Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 00:19:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081168.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_SRR3081168 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081168.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 00:19:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081168.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,684,261
Mapped reads	2,358,686 / 87.87%
Unmapped reads	325,575 / 12.13%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,707 / 0.77%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	104,322 / 3.89%
Duplication rate	3.48%
Clipped reads	1,062,802 / 39.59%

2.2. ACGT Content

Number/percentage of A's	43,823,308 / 27.8%
Number/percentage of C's	29,197,129 / 18.52%
Number/percentage of T's	49,555,698 / 31.44%
Number/percentage of G's	34,997,733 / 22.2%
Number/percentage of N's	46,992 / 0.03%
GC Percentage	40.73%

2.3. Coverage

Mean	0.0509

Standard Deviation	0.4205

2.4. Mapping Quality

Mean Mapping Quality	46.54

2.5. Mismatches and indels

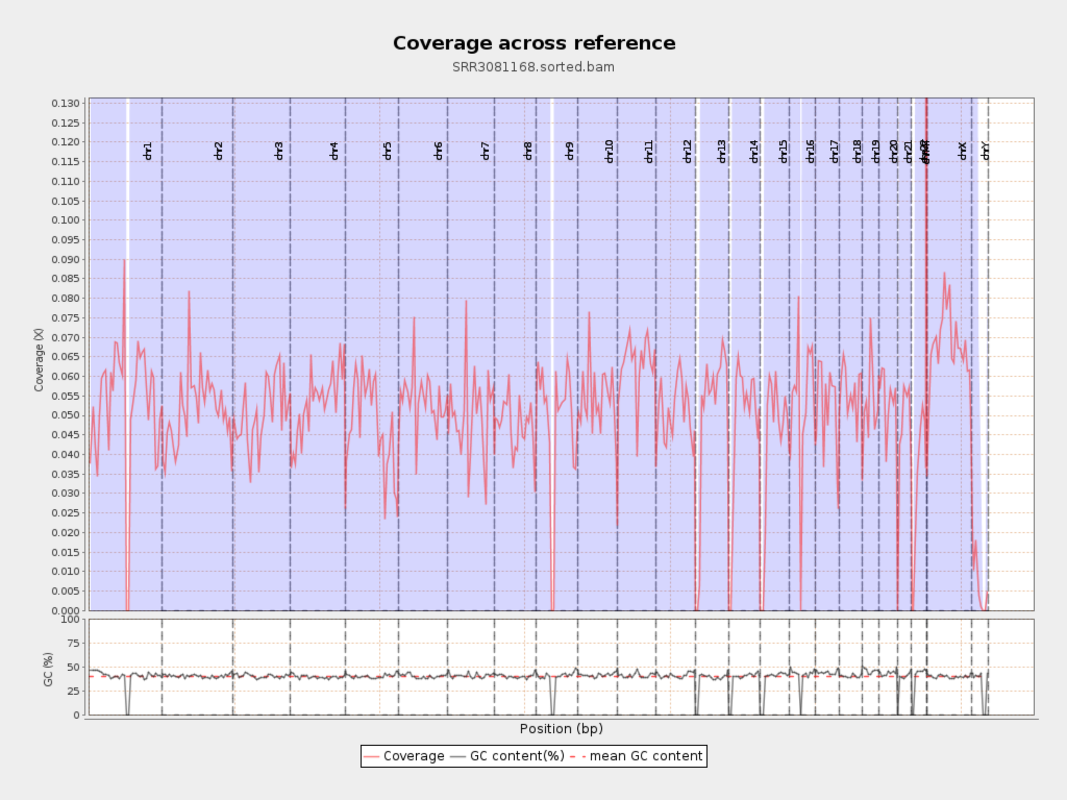
General error rate	0.85%
Mismatches	1,315,548
Insertions	12,131
Mapped reads with at least one insertion	0.51%
Deletions	34,631
Mapped reads with at least one deletion	1.45%
Homopolymer indels	47.01%

2.6. Chromosome stats

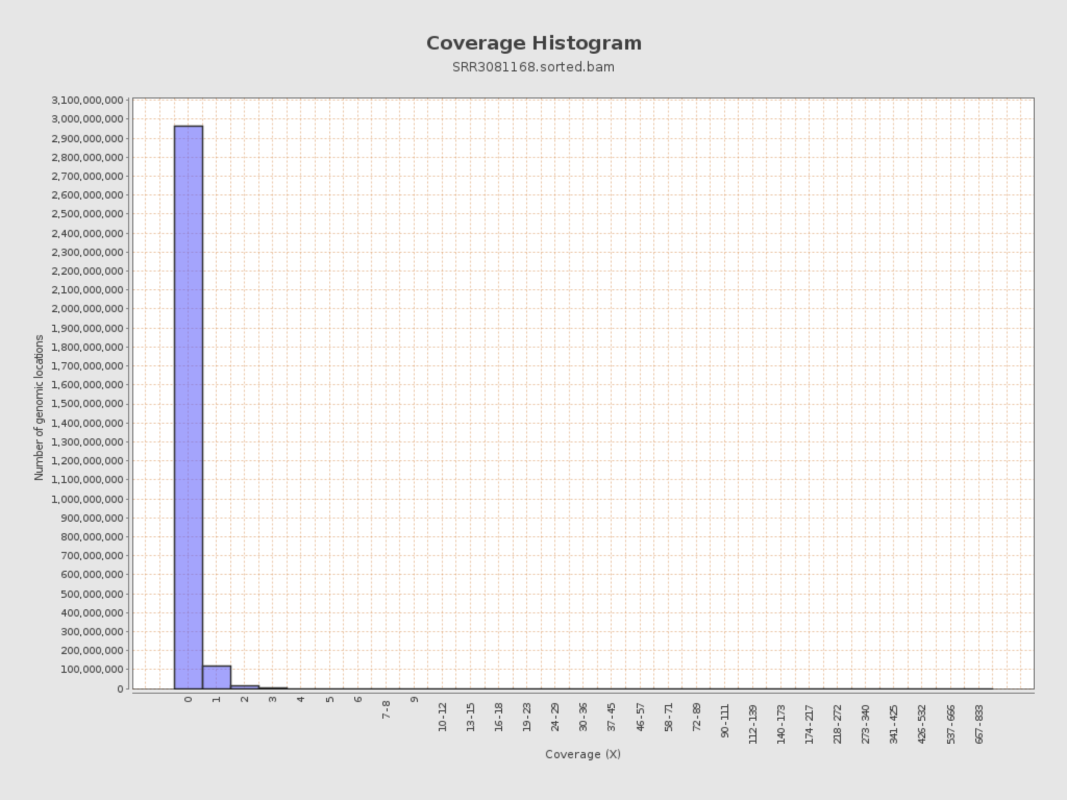
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13127102	0.0527	0.7708
chr2	243199373	12541598	0.0516	0.488
chr3	198022430	10061977	0.0508	0.2549
chr4	191154276	10238656	0.0536	0.2719
chr5	180915260	8613137	0.0476	0.2503
chr6	171115067	9192898	0.0537	0.3177
chr7	159138663	7926772	0.0498	0.6137

chr8	146364022	6918739	0.0473	0.4575
chr9	141213431	6734960	0.0477	0.3959
chr10	135534747	7392537	0.0545	0.3592
chr11	135006516	8425294	0.0624	0.4285
chr12	133851895	6859481	0.0512	0.2613
chr13	115169878	5689708	0.0494	0.2516
chr14	107349540	5007300	0.0466	0.2611
chr15	102531392	4335722	0.0423	0.2389
chr16	90354753	4833031	0.0535	0.2919
chr17	81195210	4148958	0.0511	0.3078
chr18	78077248	4404589	0.0564	0.6967
chr19	59128983	3190070	0.054	0.5707
chr20	63025520	3376645	0.0536	0.2678
chr21	48129895	2178058	0.0453	0.2594
chr22	51304566	1642324	0.032	0.2006
chrMT	16571	13690	0.8261	1.0819
chrX	155270560	10431002	0.0672	0.336
chrY	59373566	391886	0.0066	0.1292

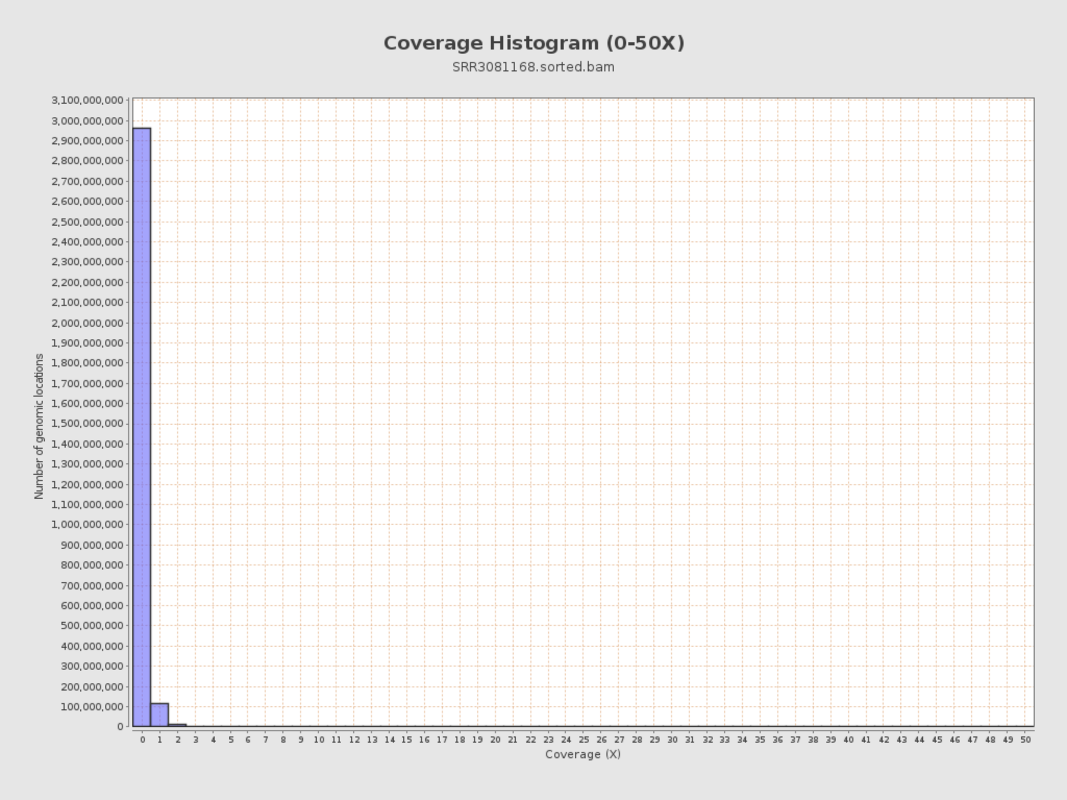
3. Results : Coverage across reference



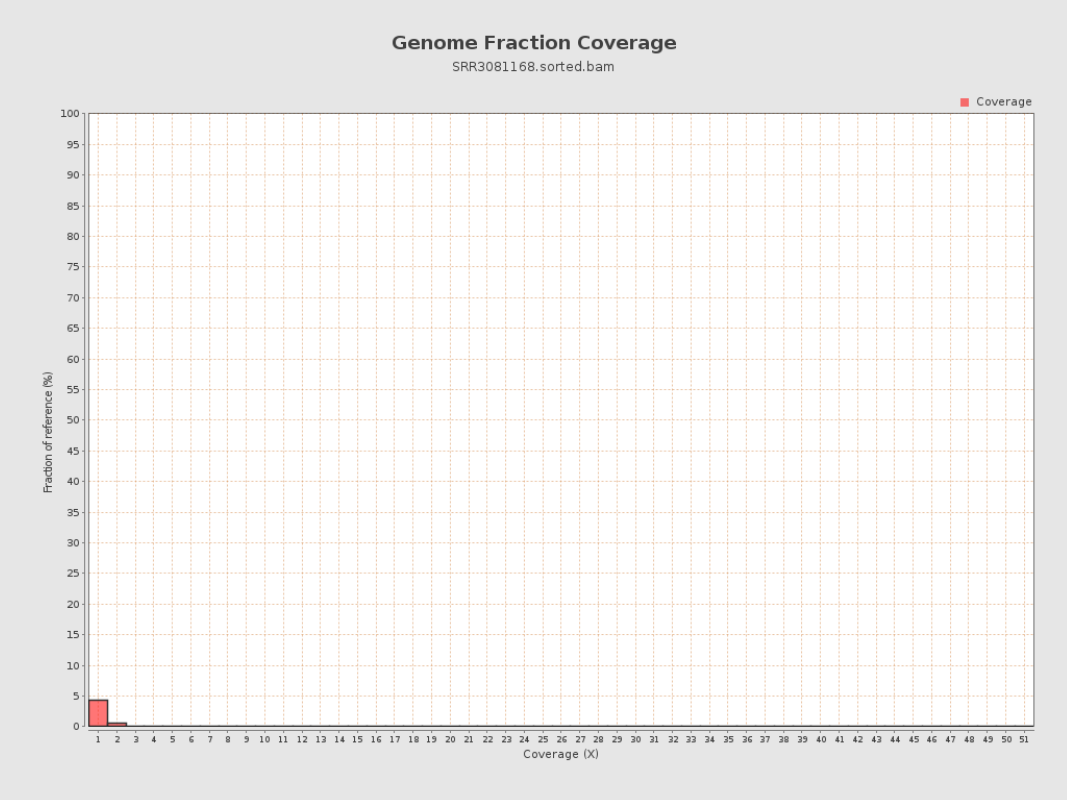
4. Results : Coverage Histogram



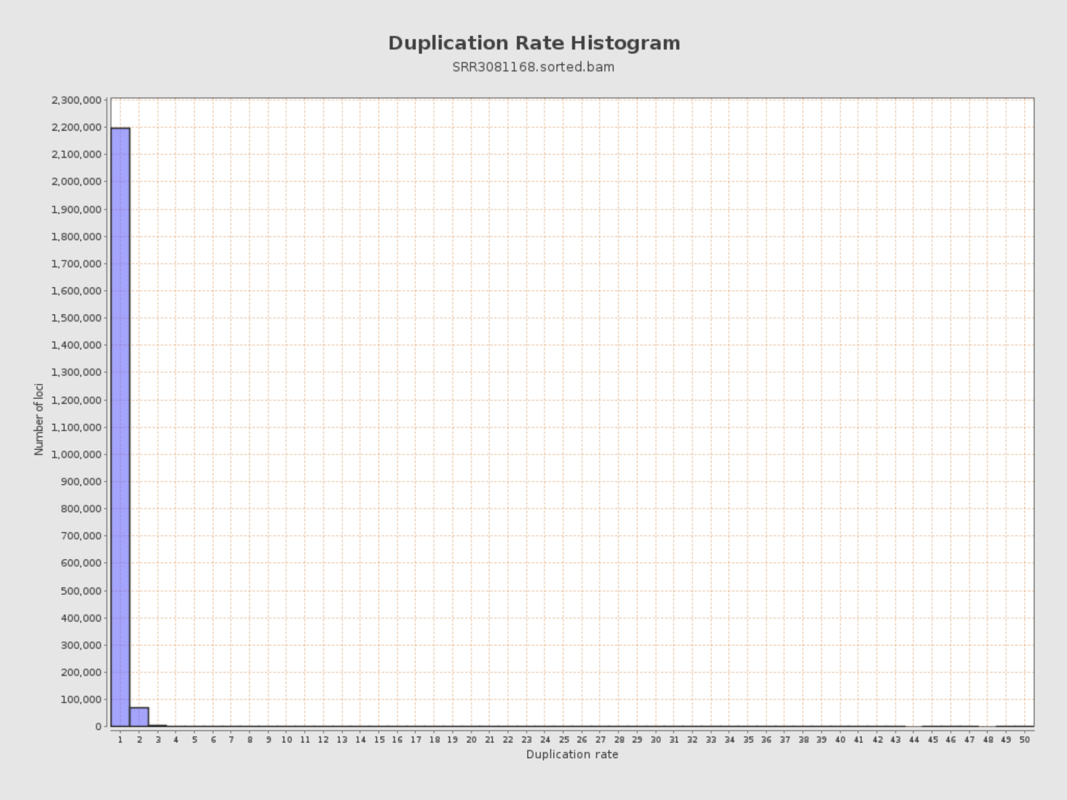
5. Results : Coverage Histogram (0-50X)



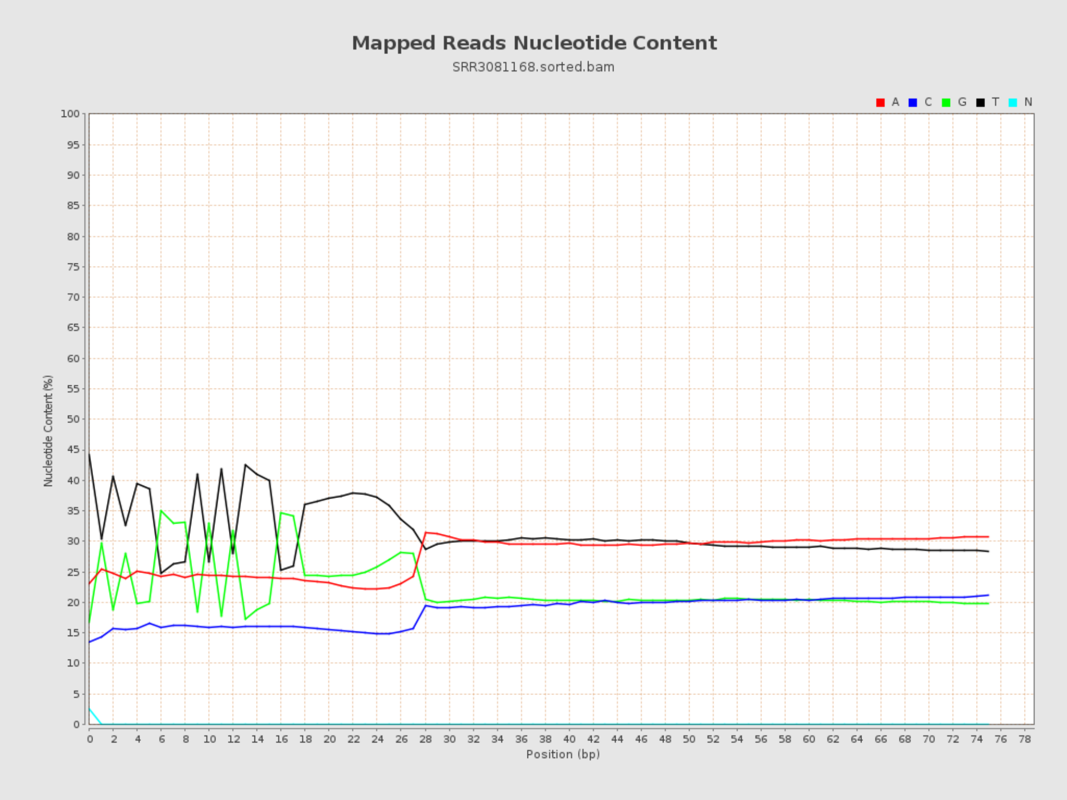
6. Results : Genome Fraction Coverage



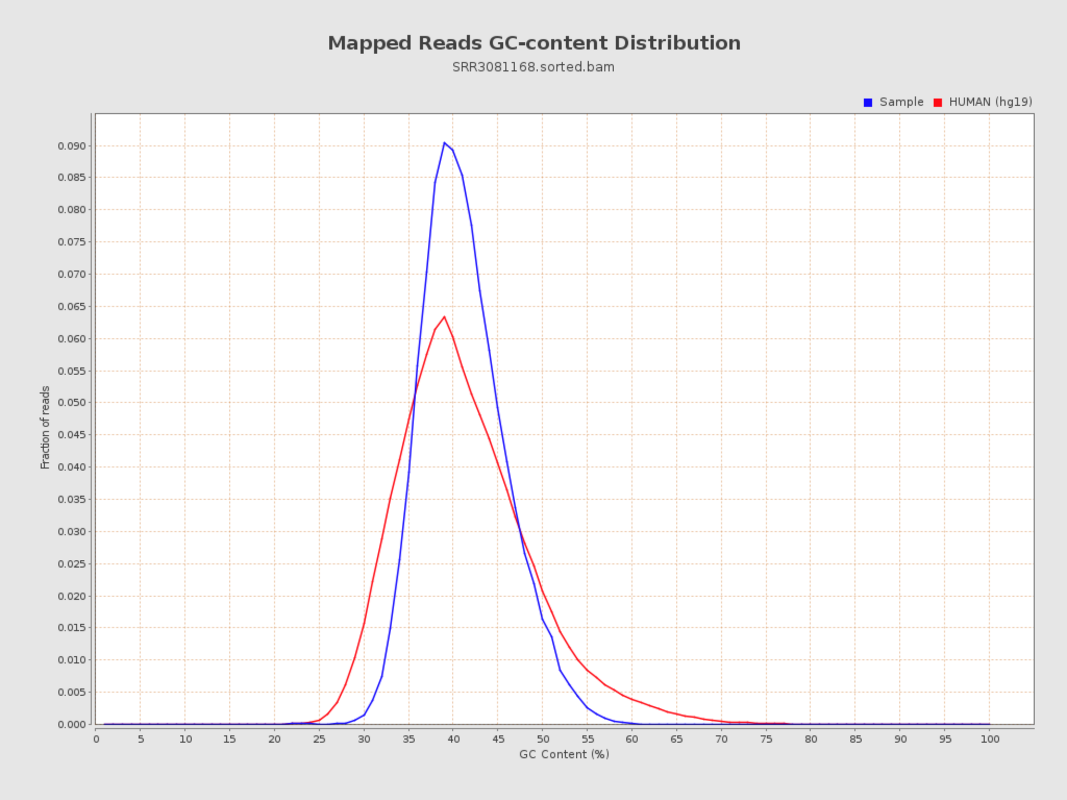
7. Results : Duplication Rate Histogram



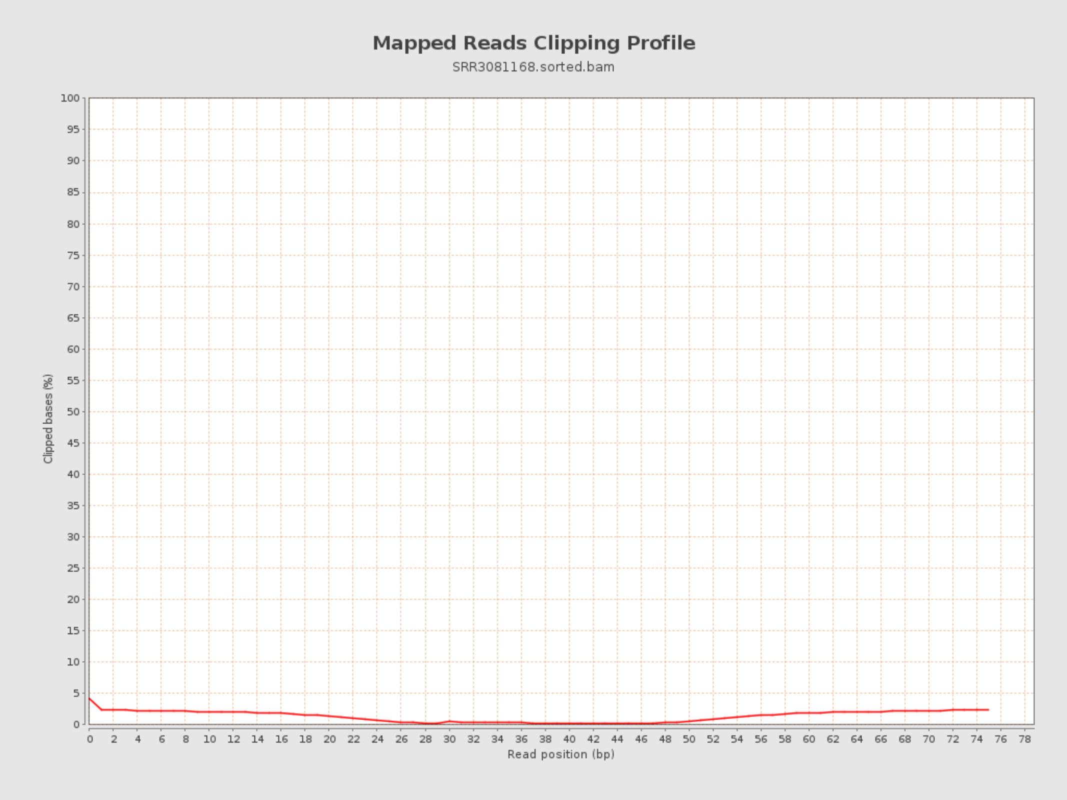
8. Results : Mapped Reads Nucleotide Content



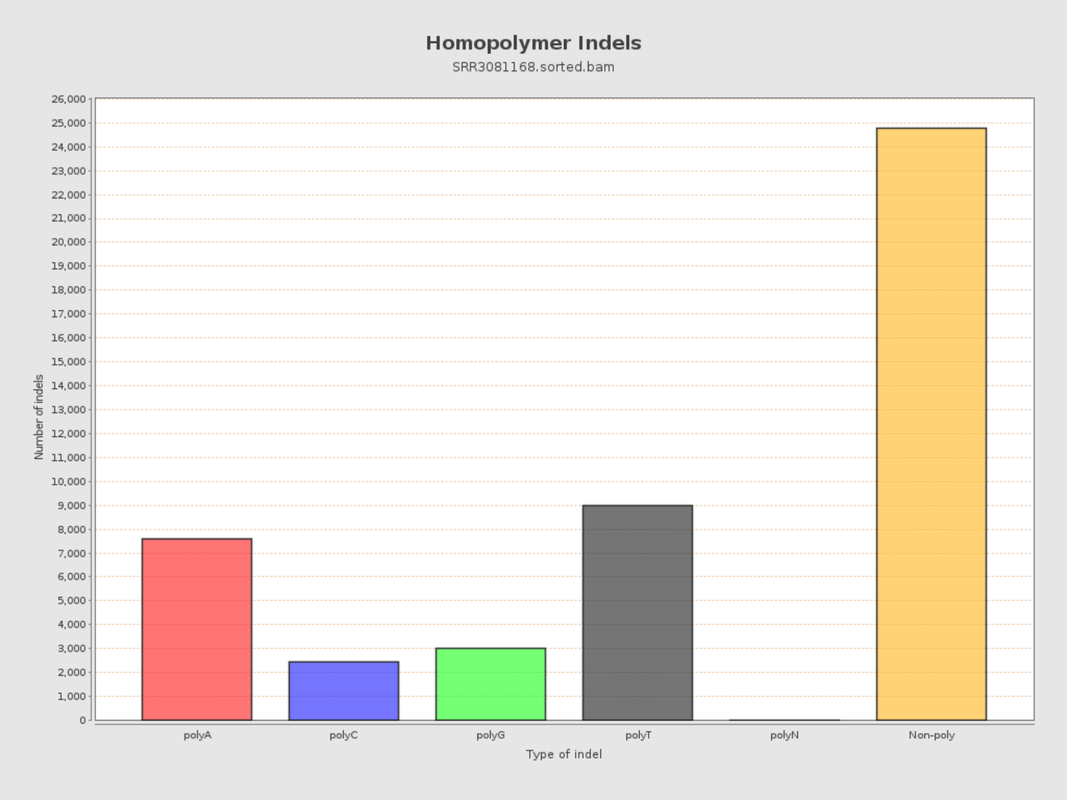
9. Results : Mapped Reads GC-content Distribution



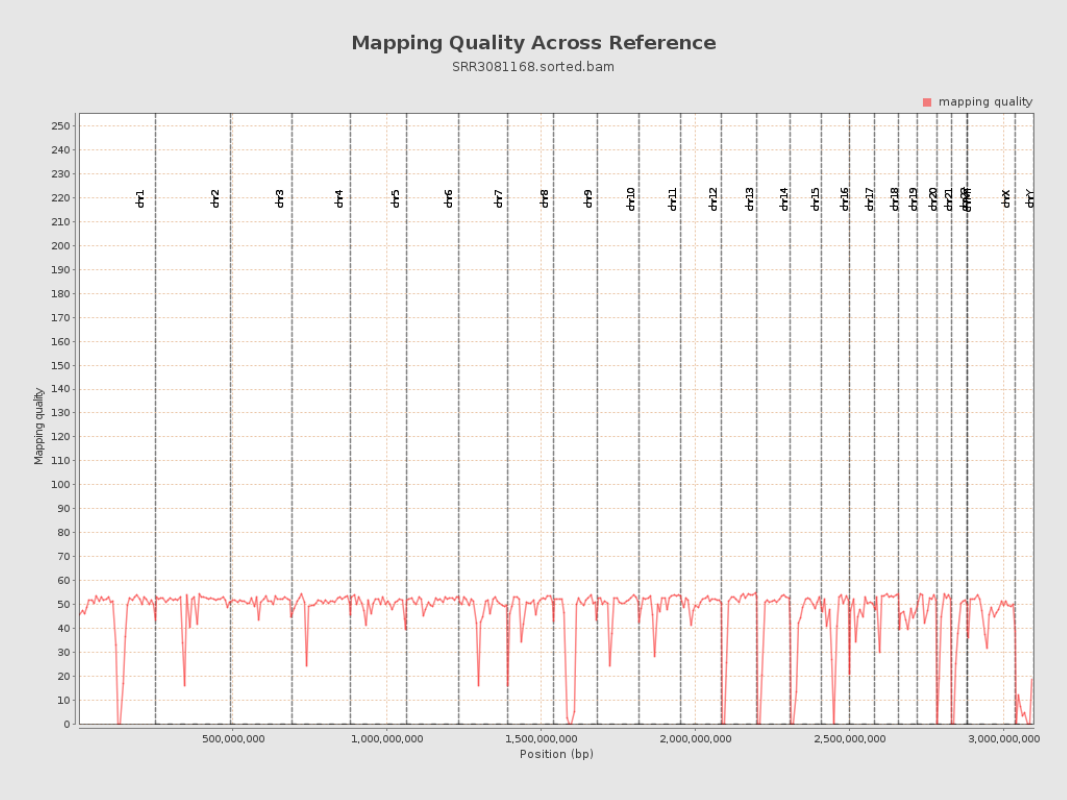
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram