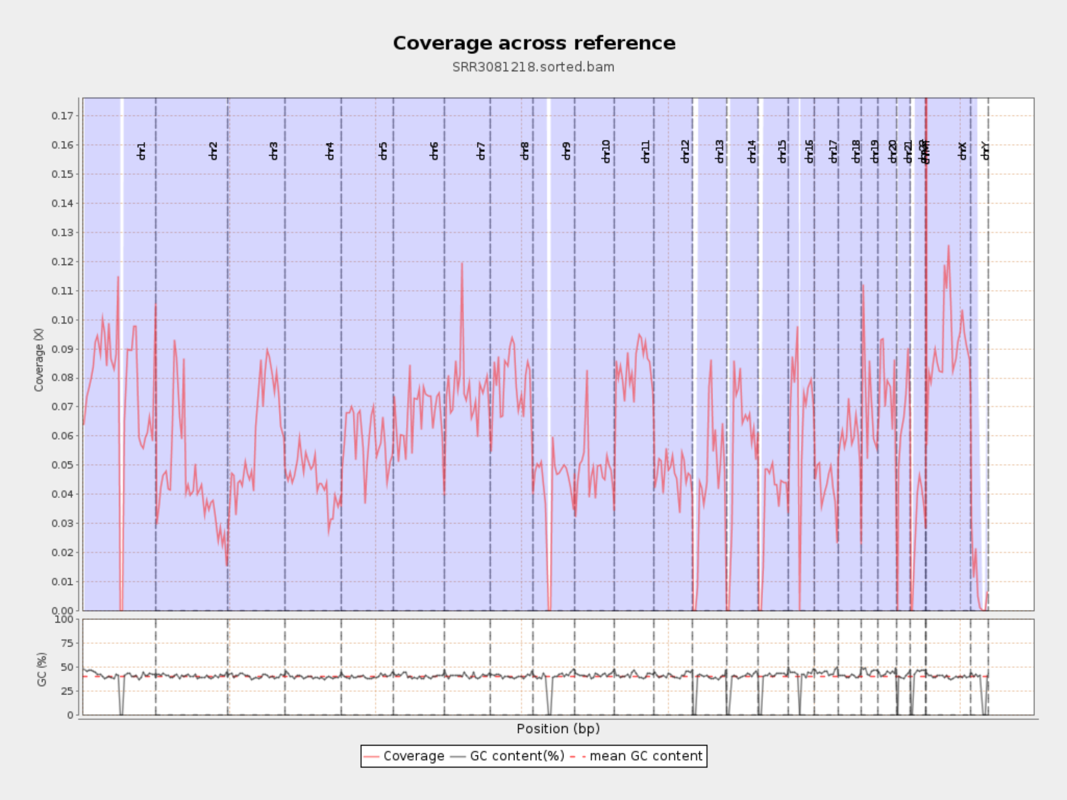
General error rate	0.91%
Mismatches	1,641,536
Insertions	13,706
Mapped reads with at least one insertion	0.48%
Deletions	41,990
Mapped reads with at least one deletion	1.47%
Homopolymer indels	47.82%

2.6. Chromosome stats

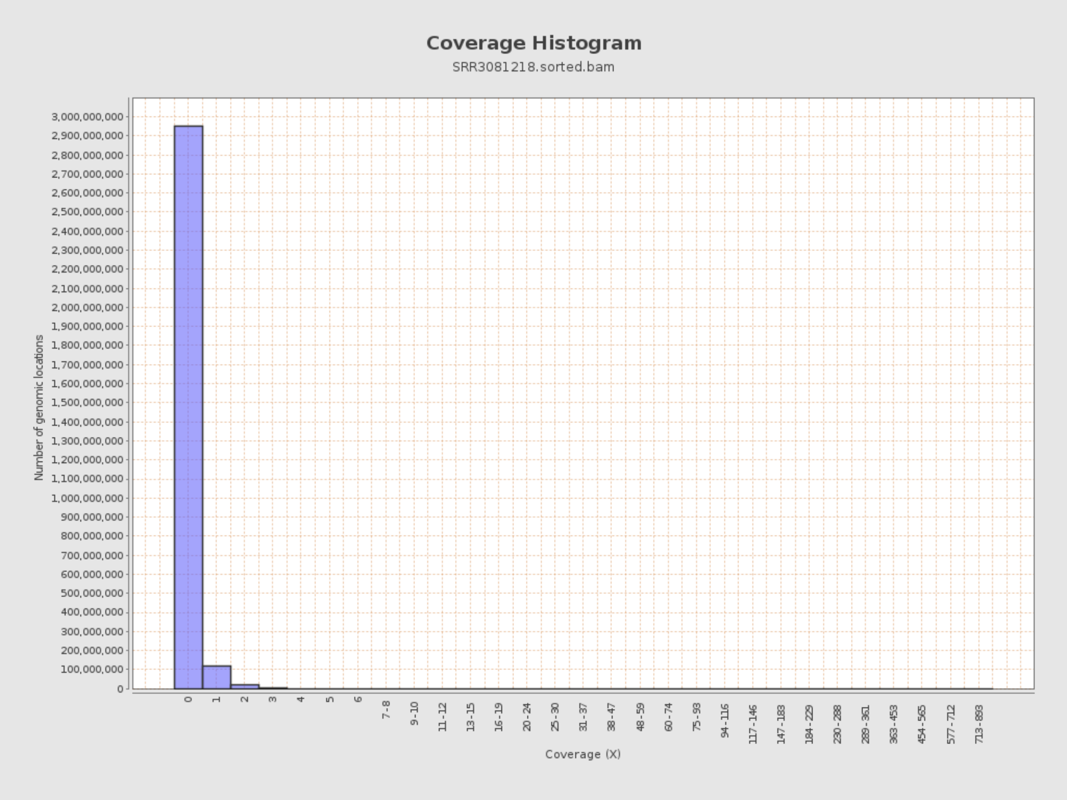
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	19076716	0.0765	0.841
chr2	243199373	10821868	0.0445	0.4855
chr3	198022430	11847282	0.0598	0.2958
chr4	191154276	8548094	0.0447	0.2622
chr5	180915260	10588626	0.0585	0.2905
chr6	171115067	11520131	0.0673	0.3797
chr7	159138663	11961867	0.0752	0.667

chr8	146364022	11405161	0.0779	0.5347
chr9	141213431	5919767	0.0419	0.3592
chr10	135534747	6596672	0.0487	0.4223
chr11	135006516	11179397	0.0828	0.5031
chr12	133851895	6348844	0.0474	0.2686
chr13	115169878	5153075	0.0447	0.2535
chr14	107349540	6137910	0.0572	0.3023
chr15	102531392	3714685	0.0362	0.233
chr16	90354753	6051178	0.067	0.3354
chr17	81195210	3501957	0.0431	0.2988
chr18	78077248	4706797	0.0603	0.565
chr19	59128983	4192201	0.0709	0.653
chr20	63025520	4881760	0.0775	0.3425
chr21	48129895	2973101	0.0618	0.3119
chr22	51304566	1482904	0.0289	0.1993
chrMT	16571	46652	2.8153	2.6539
chrX	155270560	14296172	0.0921	0.3994
chrY	59373566	502247	0.0085	0.1407

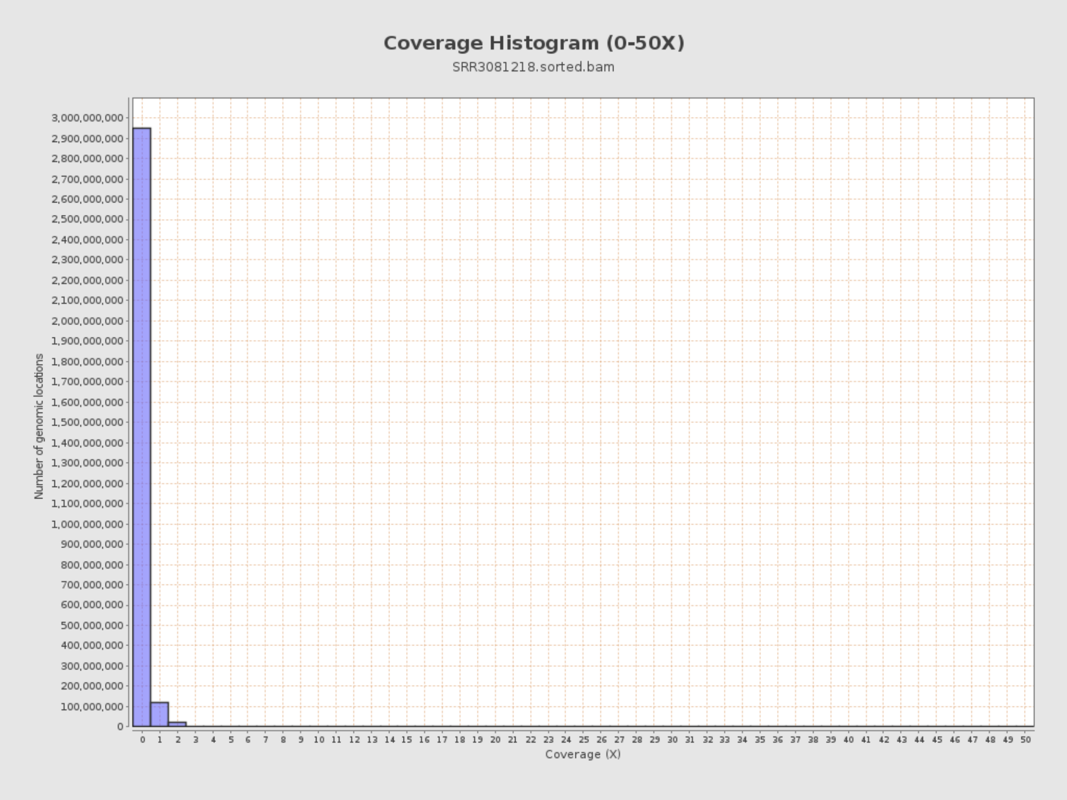
3. Results : Coverage across reference



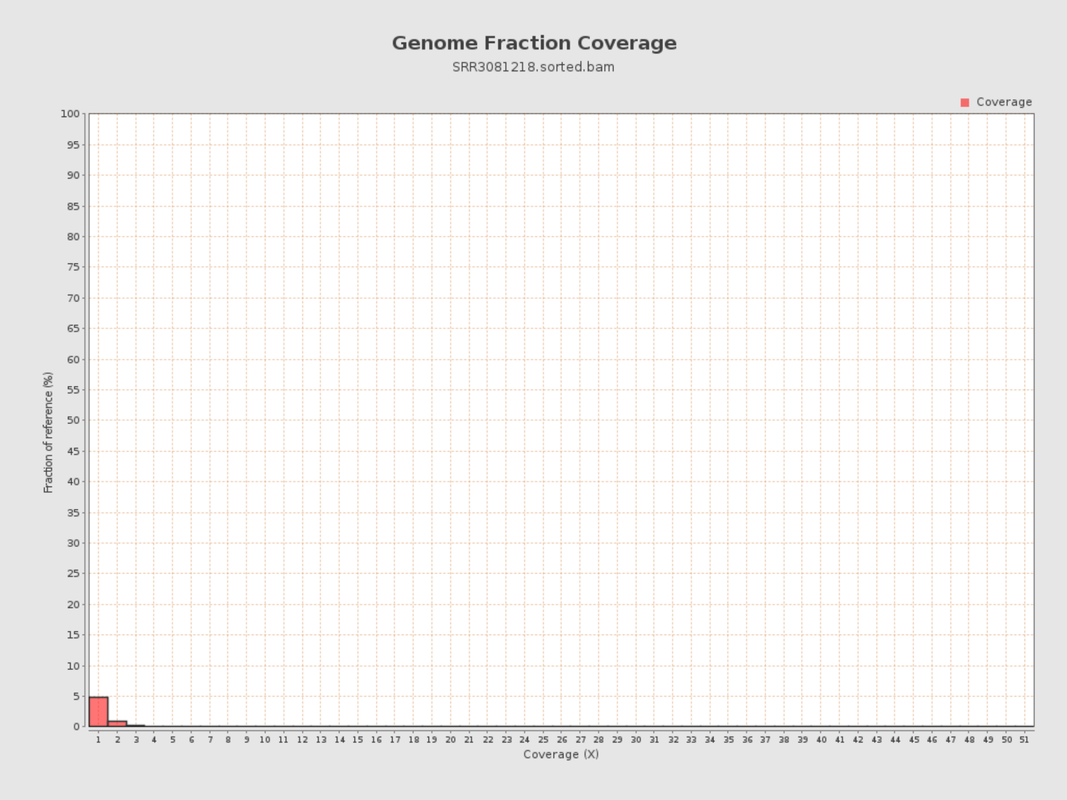
4. Results : Coverage Histogram



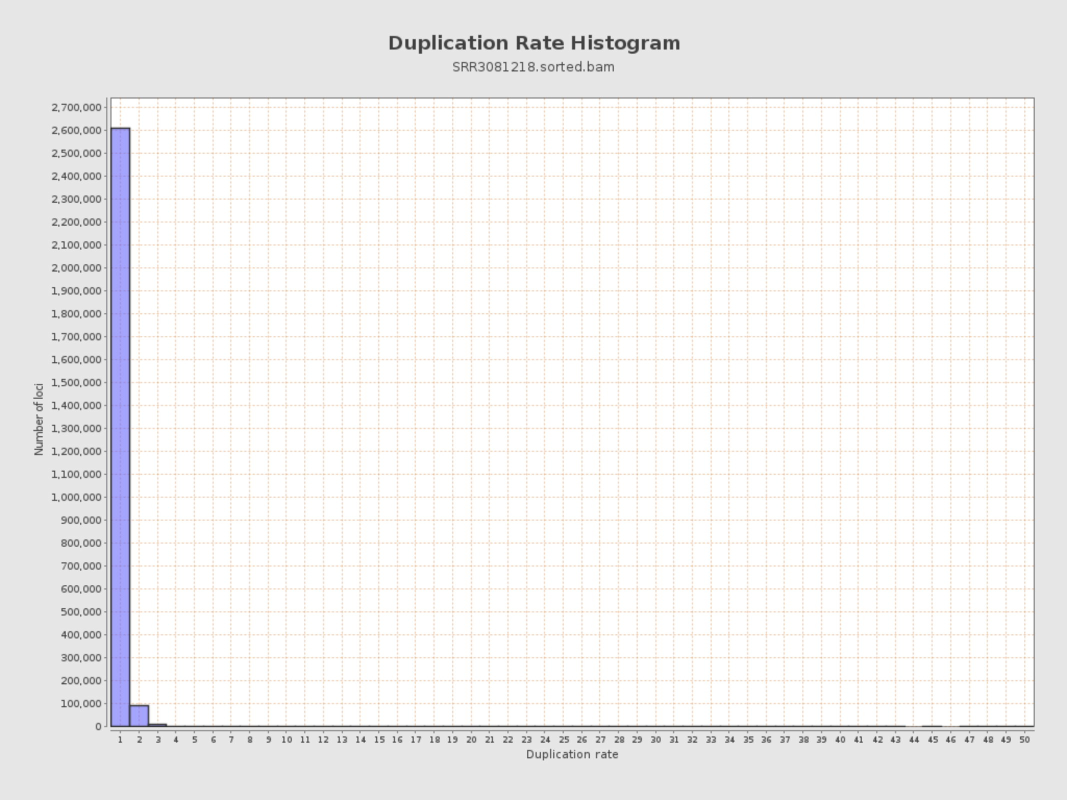
5. Results : Coverage Histogram (0-50X)



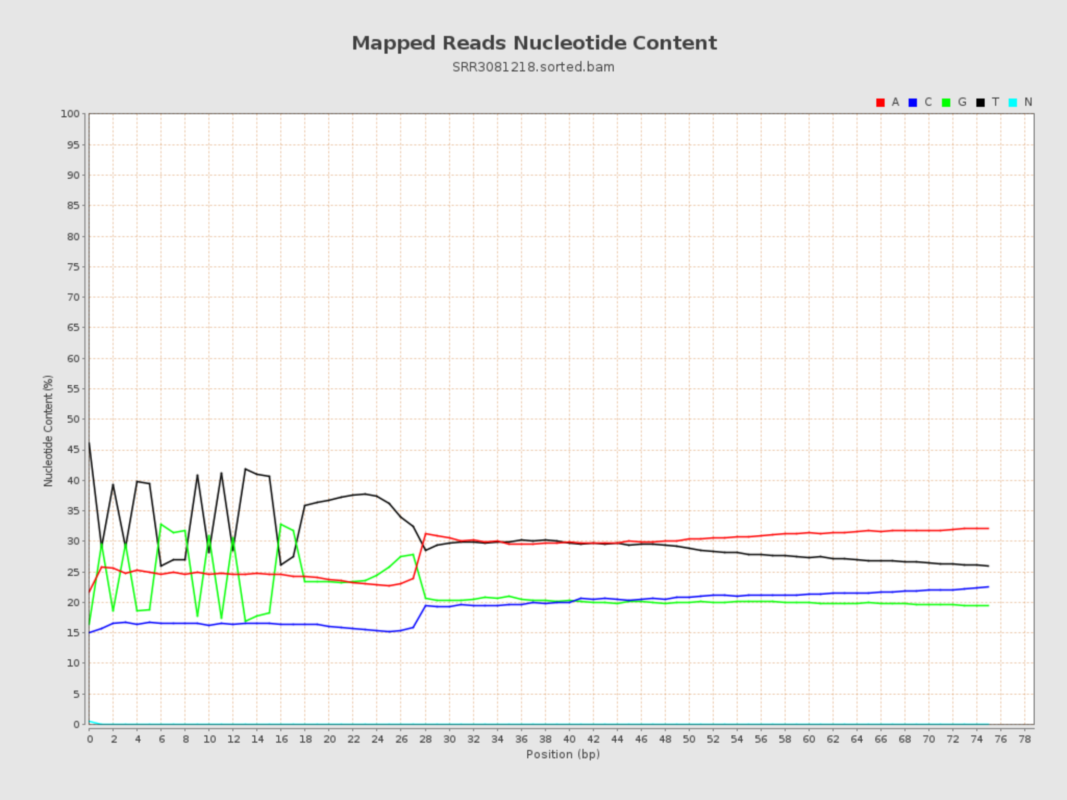
6. Results : Genome Fraction Coverage



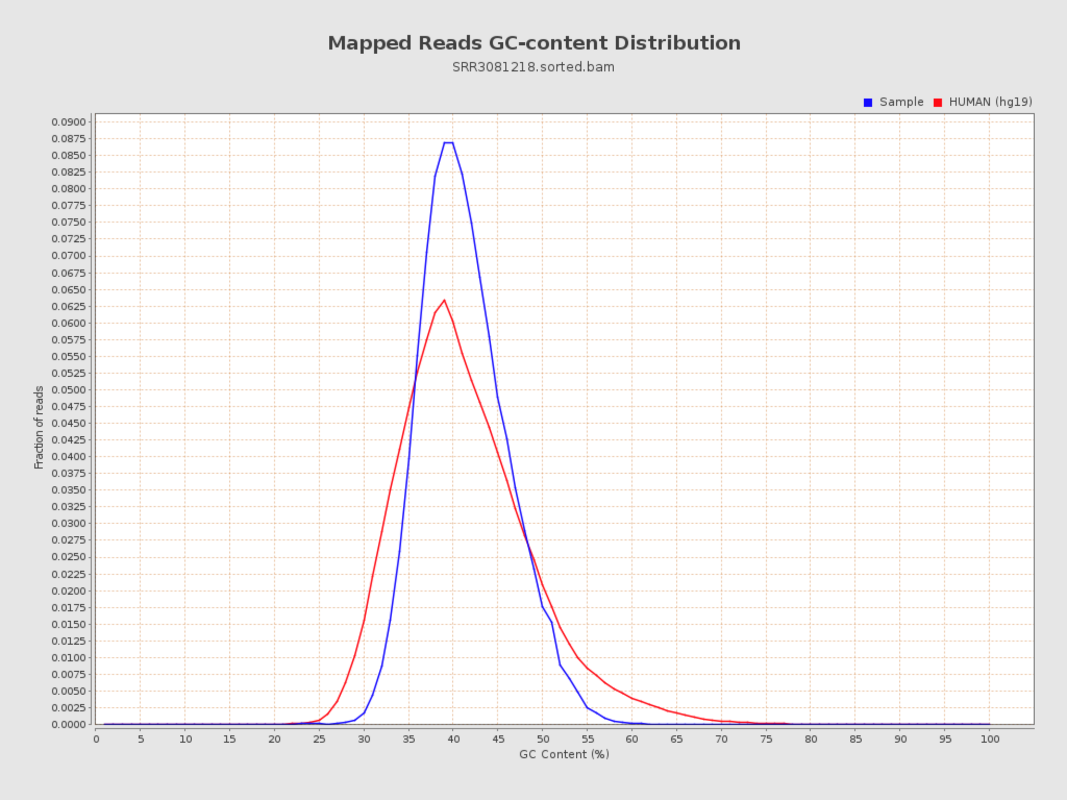
7. Results : Duplication Rate Histogram



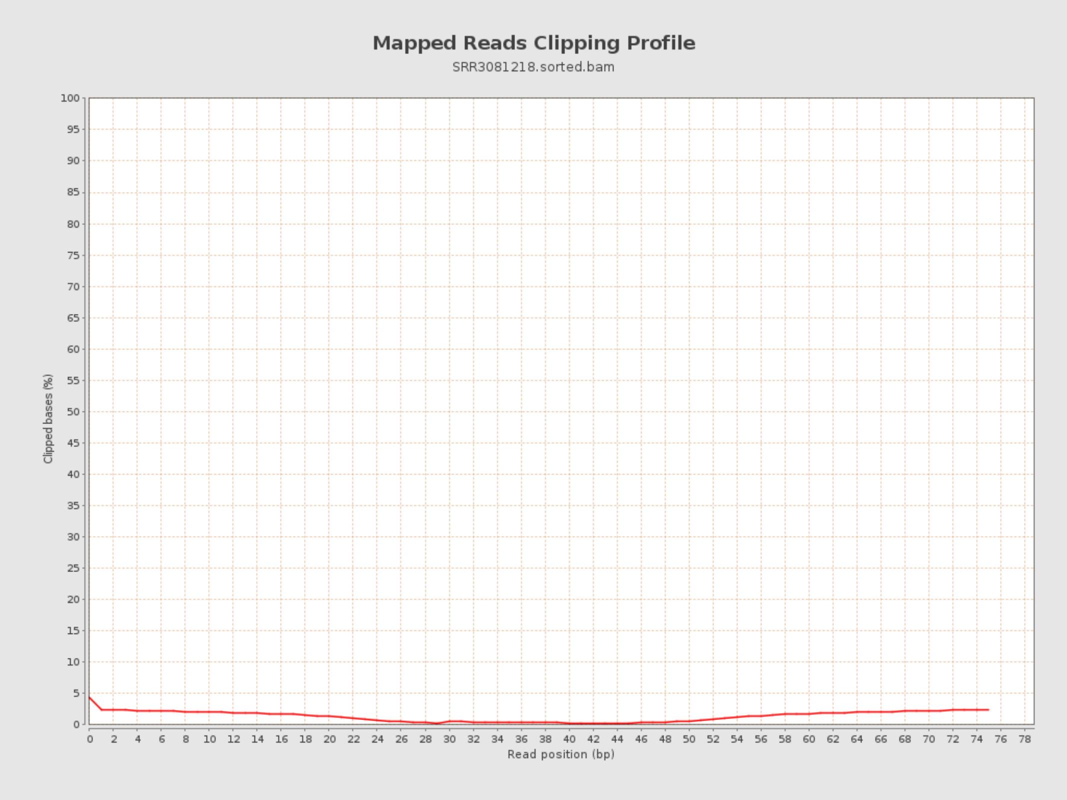
8. Results : Mapped Reads Nucleotide Content



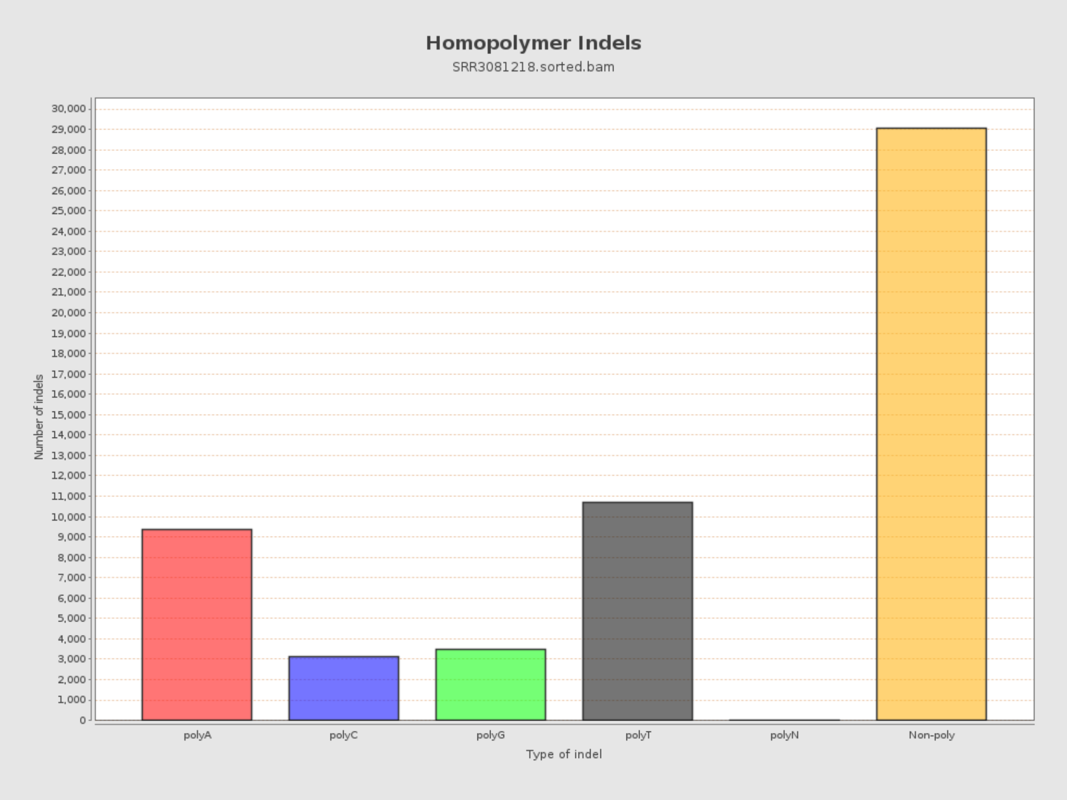
9. Results : Mapped Reads GC-content Distribution



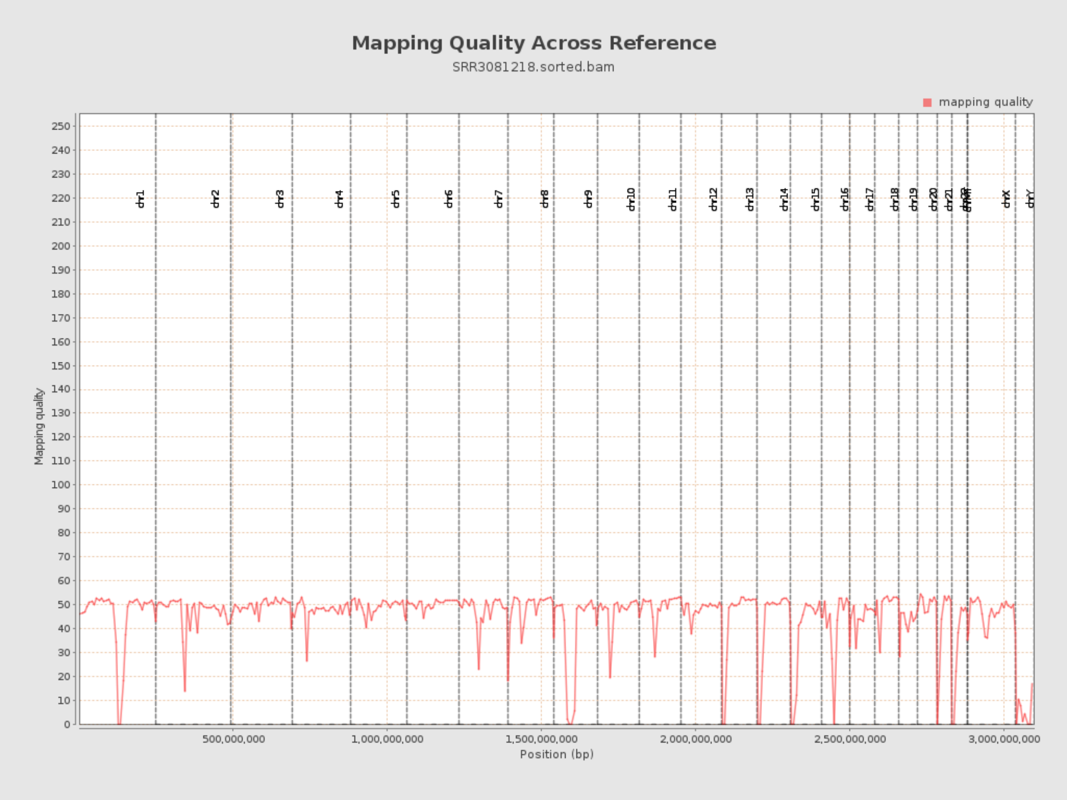
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram