Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 23:40:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081158.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_SRR3081158 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081158.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 23:40:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081158.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,488,690
Mapped reads	2,260,008 / 90.81%
Unmapped reads	228,682 / 9.19%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	25,219 / 1.01%
Read min/max/mean length	30 / 76 / 76.36
Duplicated reads (estimated)	90,407 / 3.63%
Duplication rate	3.23%
Clipped reads	973,525 / 39.12%

2.2. ACGT Content

Number/percentage of A's	43,783,419 / 28.68%
Number/percentage of C's	28,257,991 / 18.51%
Number/percentage of T's	47,993,368 / 31.44%
Number/percentage of G's	32,586,862 / 21.34%
Number/percentage of N's	45,920 / 0.03%
GC Percentage	39.85%

2.3. Coverage

Mean	0.0493

Standard Deviation	0.3773

2.4. Mapping Quality

Mean Mapping Quality	47.23

2.5. Mismatches and indels

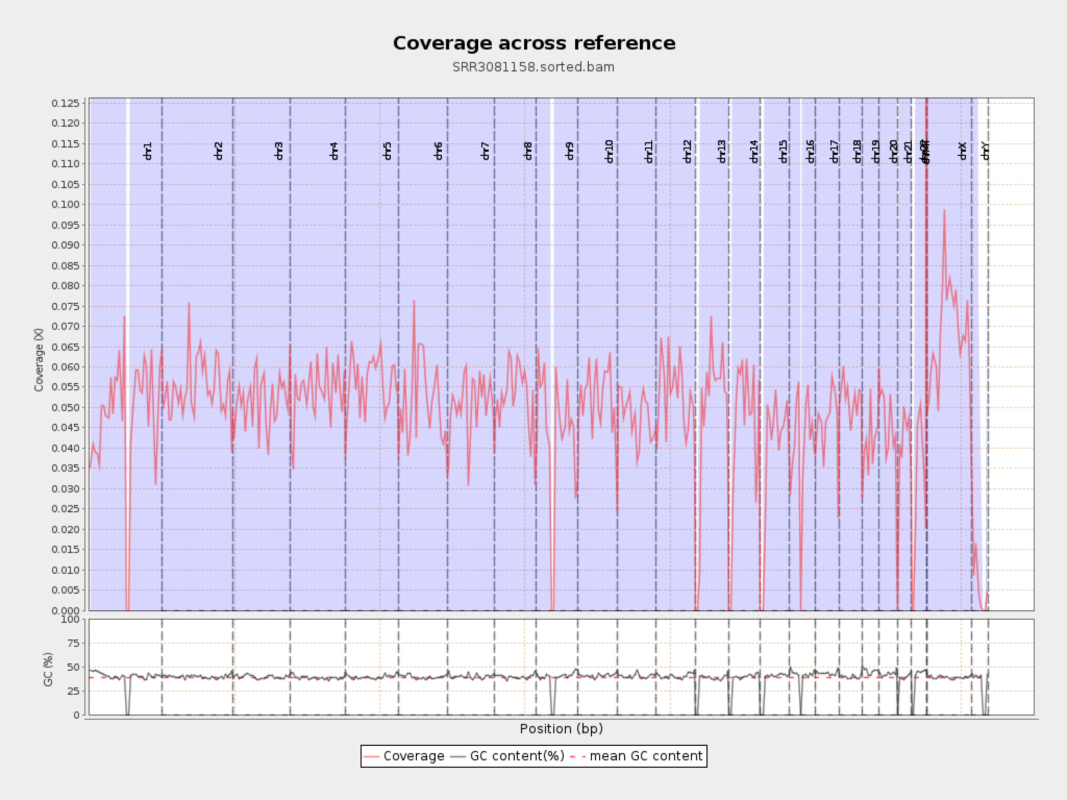
General error rate	0.83%
Mismatches	1,251,206
Insertions	11,889
Mapped reads with at least one insertion	0.52%
Deletions	35,765
Mapped reads with at least one deletion	1.57%
Homopolymer indels	47.64%

2.6. Chromosome stats

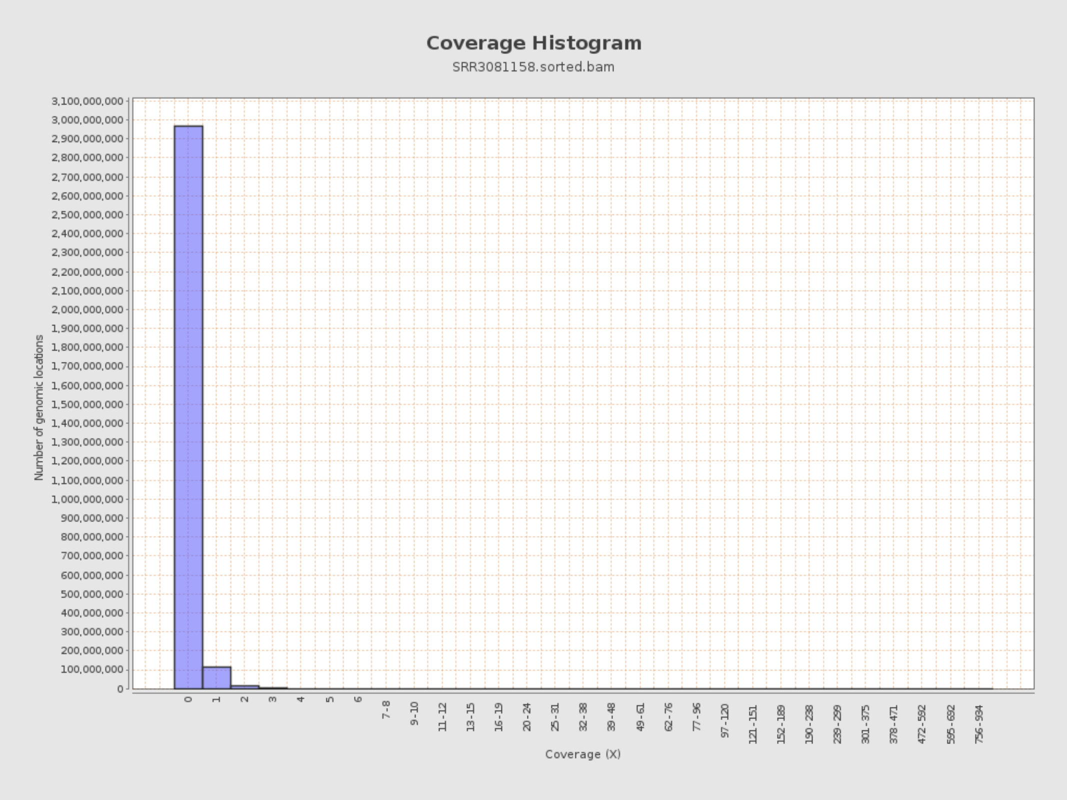
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11895575	0.0477	0.6016
chr2	243199373	13400754	0.0551	0.428
chr3	198022430	10158181	0.0513	0.2555
chr4	191154276	10299512	0.0539	0.2704
chr5	180915260	10270019	0.0568	0.2703
chr6	171115067	8813019	0.0515	0.3495
chr7	159138663	8105350	0.0509	0.4304

chr8	146364022	7691807	0.0526	0.6047
chr9	141213431	6184956	0.0438	0.3492
chr10	135534747	7158551	0.0528	0.3272
chr11	135006516	6421334	0.0476	0.3221
chr12	133851895	7117947	0.0532	0.266
chr13	115169878	5469694	0.0475	0.2465
chr14	107349540	4615160	0.043	0.2527
chr15	102531392	3918635	0.0382	0.2278
chr16	90354753	3652892	0.0404	0.2644
chr17	81195210	3756506	0.0463	0.2692
chr18	78077248	4091772	0.0524	0.6859
chr19	59128983	2471081	0.0418	0.4389
chr20	63025520	2838287	0.045	0.2471
chr21	48129895	1873703	0.0389	0.2386
chr22	51304566	1480631	0.0289	0.1898
chrMT	16571	10957	0.6612	0.9931
chrX	155270560	10645211	0.0686	0.3364
chrY	59373566	384034	0.0065	0.1177

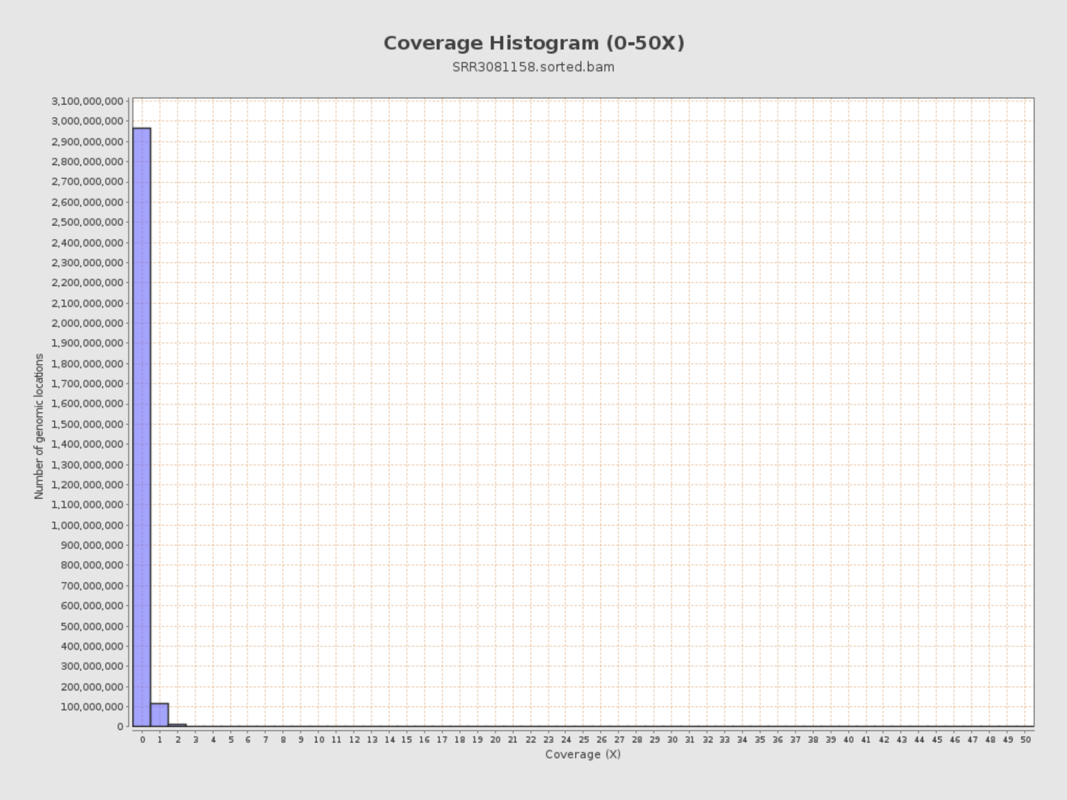
3. Results : Coverage across reference



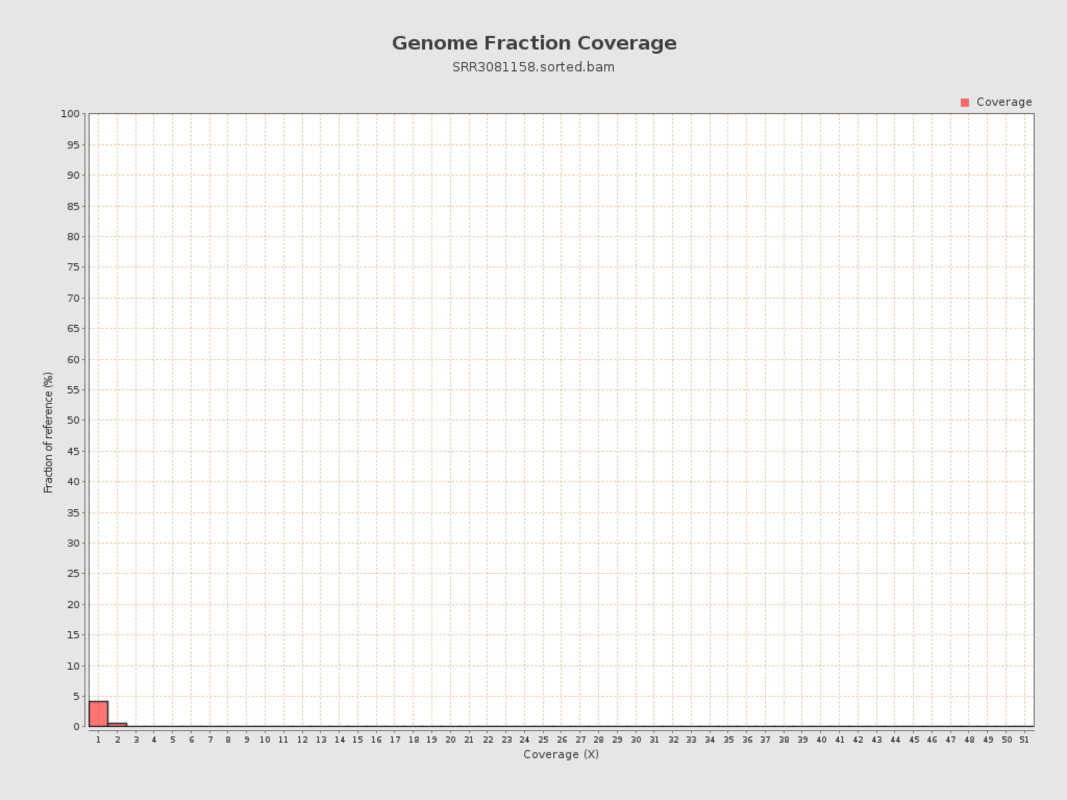
4. Results : Coverage Histogram



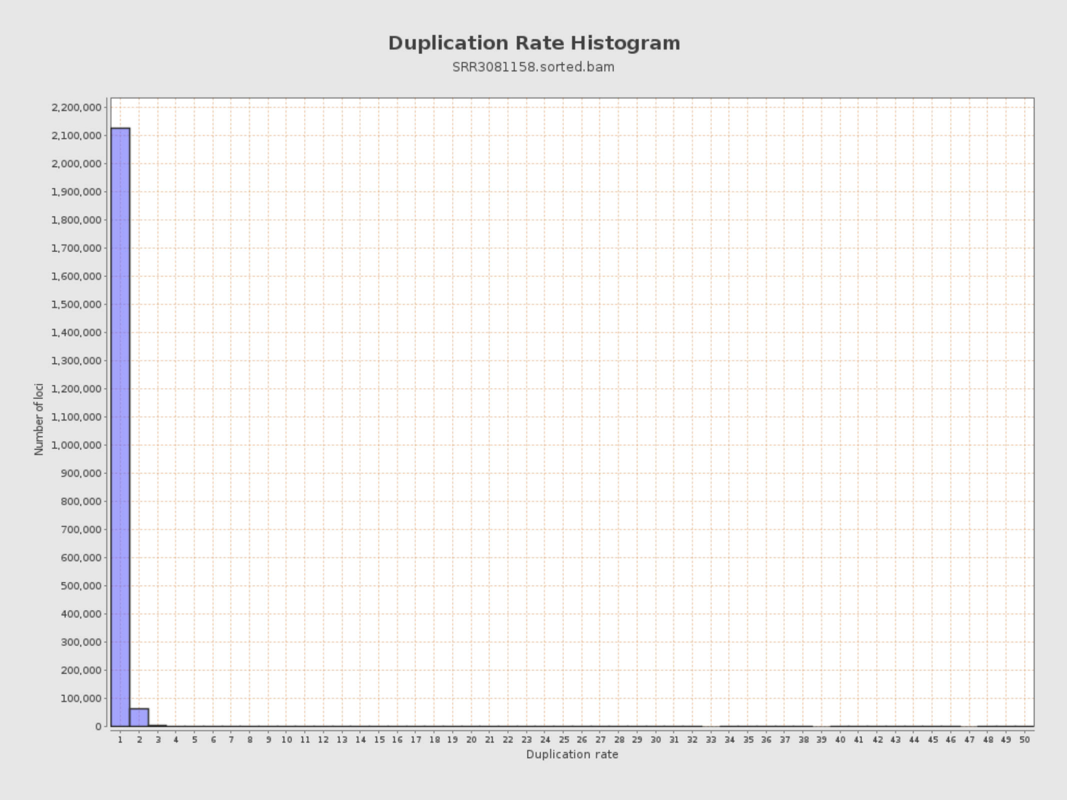
5. Results : Coverage Histogram (0-50X)



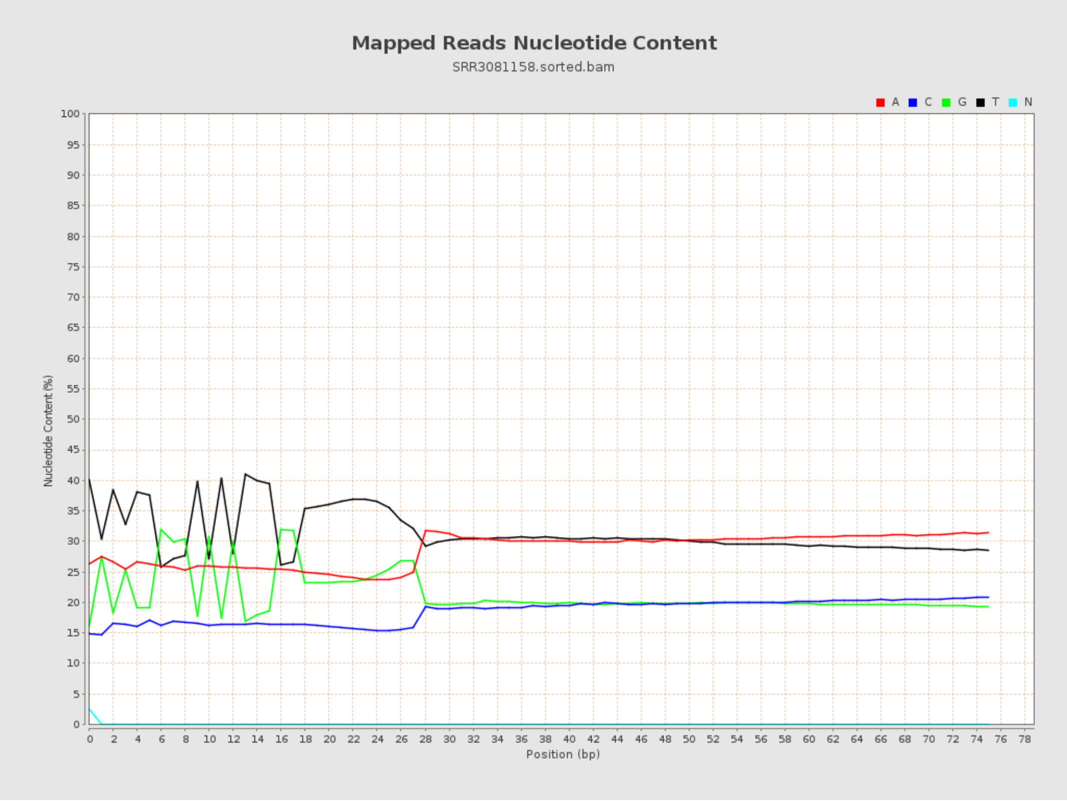
6. Results : Genome Fraction Coverage



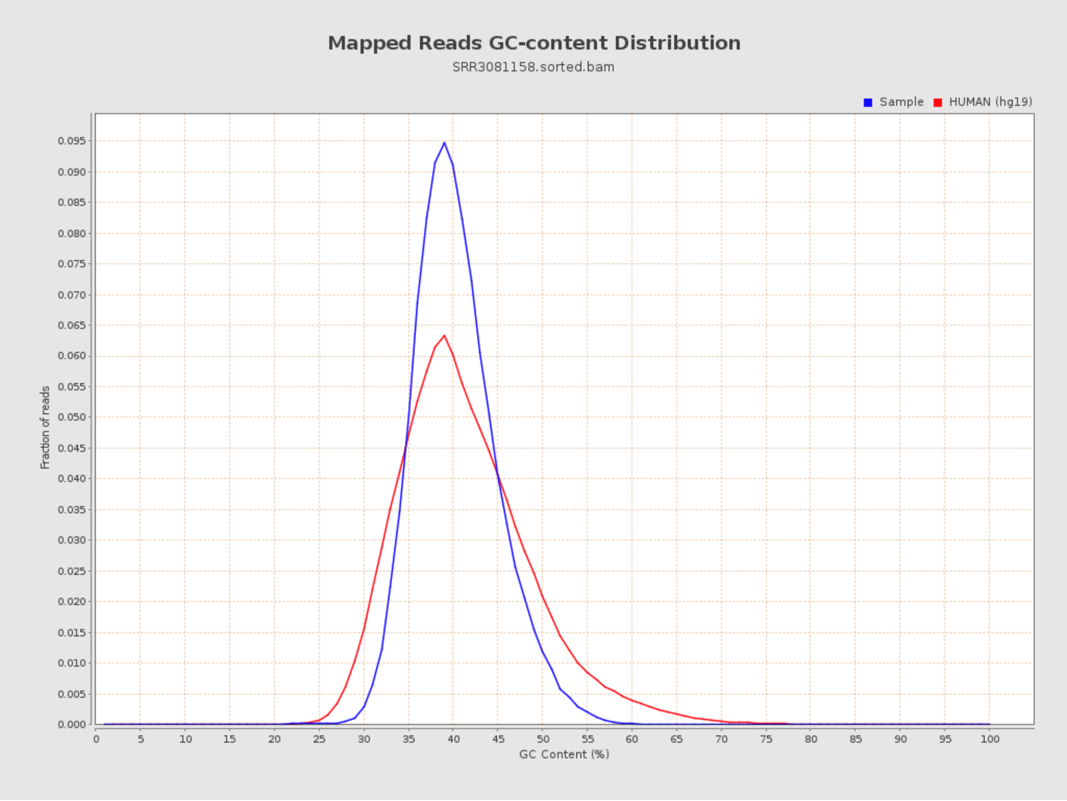
7. Results : Duplication Rate Histogram



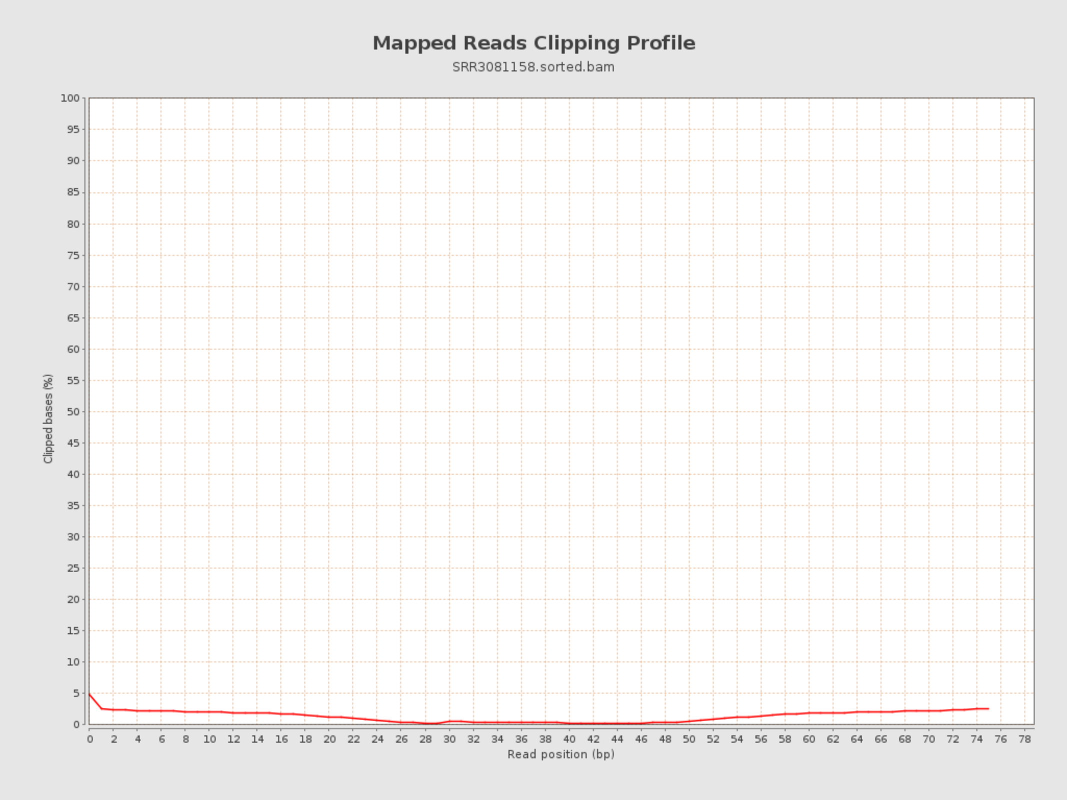
8. Results : Mapped Reads Nucleotide Content



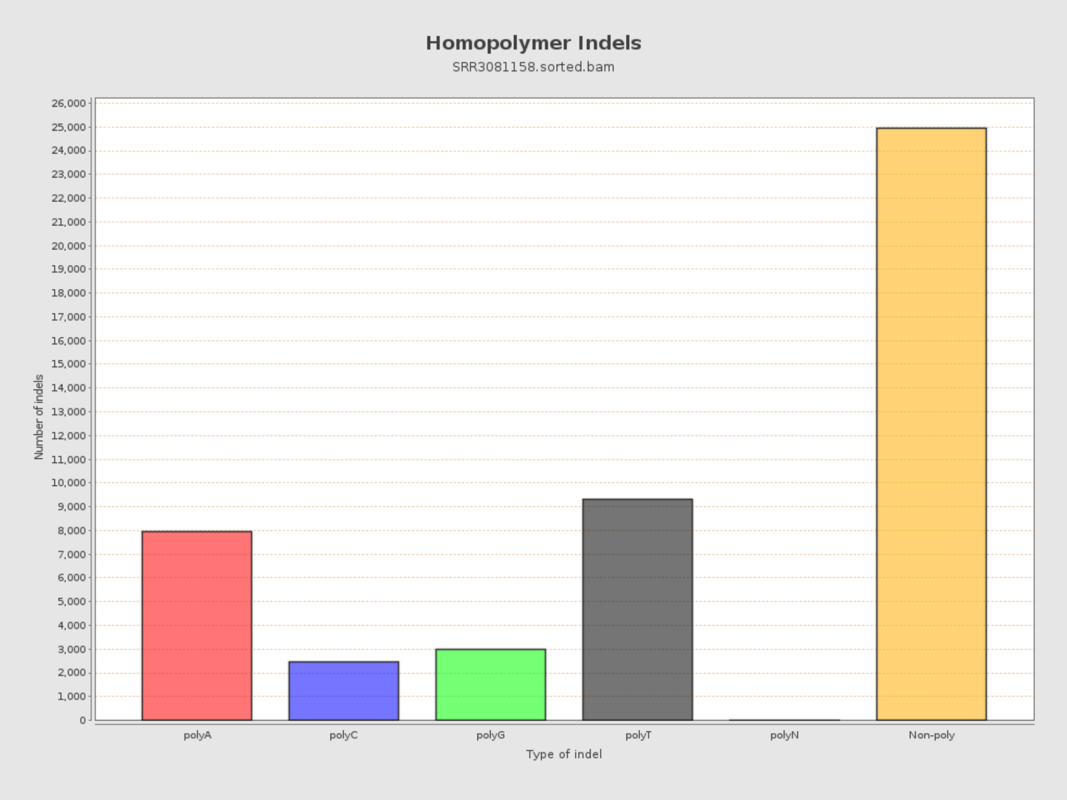
9. Results : Mapped Reads GC-content Distribution



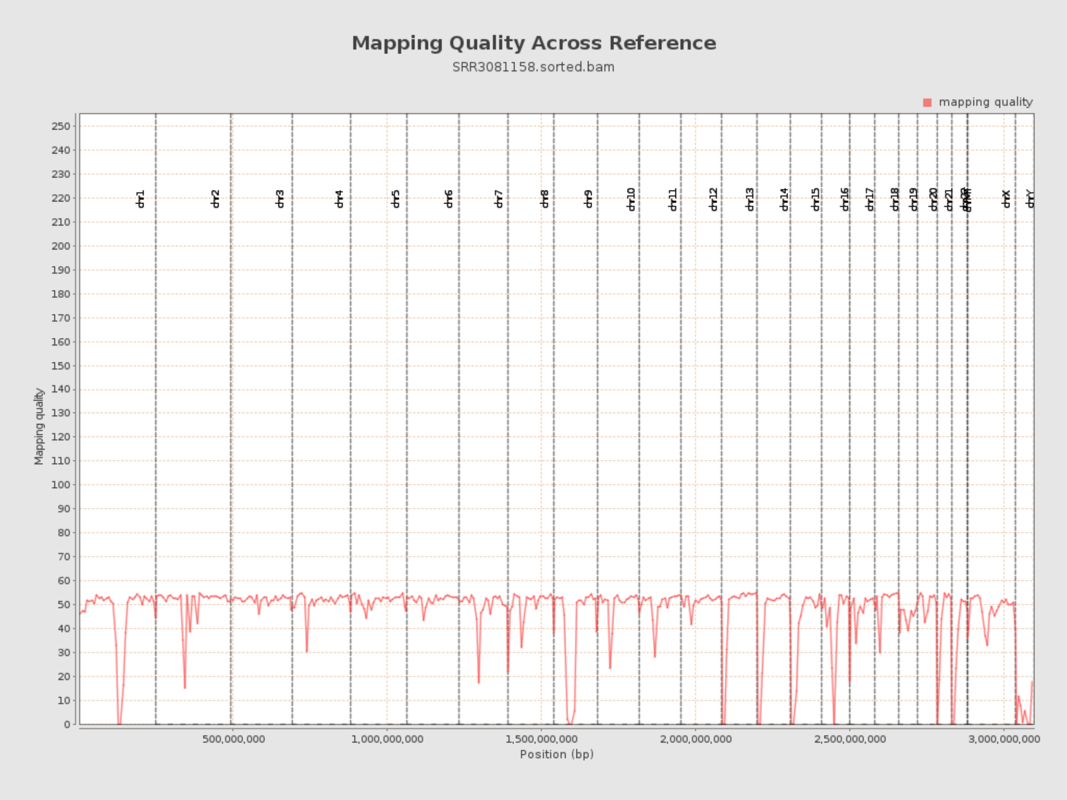
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram