Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 05:22:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081251.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_SRR3081251 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081251.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 05:22:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081251.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,544,756
Mapped reads	2,861,560 / 80.73%
Unmapped reads	683,196 / 19.27%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	27,613 / 0.78%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	154,400 / 4.36%
Duplication rate	4.36%
Clipped reads	1,132,773 / 31.96%

2.2. ACGT Content

Number/percentage of A's	54,113,837 / 27.88%
Number/percentage of C's	35,641,226 / 18.36%
Number/percentage of T's	61,992,703 / 31.93%
Number/percentage of G's	42,323,223 / 21.8%
Number/percentage of N's	51,760 / 0.03%
GC Percentage	40.16%

2.3. Coverage

Mean	0.0627

Standard Deviation	0.5072

2.4. Mapping Quality

Mean Mapping Quality	47.11

2.5. Mismatches and indels

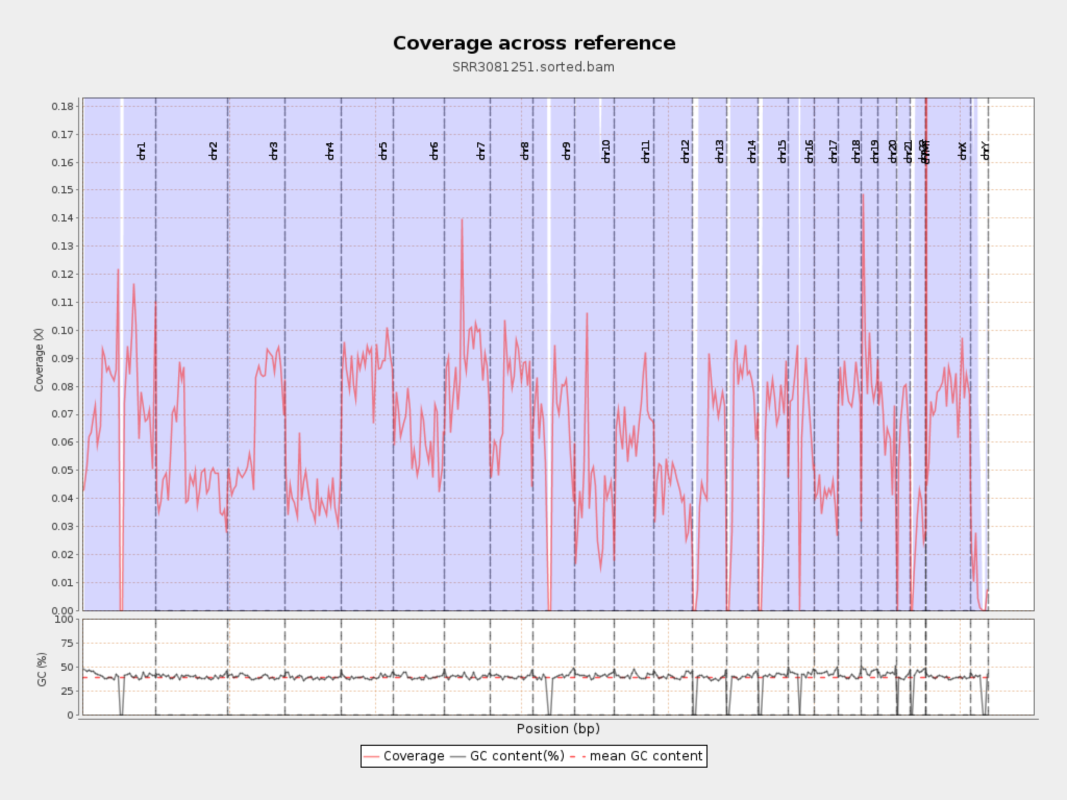
General error rate	0.89%
Mismatches	1,694,379
Insertions	15,860
Mapped reads with at least one insertion	0.55%
Deletions	49,719
Mapped reads with at least one deletion	1.72%
Homopolymer indels	50.07%

2.6. Chromosome stats

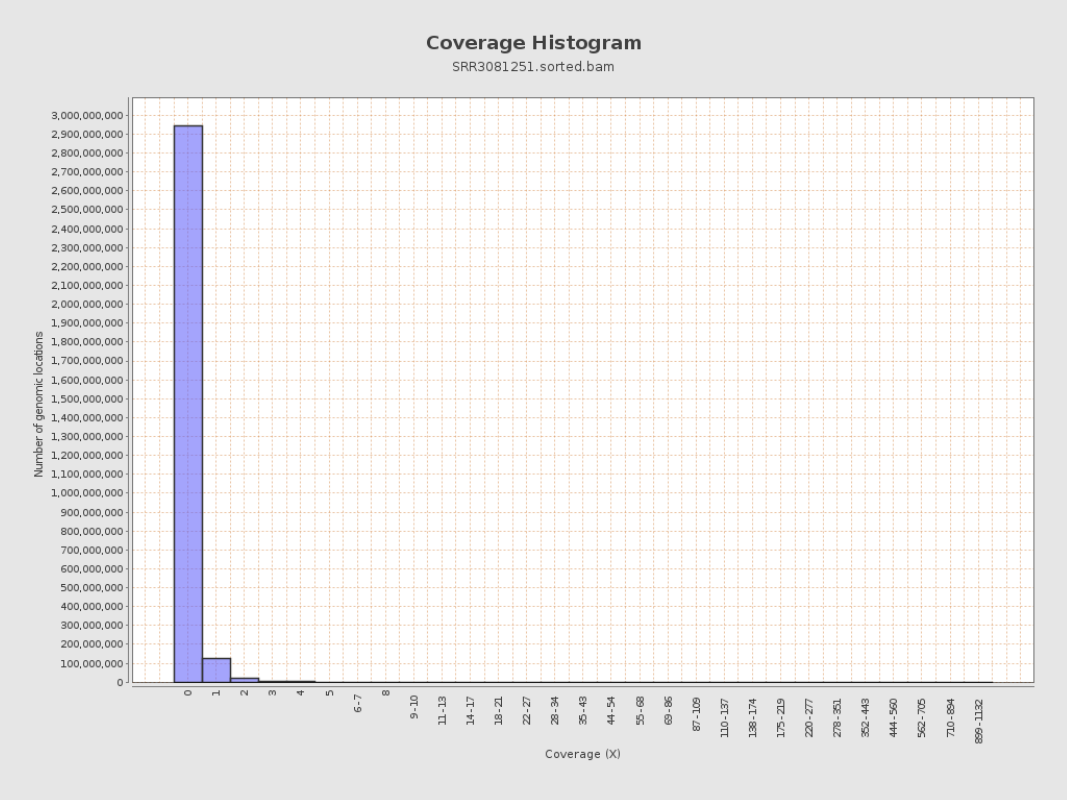
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	18363837	0.0737	1.0232
chr2	243199373	12164367	0.05	0.4496
chr3	198022430	13454784	0.0679	0.3222
chr4	191154276	7766448	0.0406	0.2808
chr5	180915260	15838711	0.0875	0.3645
chr6	171115067	10617576	0.062	0.3433
chr7	159138663	14243859	0.0895	0.8365

chr8	146364022	11143069	0.0761	0.5592
chr9	141213431	8907569	0.0631	0.4196
chr10	135534747	5549902	0.0409	0.5276
chr11	135006516	9003769	0.0667	0.4322
chr12	133851895	5672774	0.0424	0.2548
chr13	115169878	6222636	0.054	0.2812
chr14	107349540	7421719	0.0691	0.3289
chr15	102531392	6249757	0.061	0.2995
chr16	90354753	6039300	0.0668	0.3341
chr17	81195210	3335632	0.0411	0.2807
chr18	78077248	6241994	0.0799	0.6488
chr19	59128983	5376905	0.0909	0.7791
chr20	63025520	4025374	0.0639	0.3126
chr21	48129895	2957210	0.0614	0.3331
chr22	51304566	1267128	0.0247	0.1861
chrMT	16571	103794	6.2636	3.8472
chrX	155270560	11734675	0.0756	0.3611
chrY	59373566	503448	0.0085	0.1961

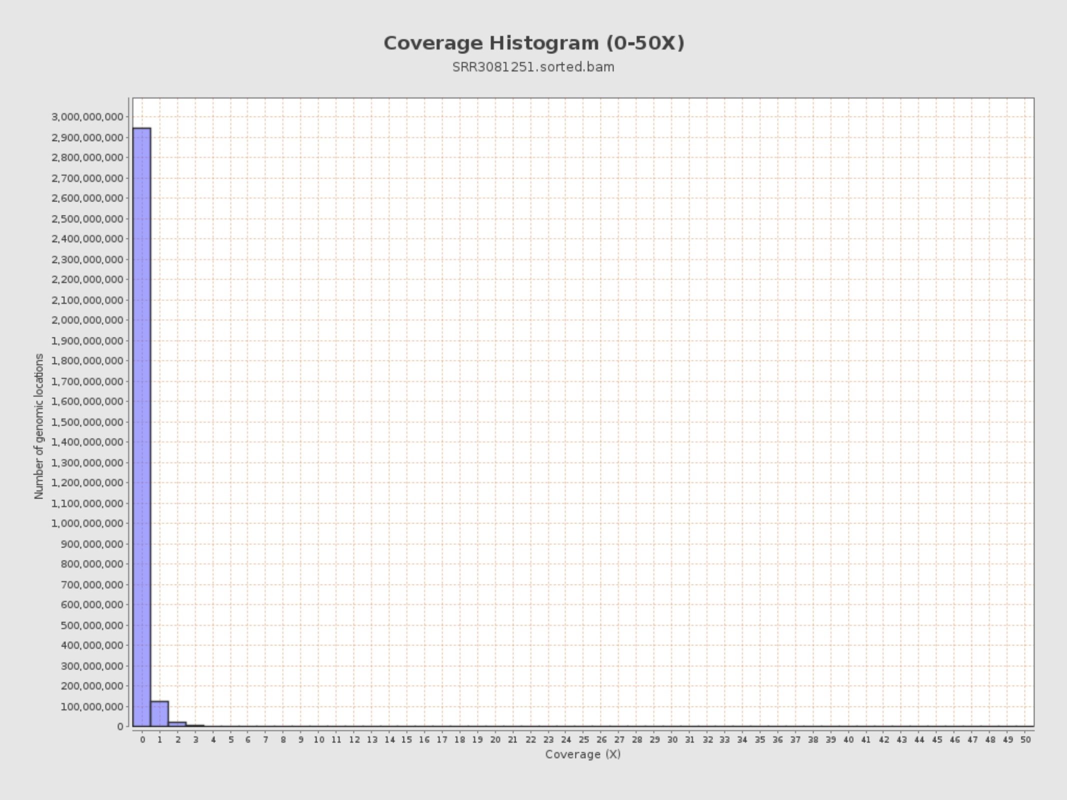
3. Results : Coverage across reference



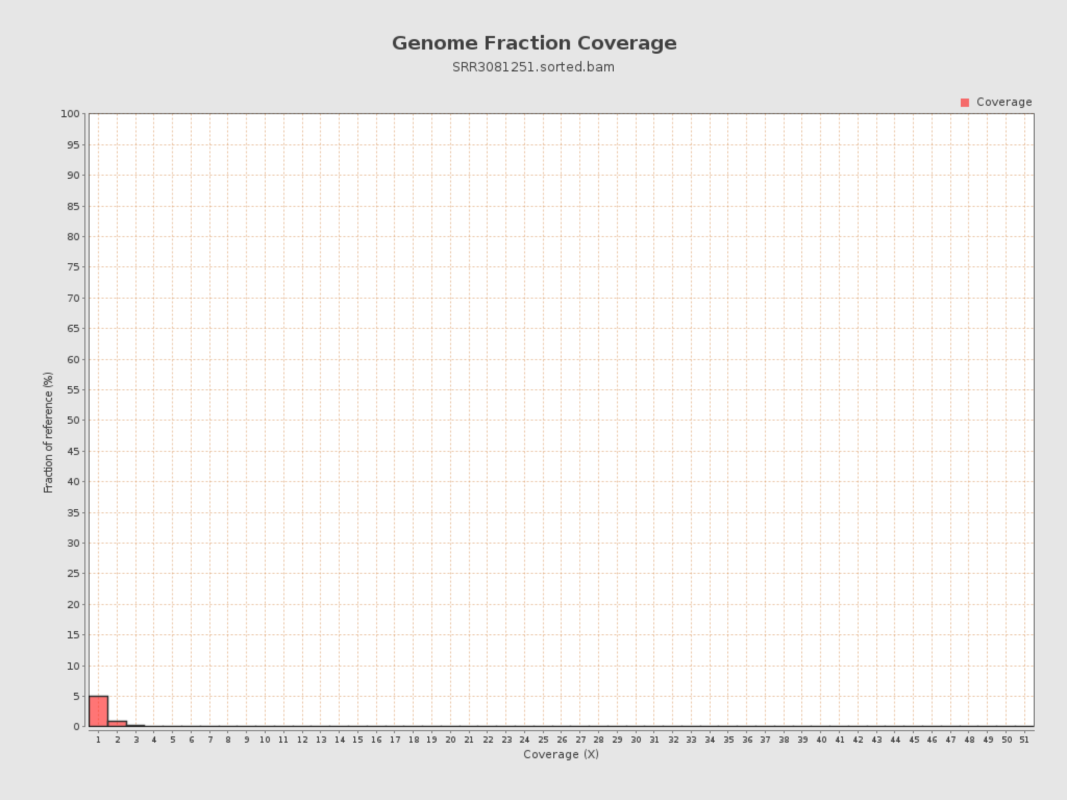
4. Results : Coverage Histogram



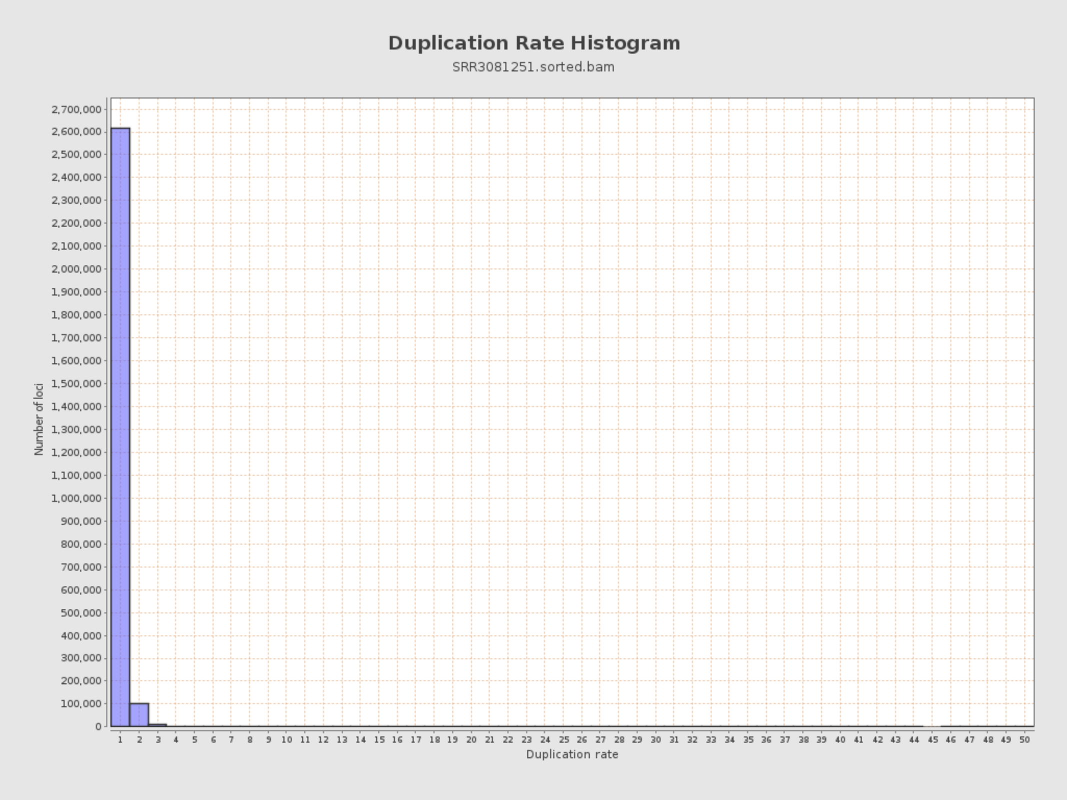
5. Results : Coverage Histogram (0-50X)



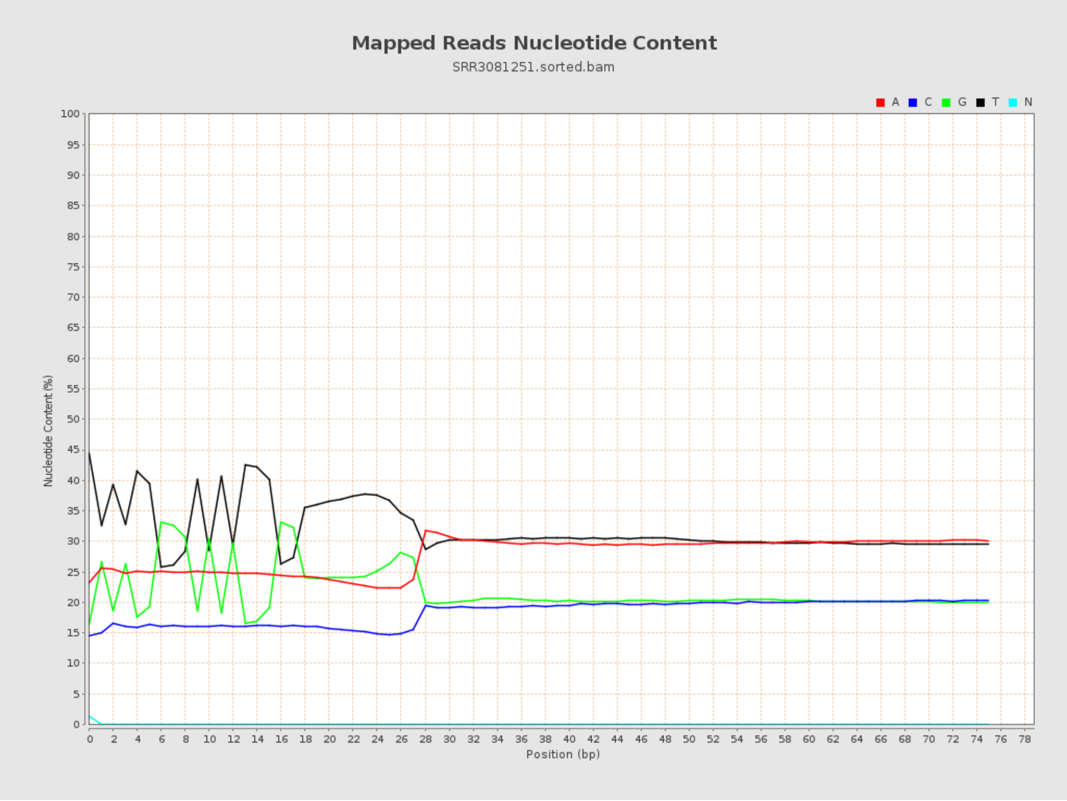
6. Results : Genome Fraction Coverage



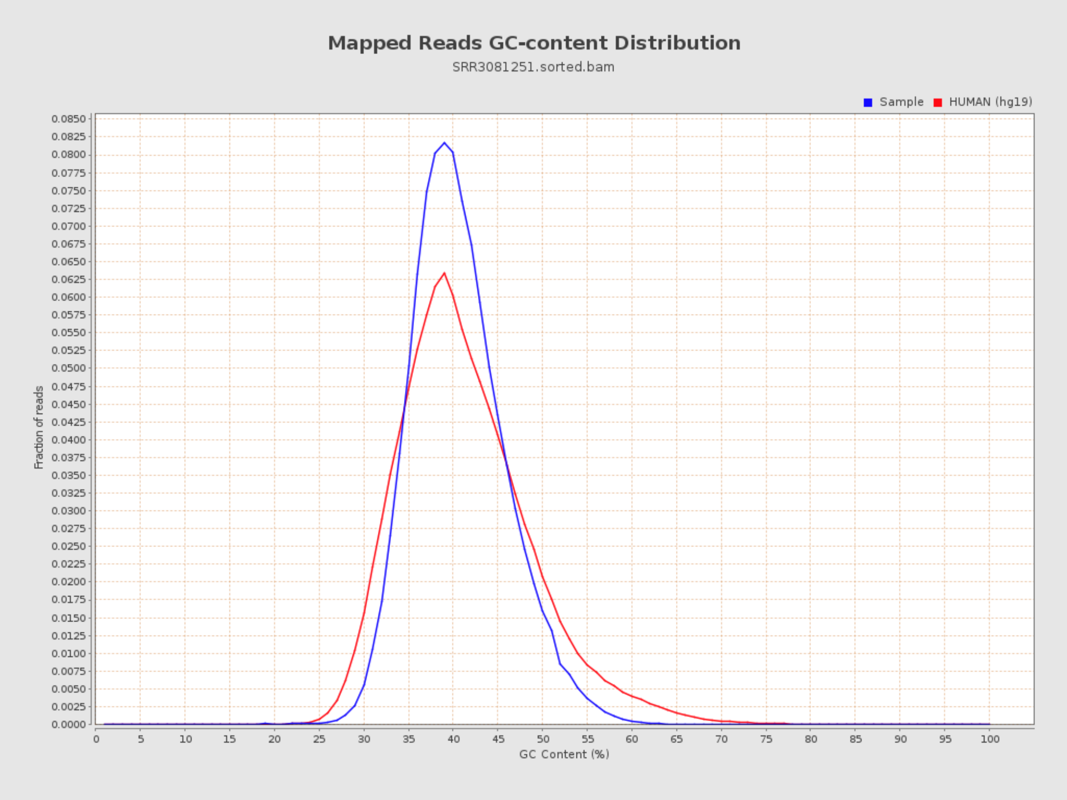
7. Results : Duplication Rate Histogram



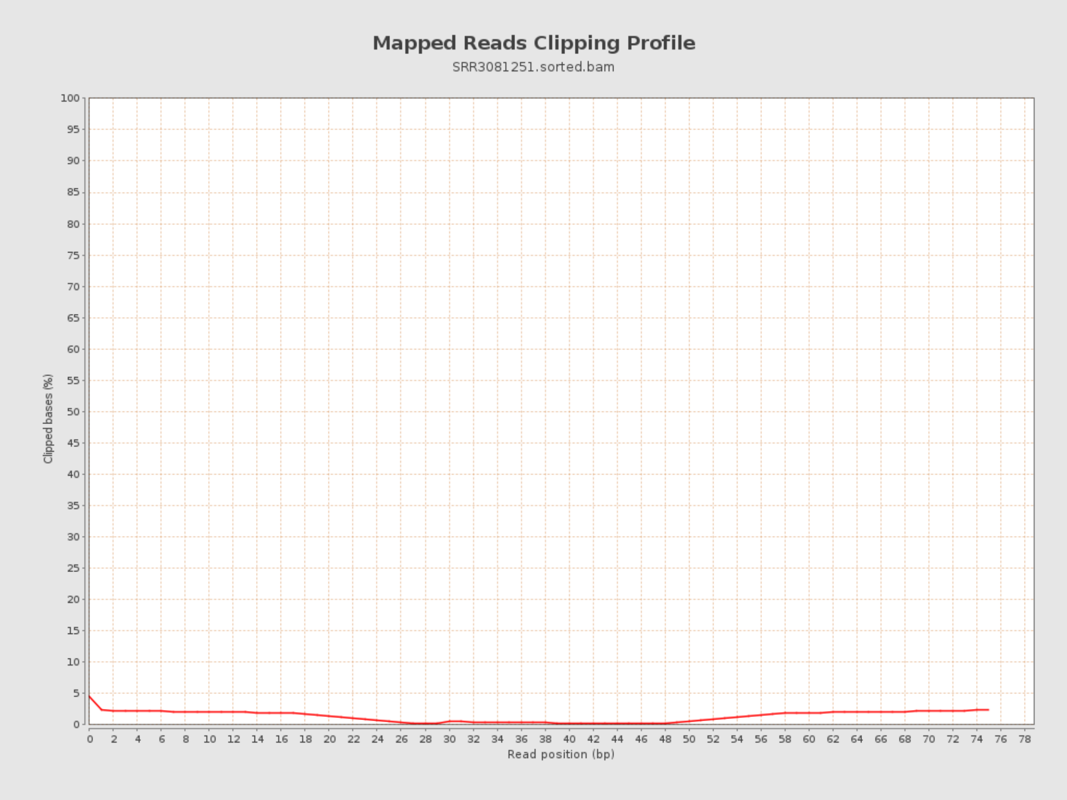
8. Results : Mapped Reads Nucleotide Content



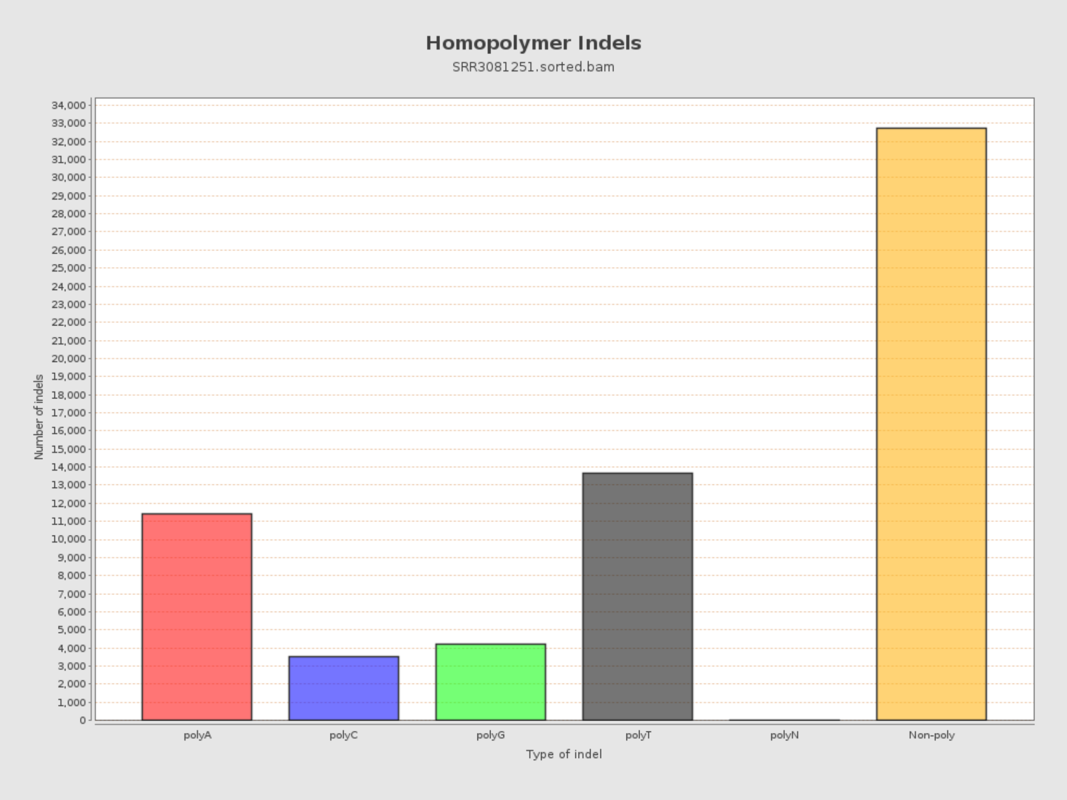
9. Results : Mapped Reads GC-content Distribution



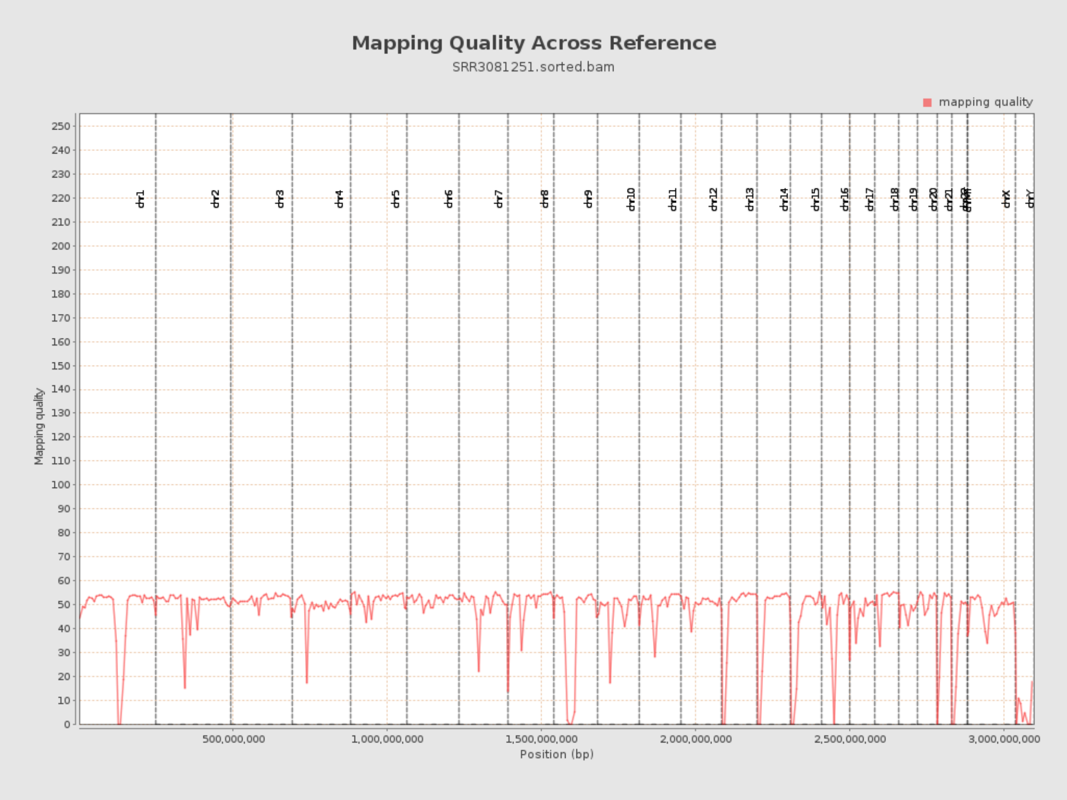
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram