Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 10:28:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081926.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_SRR3081926 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081926.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 10:28:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081926.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,731,989
Mapped reads	2,510,299 / 91.89%
Unmapped reads	221,690 / 8.11%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,037 / 0.59%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	118,923 / 4.35%
Duplication rate	3.89%
Clipped reads	968,470 / 35.45%

2.2. ACGT Content

Number/percentage of A's	48,200,912 / 28.3%
Number/percentage of C's	31,225,383 / 18.34%
Number/percentage of T's	54,158,218 / 31.8%
Number/percentage of G's	36,697,696 / 21.55%
Number/percentage of N's	21,584 / 0.01%
GC Percentage	39.88%

2.3. Coverage

Mean	0.055

Standard Deviation	0.3968

2.4. Mapping Quality

Mean Mapping Quality	46.63

2.5. Mismatches and indels

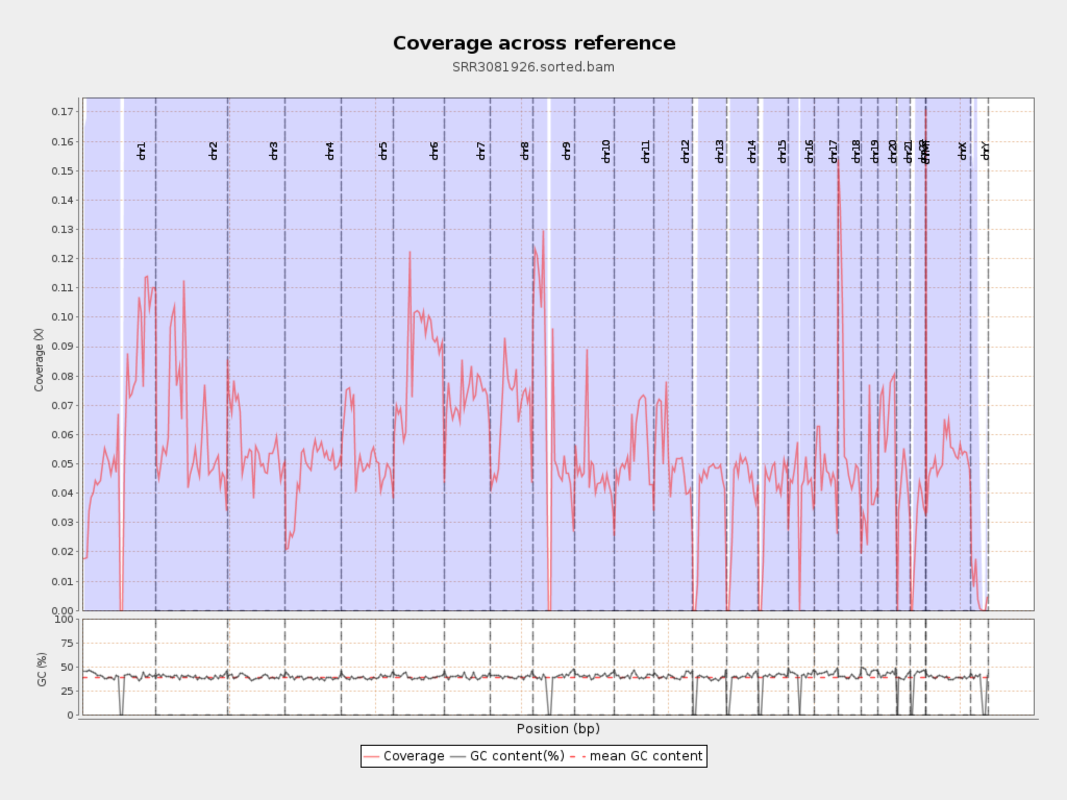
General error rate	0.76%
Mismatches	1,265,485
Insertions	11,880
Mapped reads with at least one insertion	0.47%
Deletions	35,711
Mapped reads with at least one deletion	1.41%
Homopolymer indels	48.25%

2.6. Chromosome stats

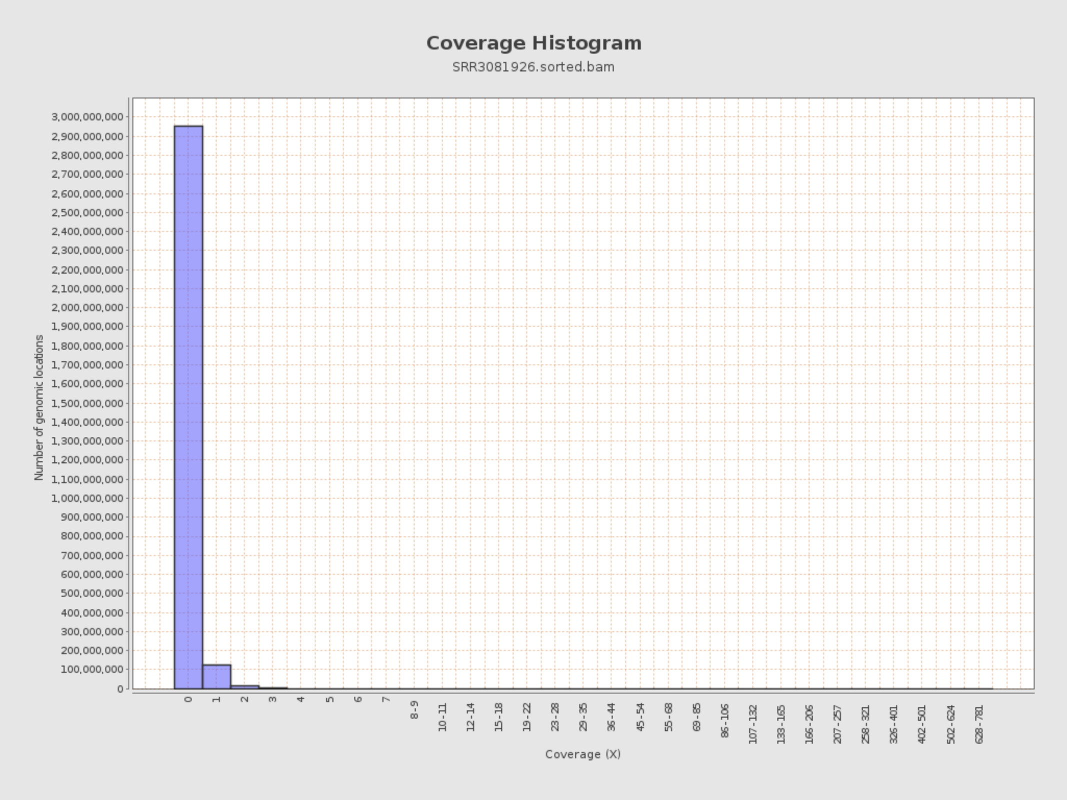
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15474628	0.0621	0.5527
chr2	243199373	14847995	0.0611	0.5592
chr3	198022430	11195542	0.0565	0.2717
chr4	191154276	8867167	0.0464	0.2579
chr5	180915260	9707736	0.0537	0.2645
chr6	171115067	14984012	0.0876	0.4146
chr7	159138663	11505334	0.0723	0.4662

chr8	146364022	9837581	0.0672	0.5884
chr9	141213431	9290486	0.0658	0.4616
chr10	135534747	6455242	0.0476	0.4011
chr11	135006516	7449191	0.0552	0.3177
chr12	133851895	7054204	0.0527	0.2708
chr13	115169878	4489995	0.039	0.2247
chr14	107349540	4228770	0.0394	0.254
chr15	102531392	3839179	0.0374	0.2193
chr16	90354753	3681654	0.0407	0.2626
chr17	81195210	3948499	0.0486	0.2676
chr18	78077248	5181060	0.0664	0.6677
chr19	59128983	2271164	0.0384	0.498
chr20	63025520	4349979	0.069	0.3045
chr21	48129895	1851979	0.0385	0.2515
chr22	51304566	1385152	0.027	0.1842
chrMT	16571	2830	0.1708	0.4383
chrX	155270560	8108528	0.0522	0.2964
chrY	59373566	359372	0.0061	0.128

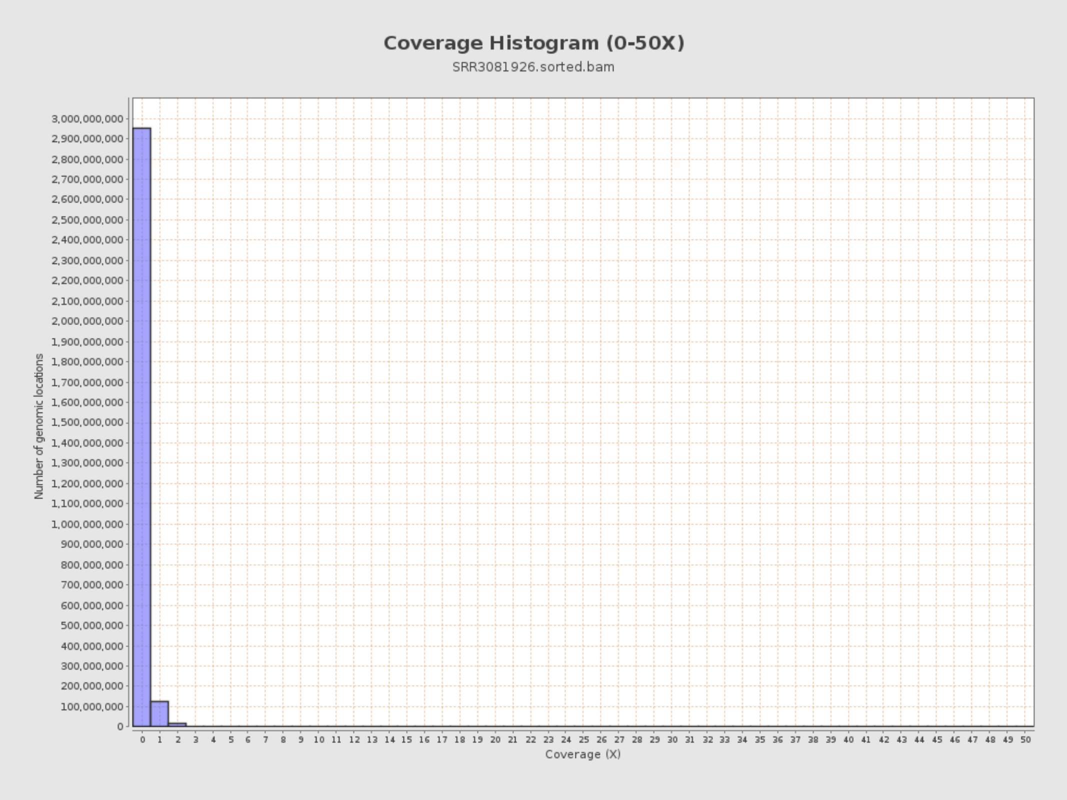
3. Results : Coverage across reference



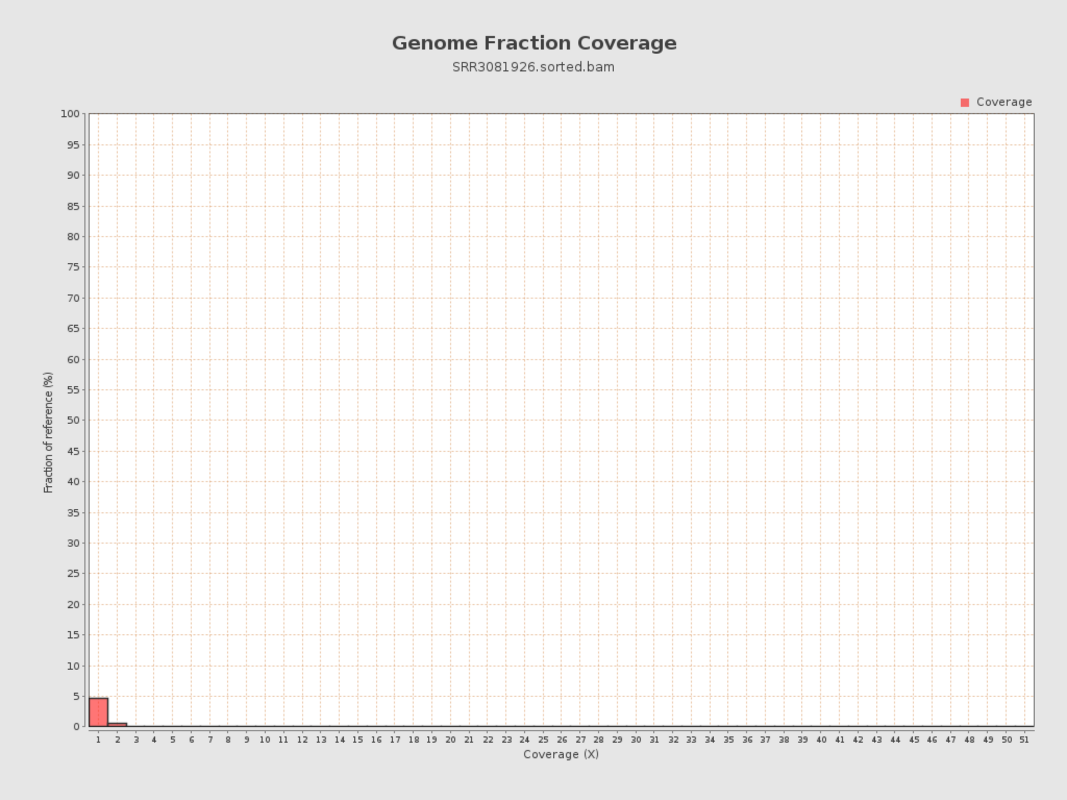
4. Results : Coverage Histogram



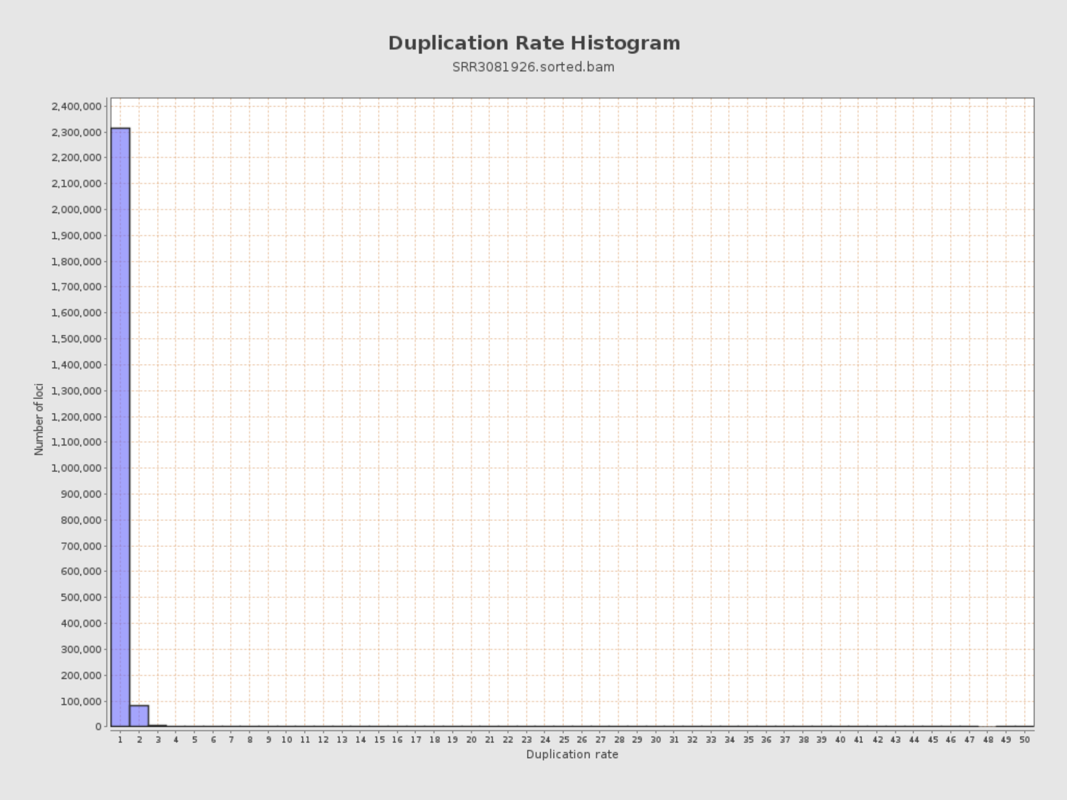
5. Results : Coverage Histogram (0-50X)



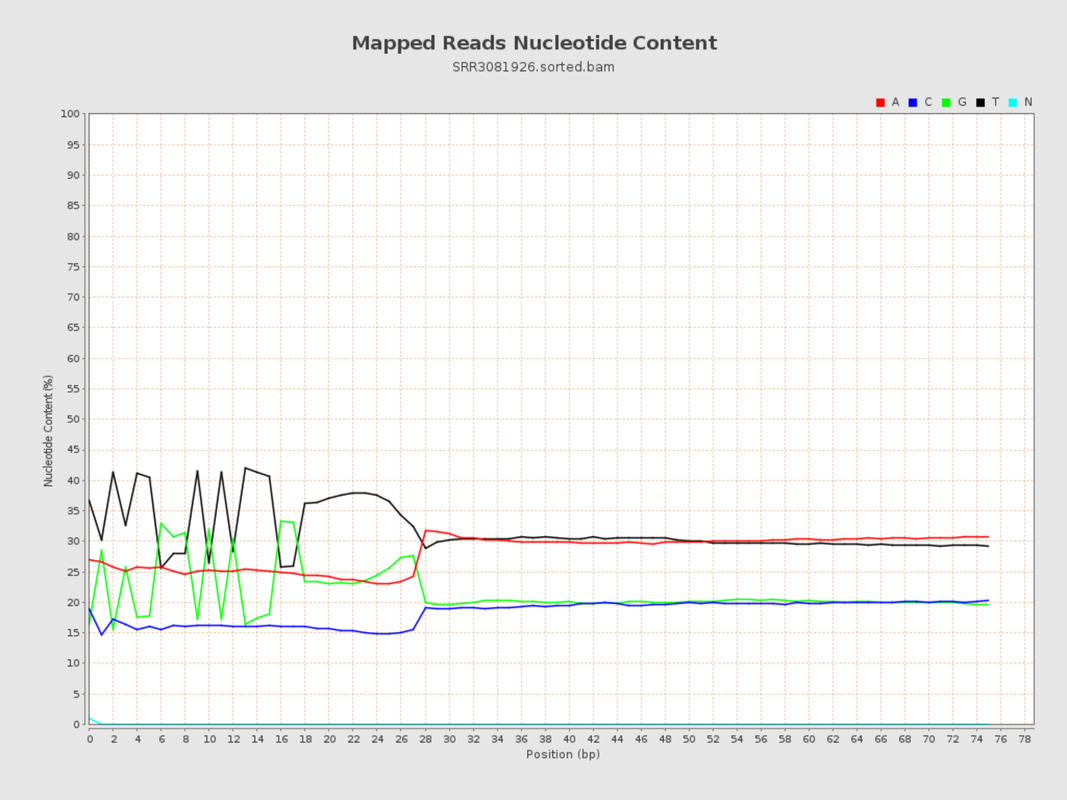
6. Results : Genome Fraction Coverage



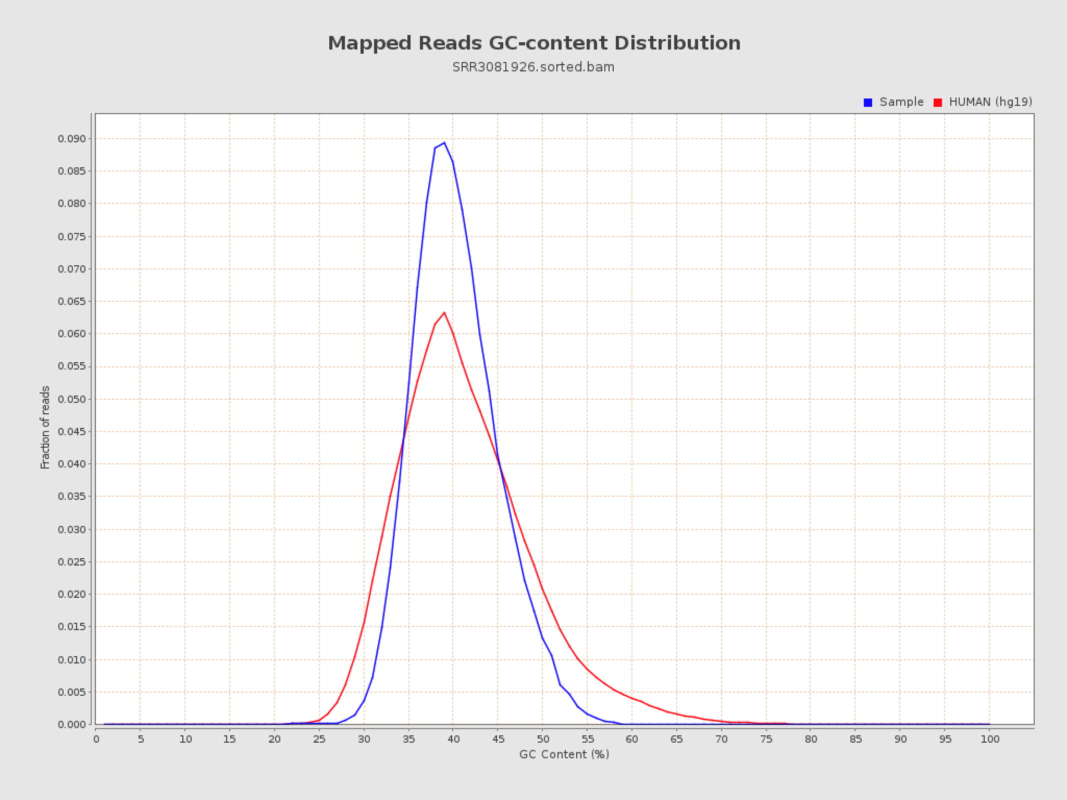
7. Results : Duplication Rate Histogram



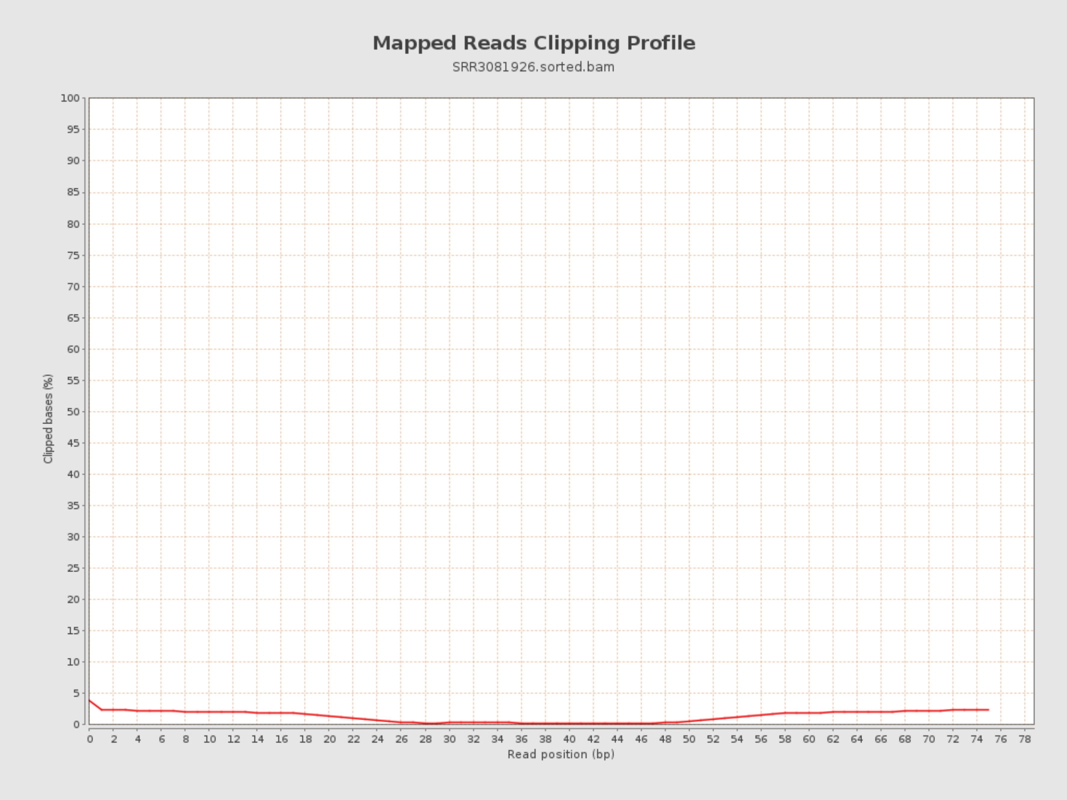
8. Results : Mapped Reads Nucleotide Content



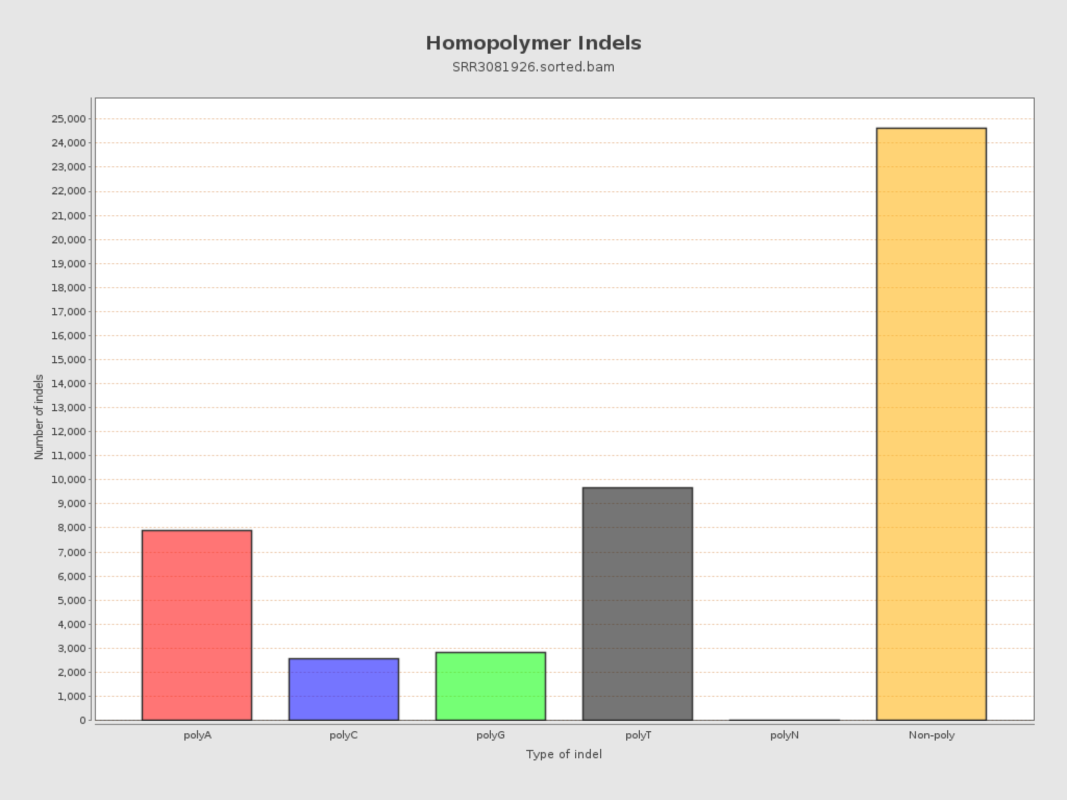
9. Results : Mapped Reads GC-content Distribution



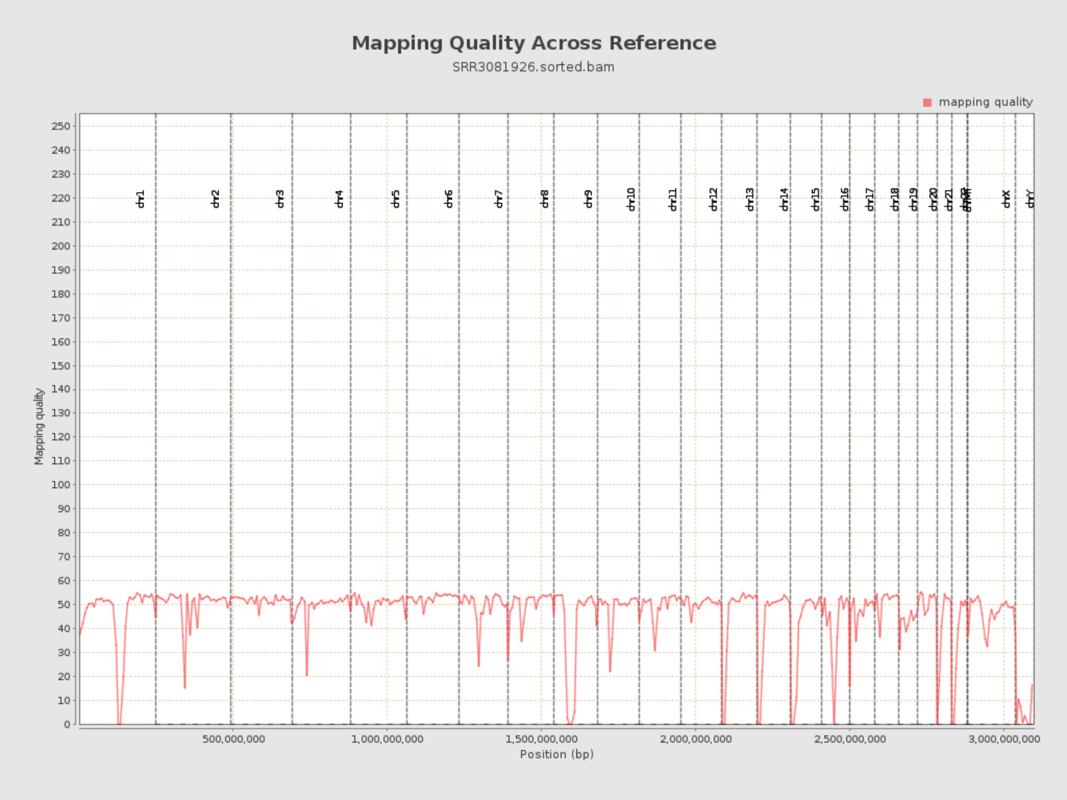
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram