Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 22:56:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081147.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_SRR3081147 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081147.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 22:56:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081147.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,811,145
Mapped reads	2,529,250 / 89.97%
Unmapped reads	281,895 / 10.03%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	23,976 / 0.85%
Read min/max/mean length	30 / 76 / 76.3
Duplicated reads (estimated)	101,862 / 3.62%
Duplication rate	3.24%
Clipped reads	1,074,902 / 38.24%

2.2. ACGT Content

Number/percentage of A's	49,056,680 / 28.73%
Number/percentage of C's	31,549,105 / 18.48%
Number/percentage of T's	53,630,624 / 31.41%
Number/percentage of G's	36,447,751 / 21.35%
Number/percentage of N's	51,214 / 0.03%
GC Percentage	39.83%

2.3. Coverage

Mean	0.0552

Standard Deviation	0.4041

2.4. Mapping Quality

Mean Mapping Quality	47.3

2.5. Mismatches and indels

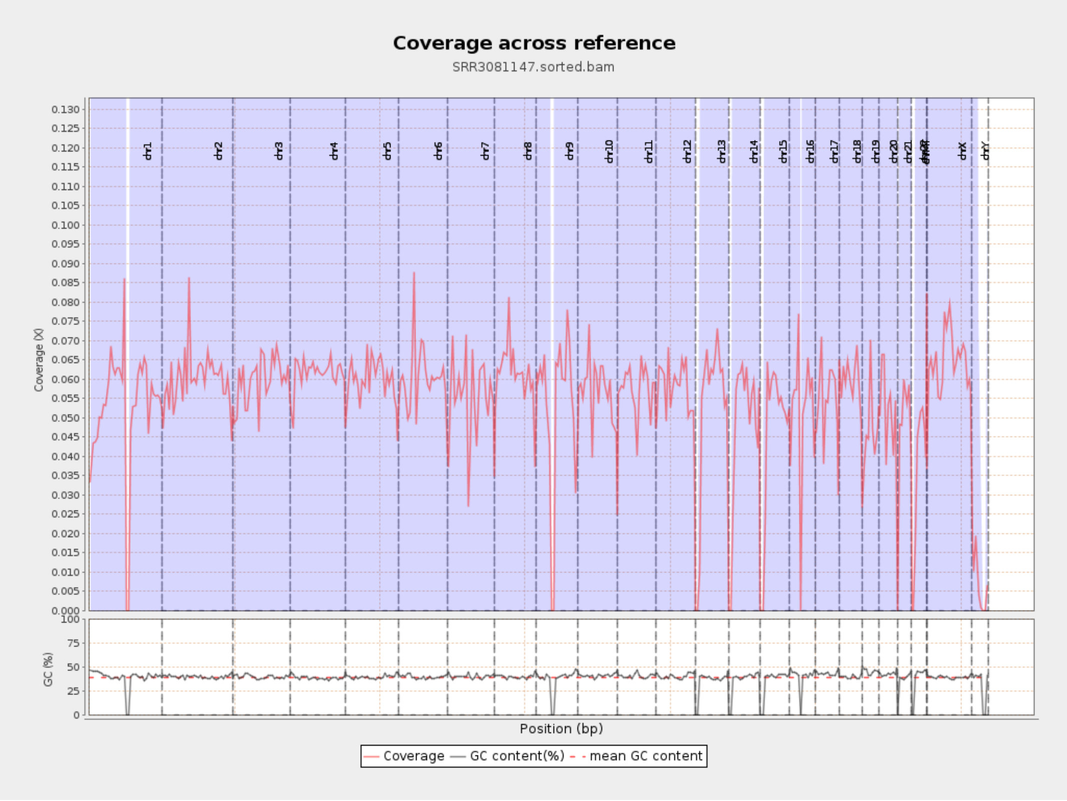
General error rate	0.83%
Mismatches	1,395,708
Insertions	13,459
Mapped reads with at least one insertion	0.53%
Deletions	38,912
Mapped reads with at least one deletion	1.52%
Homopolymer indels	47.68%

2.6. Chromosome stats

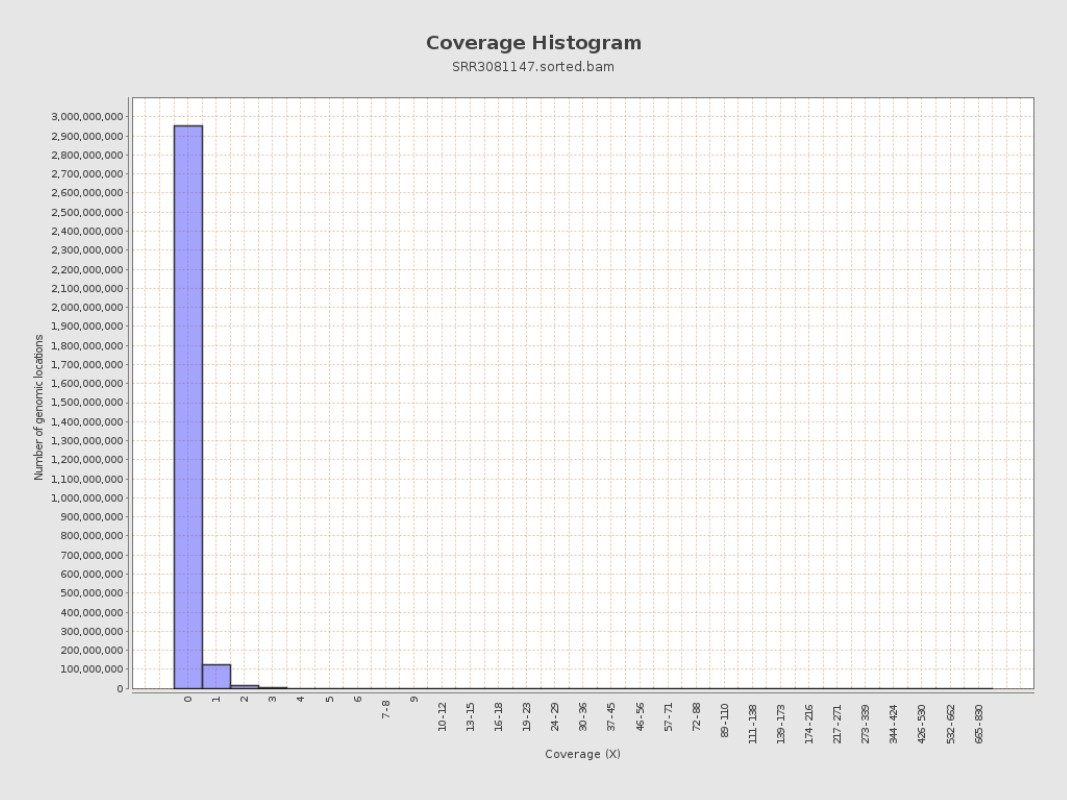
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13190195	0.0529	0.6812
chr2	243199373	14627510	0.0601	0.4689
chr3	198022430	11818930	0.0597	0.2759
chr4	191154276	11769179	0.0616	0.2923
chr5	180915260	10871256	0.0601	0.2794
chr6	171115067	10328440	0.0604	0.3908
chr7	159138663	8867906	0.0557	0.4905

chr8	146364022	8958404	0.0612	0.5829
chr9	141213431	7448550	0.0527	0.3744
chr10	135534747	7768060	0.0573	0.3647
chr11	135006516	7701744	0.057	0.3658
chr12	133851895	7741915	0.0578	0.2782
chr13	115169878	5846740	0.0508	0.2559
chr14	107349540	5040834	0.047	0.2611
chr15	102531392	4692516	0.0458	0.2449
chr16	90354753	4650793	0.0515	0.2861
chr17	81195210	4371825	0.0538	0.3069
chr18	78077248	4697659	0.0602	0.6492
chr19	59128983	2762509	0.0467	0.4972
chr20	63025520	3274988	0.052	0.267
chr21	48129895	2273428	0.0472	0.2666
chr22	51304566	1734445	0.0338	0.206
chrMT	16571	1365	0.0824	0.2843
chrX	155270560	9955774	0.0641	0.3147
chrY	59373566	403571	0.0068	0.1352

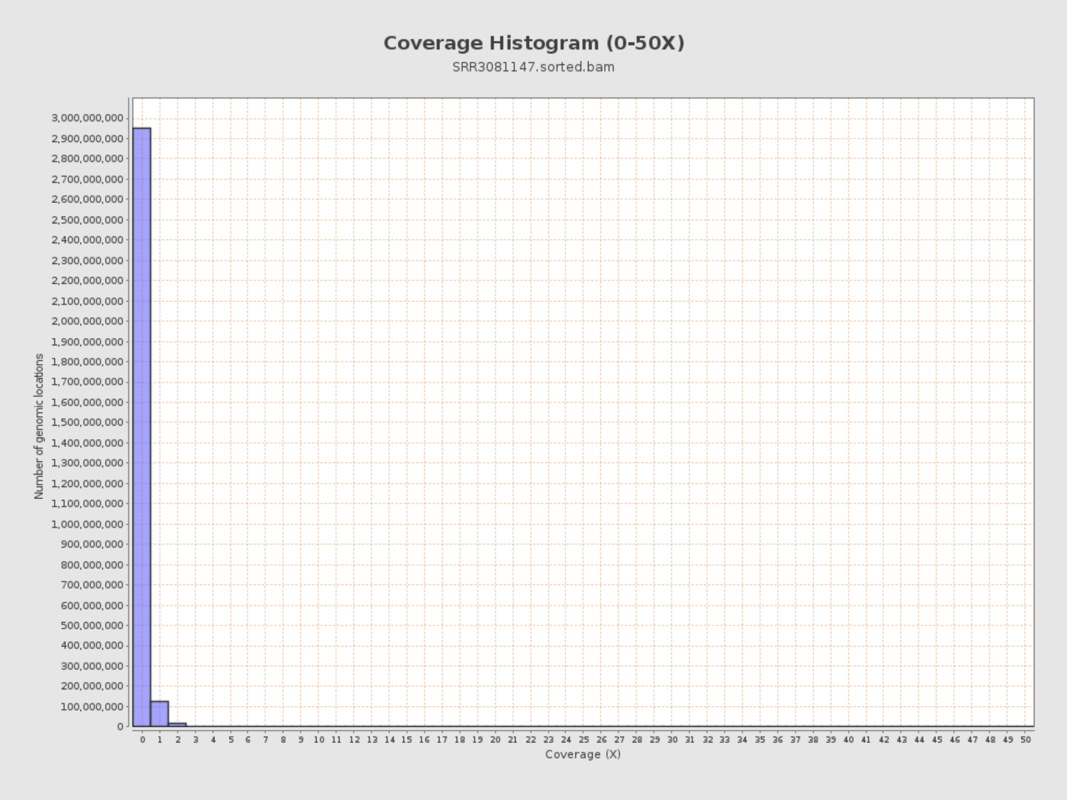
3. Results : Coverage across reference



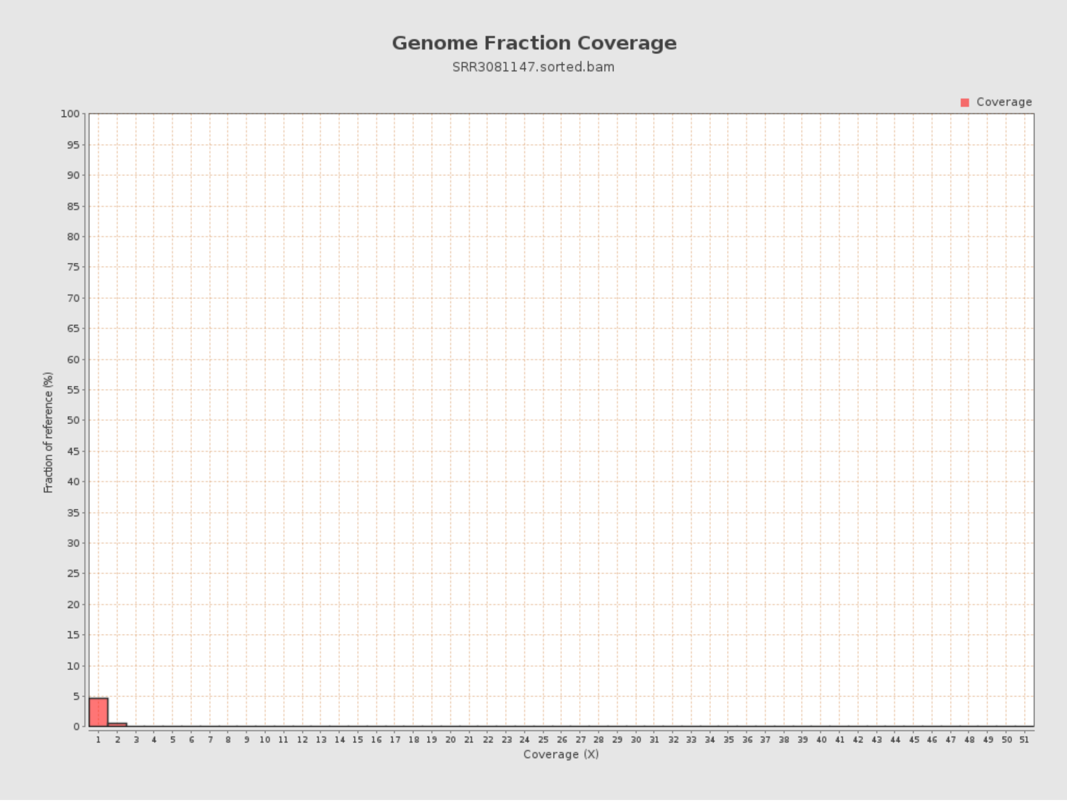
4. Results : Coverage Histogram



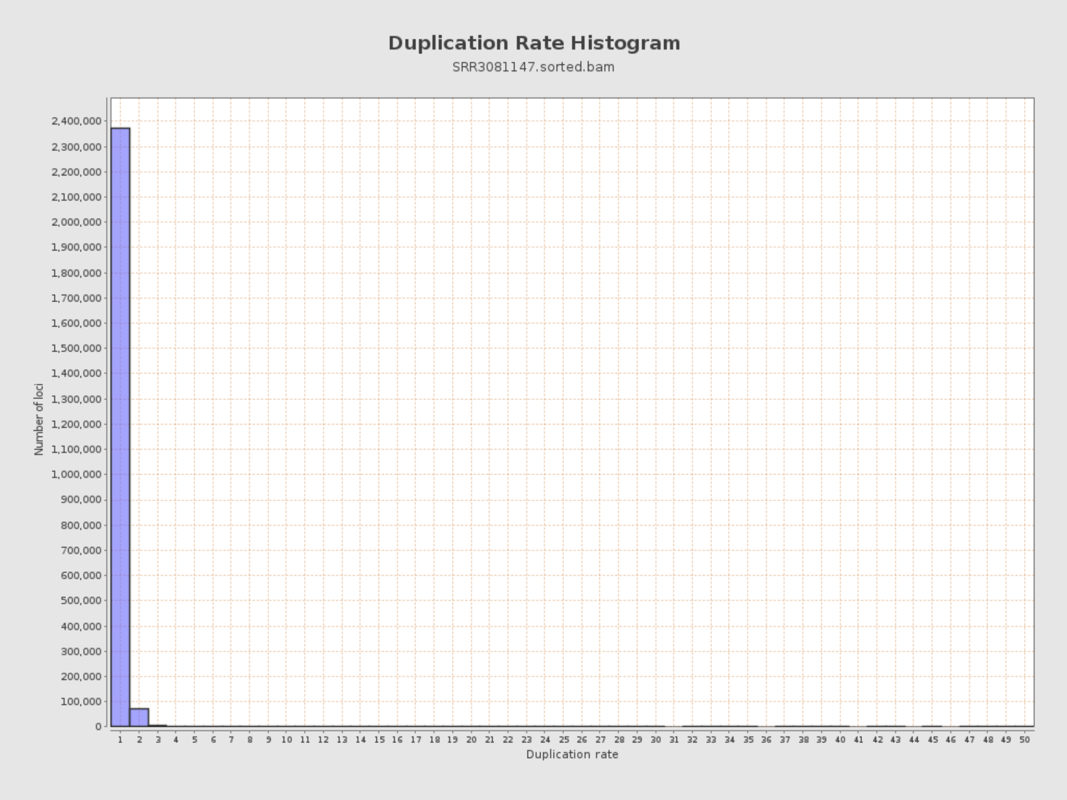
5. Results : Coverage Histogram (0-50X)



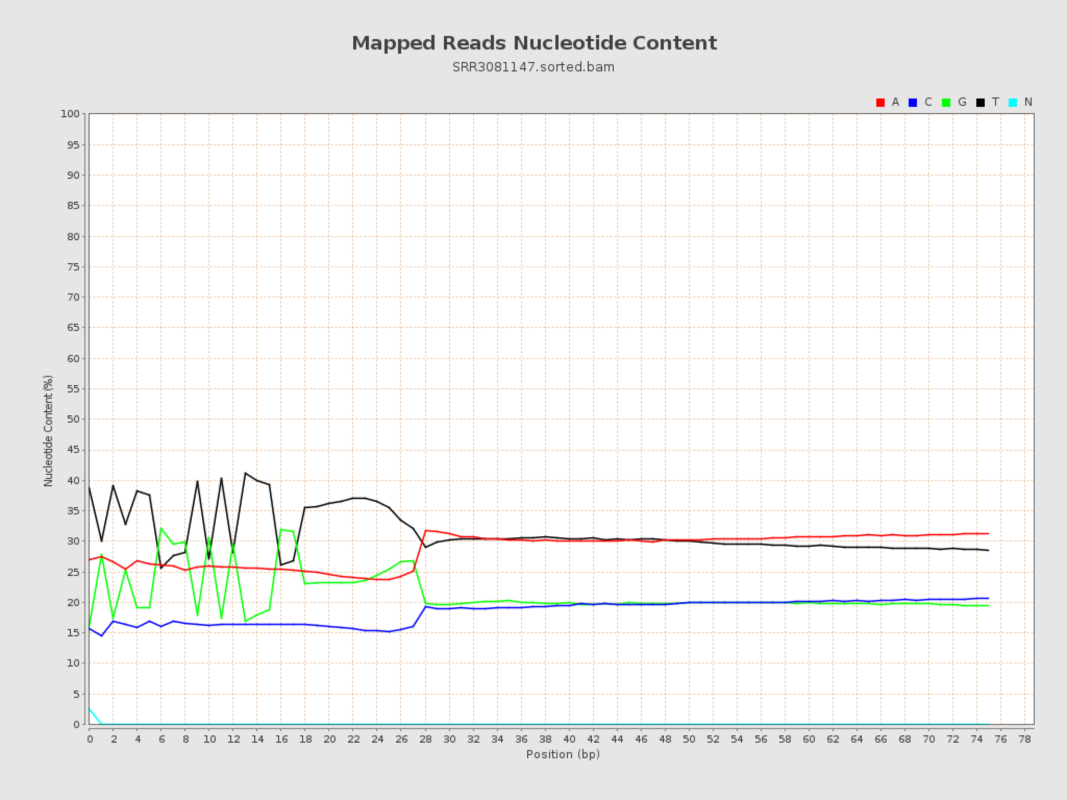
6. Results : Genome Fraction Coverage



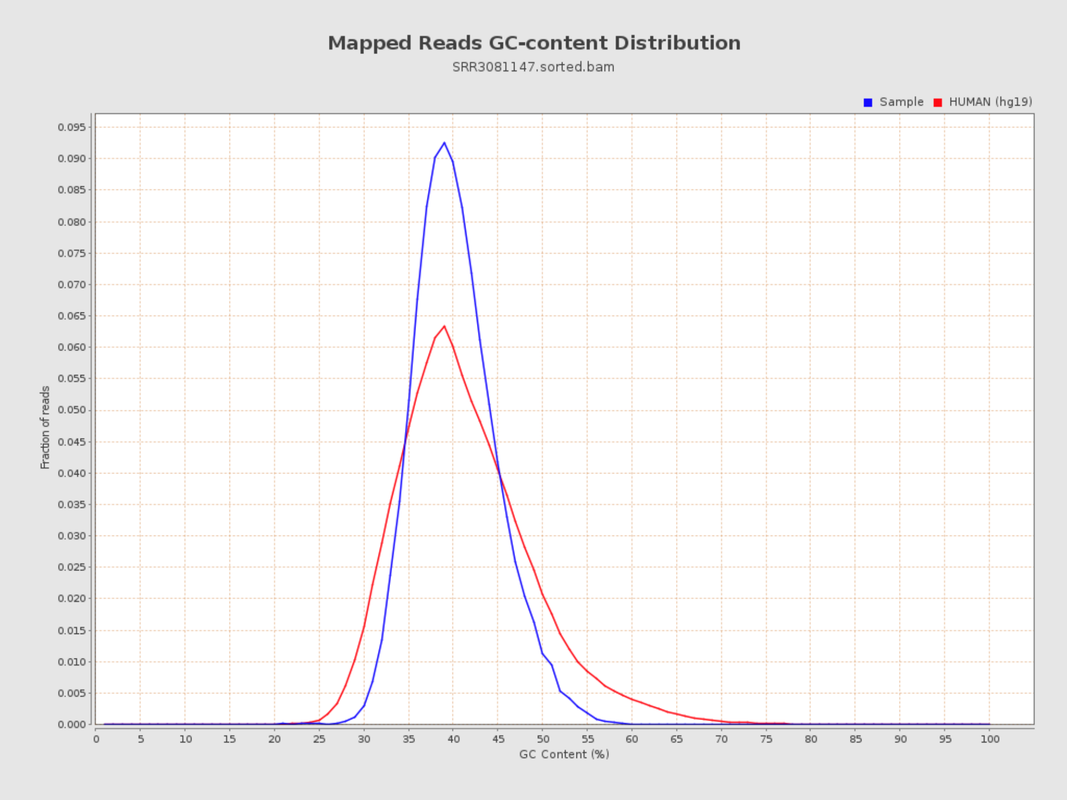
7. Results : Duplication Rate Histogram



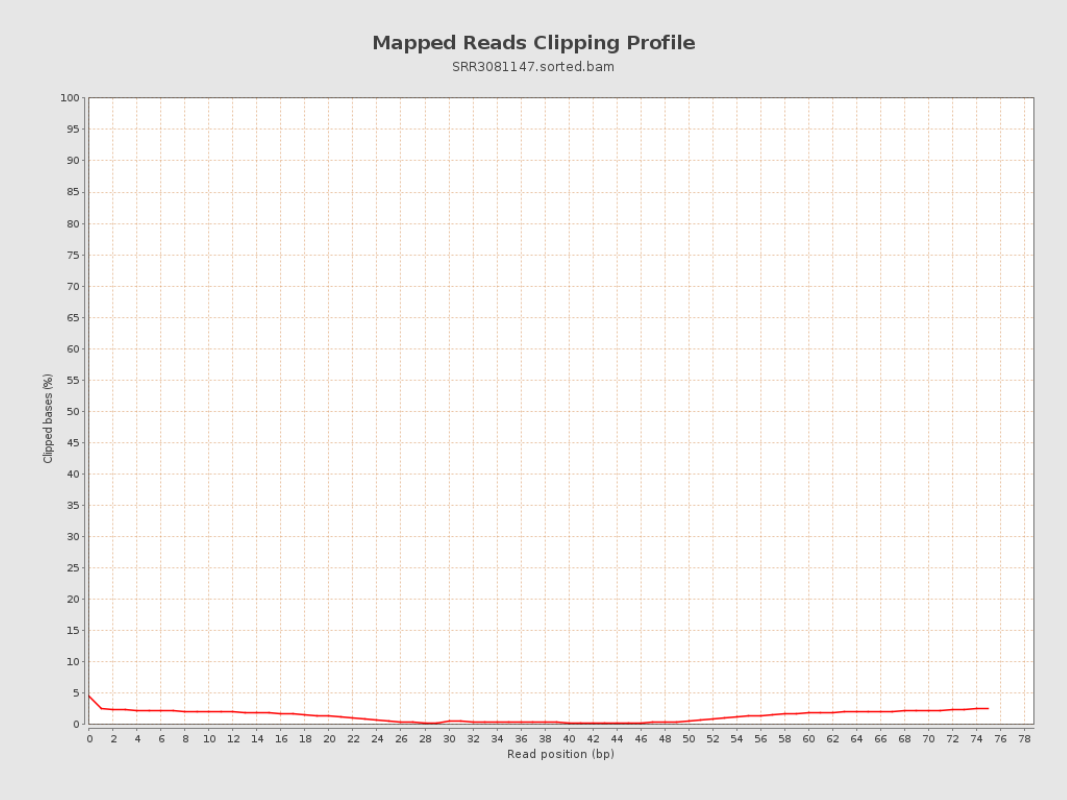
8. Results : Mapped Reads Nucleotide Content



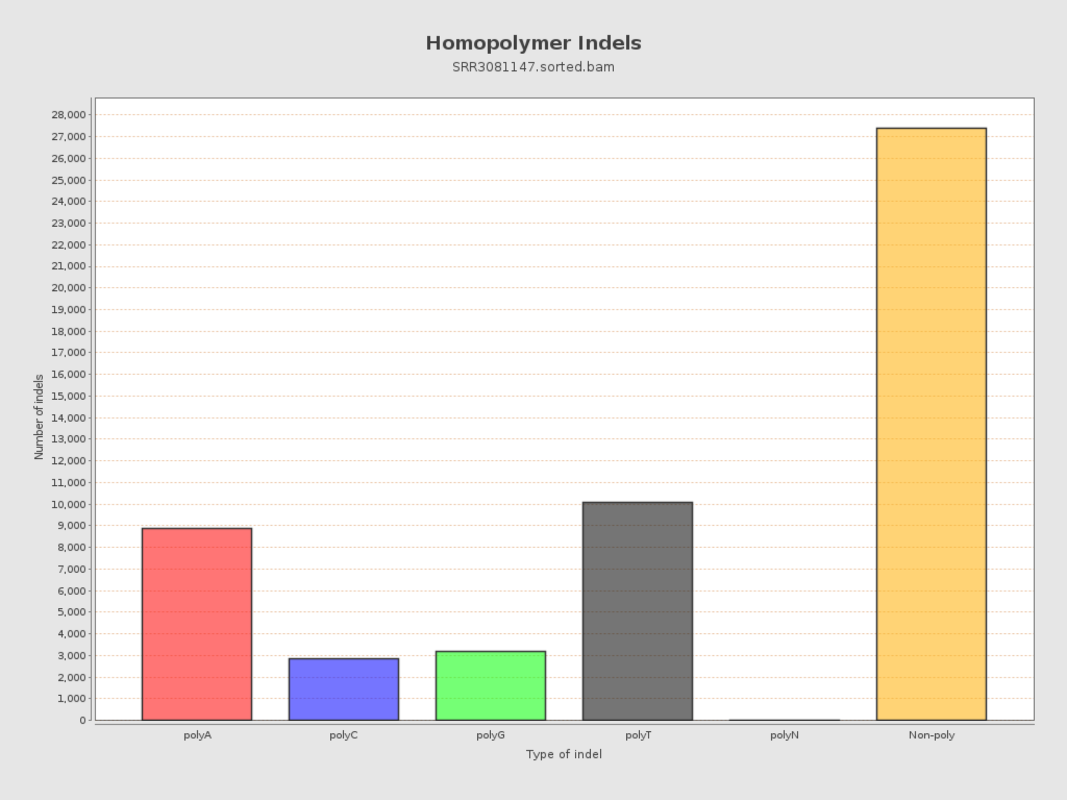
9. Results : Mapped Reads GC-content Distribution



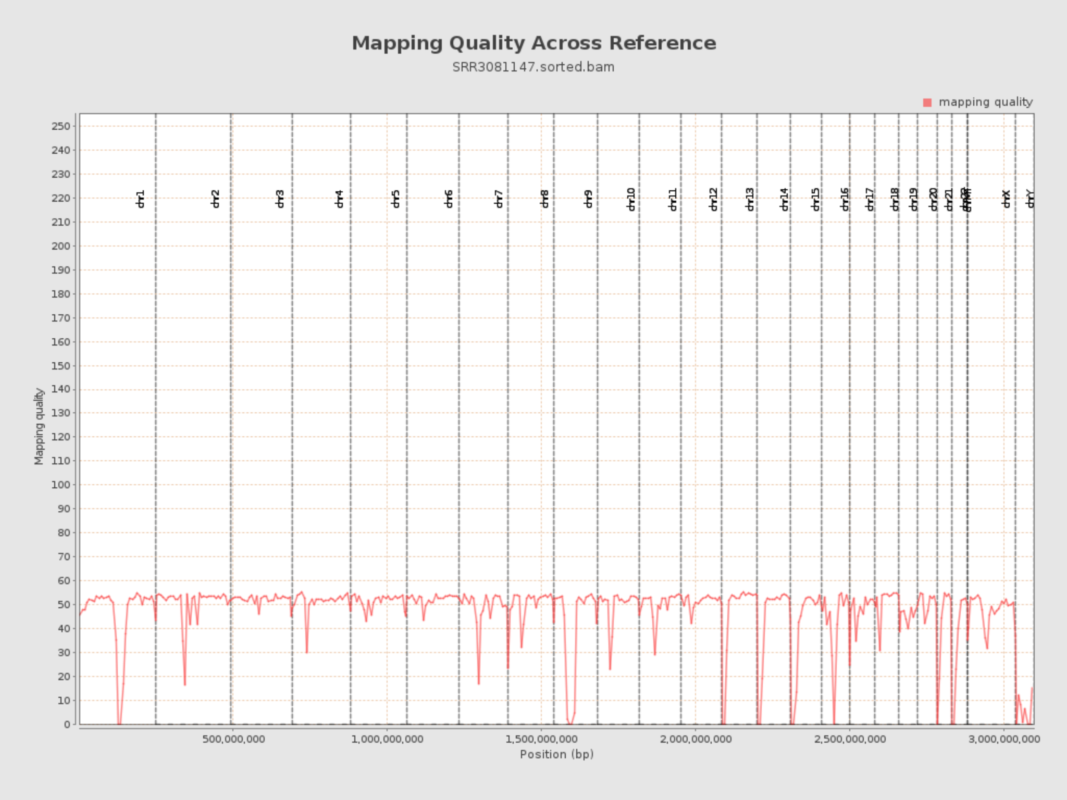
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram