Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 06:20:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081693.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_SRR3081693 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081693.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 06:20:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081693.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,487,632
Mapped reads	2,171,704 / 87.3%
Unmapped reads	315,928 / 12.7%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	25,939 / 1.04%
Read min/max/mean length	30 / 76 / 76.36
Duplicated reads (estimated)	111,030 / 4.46%
Duplication rate	4.18%
Clipped reads	914,837 / 36.78%

2.2. ACGT Content

Number/percentage of A's	41,271,801 / 28.16%
Number/percentage of C's	26,199,751 / 17.88%
Number/percentage of T's	47,493,811 / 32.41%
Number/percentage of G's	31,467,885 / 21.47%
Number/percentage of N's	106,423 / 0.07%
GC Percentage	39.35%

2.3. Coverage

Mean	0.0474

Standard Deviation	0.3771

2.4. Mapping Quality

Mean Mapping Quality	47.44

2.5. Mismatches and indels

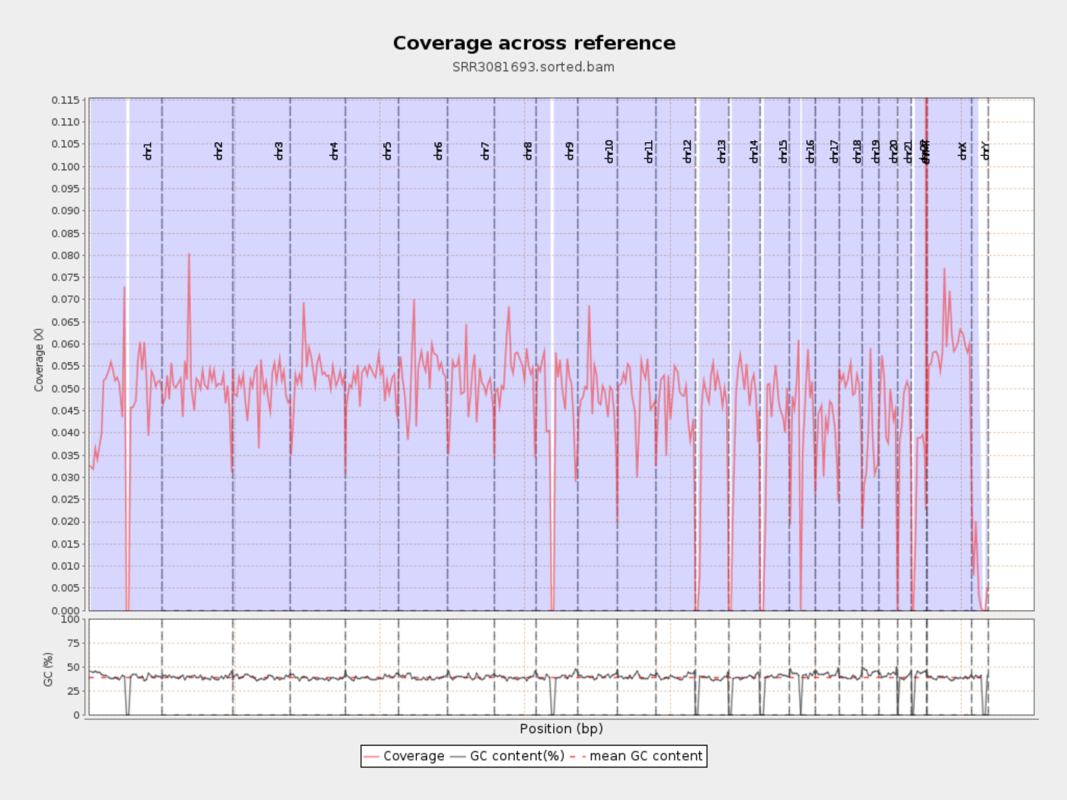
General error rate	0.89%
Mismatches	1,276,507
Insertions	12,508
Mapped reads with at least one insertion	0.57%
Deletions	33,446
Mapped reads with at least one deletion	1.53%
Homopolymer indels	49.44%

2.6. Chromosome stats

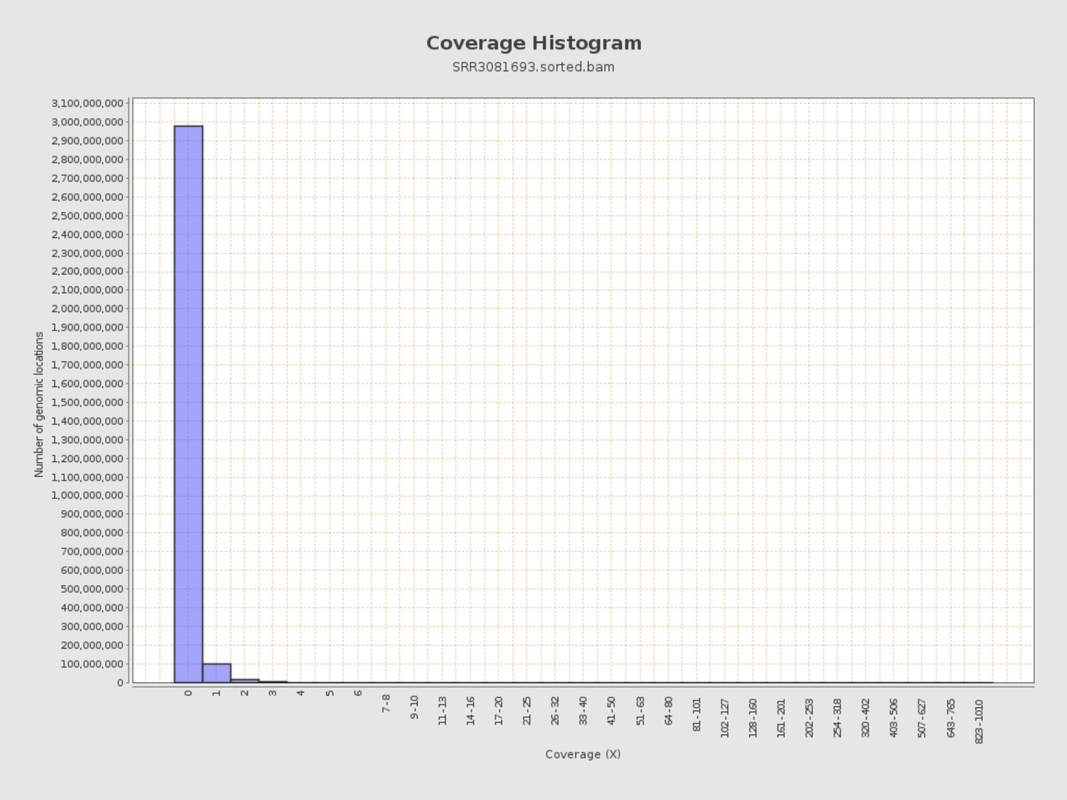
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11493114	0.0461	0.5786
chr2	243199373	12457165	0.0512	0.4009
chr3	198022430	9985329	0.0504	0.2694
chr4	191154276	10150151	0.0531	0.2945
chr5	180915260	9356844	0.0517	0.2734
chr6	171115067	9186590	0.0537	0.3301
chr7	159138663	8126924	0.0511	0.4128

chr8	146364022	7881832	0.0539	0.6773
chr9	141213431	6275738	0.0444	0.3535
chr10	135534747	6650026	0.0491	0.355
chr11	135006516	6582844	0.0488	0.3537
chr12	133851895	6240805	0.0466	0.2617
chr13	115169878	4738528	0.0411	0.2427
chr14	107349540	4540216	0.0423	0.2595
chr15	102531392	3936911	0.0384	0.2335
chr16	90354753	3871110	0.0428	0.2656
chr17	81195210	3217256	0.0396	0.2673
chr18	78077248	3985075	0.051	0.6131
chr19	59128983	2172324	0.0367	0.4401
chr20	63025520	2855387	0.0453	0.2679
chr21	48129895	1948503	0.0405	0.2612
chr22	51304566	1345581	0.0262	0.1924
chrMT	16571	49935	3.0134	2.2726
chrX	155270560	9182772	0.0591	0.3152
chrY	59373566	362916	0.0061	0.1575

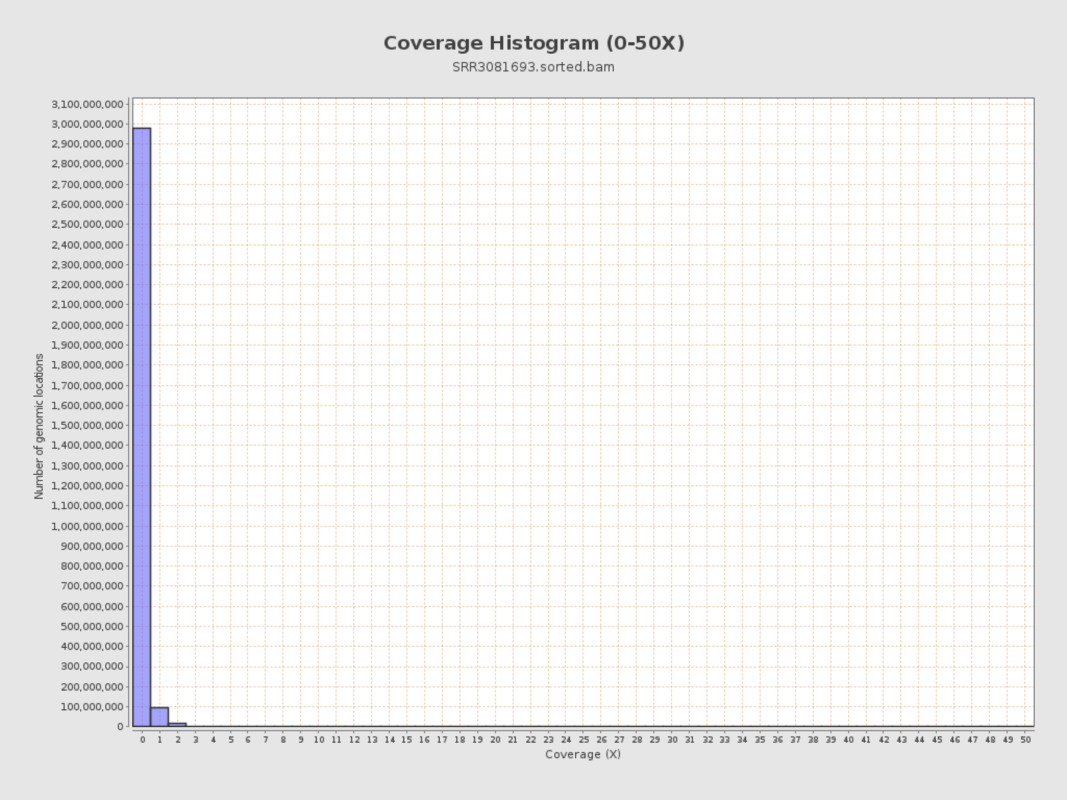
3. Results : Coverage across reference



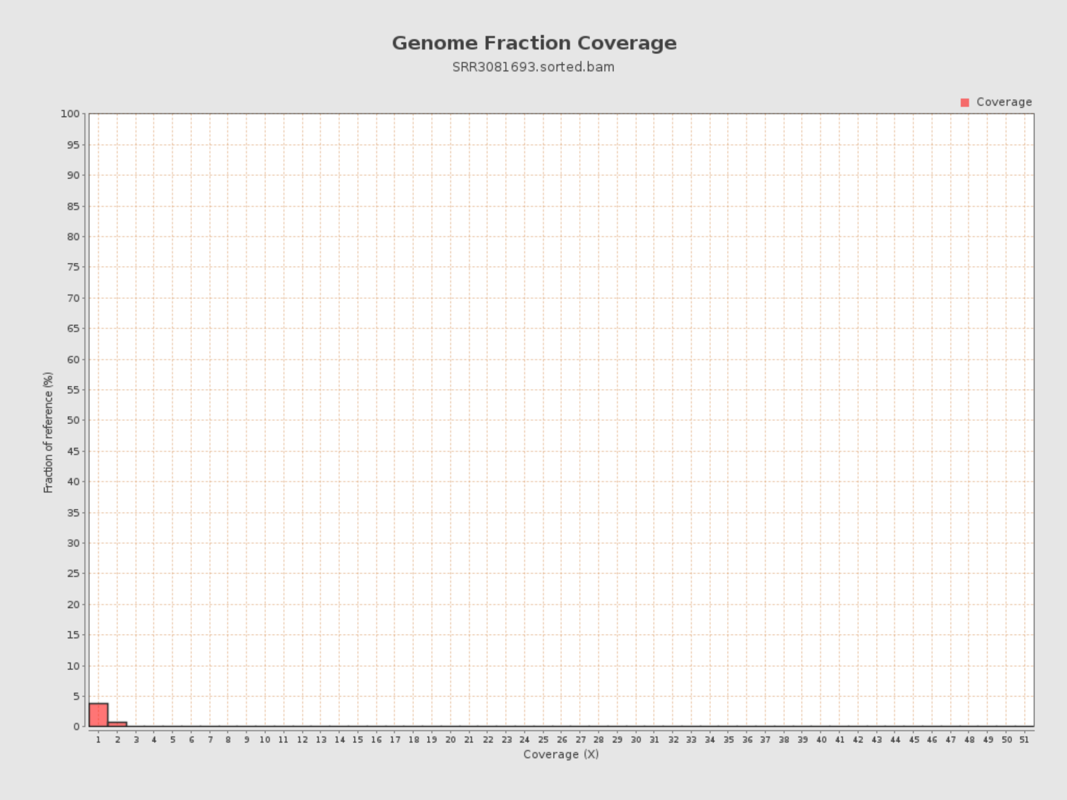
4. Results : Coverage Histogram



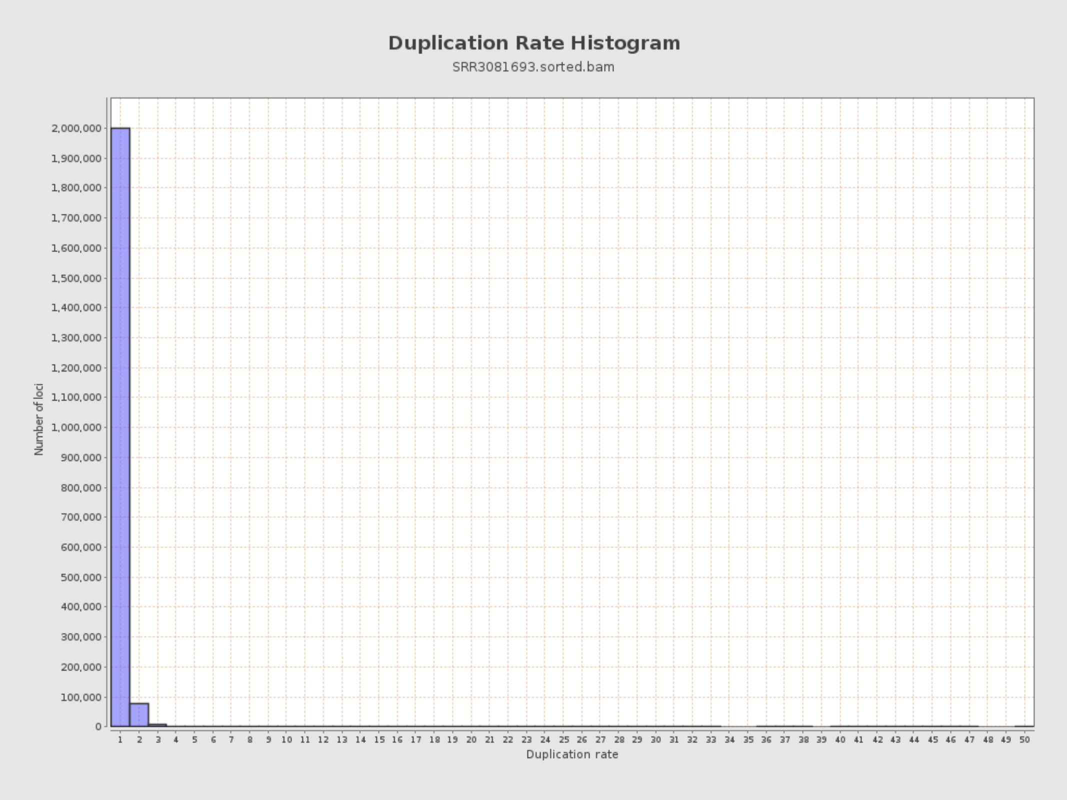
5. Results : Coverage Histogram (0-50X)



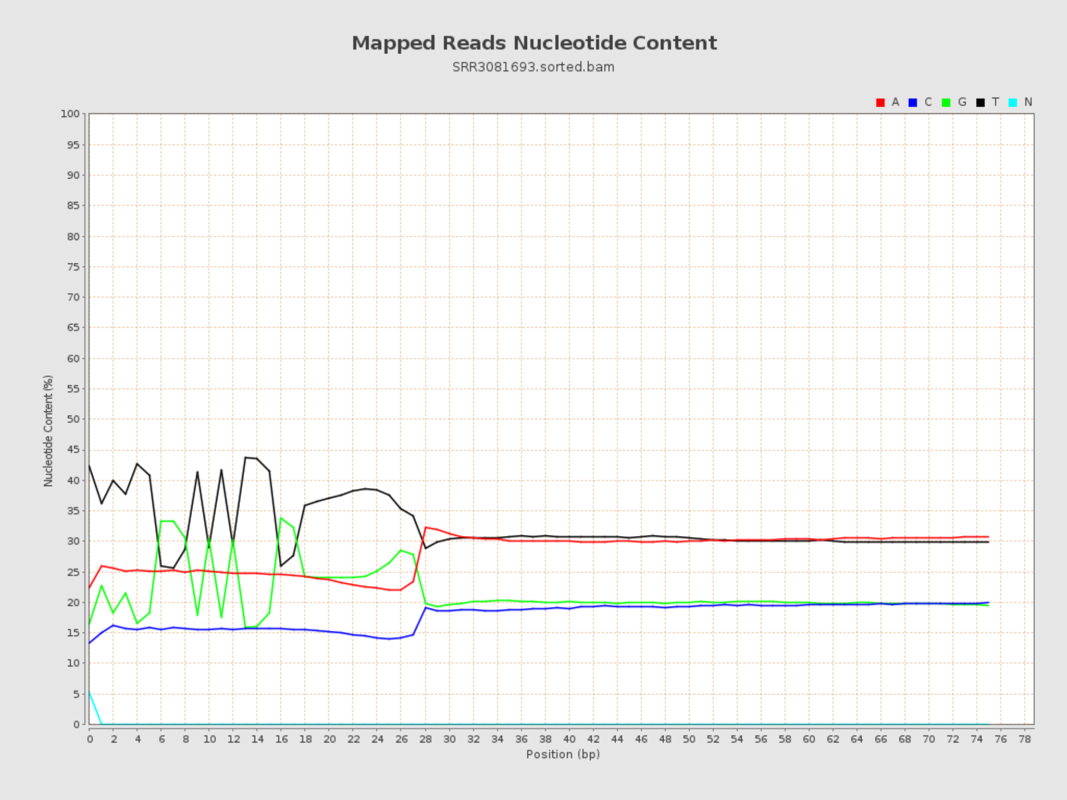
6. Results : Genome Fraction Coverage



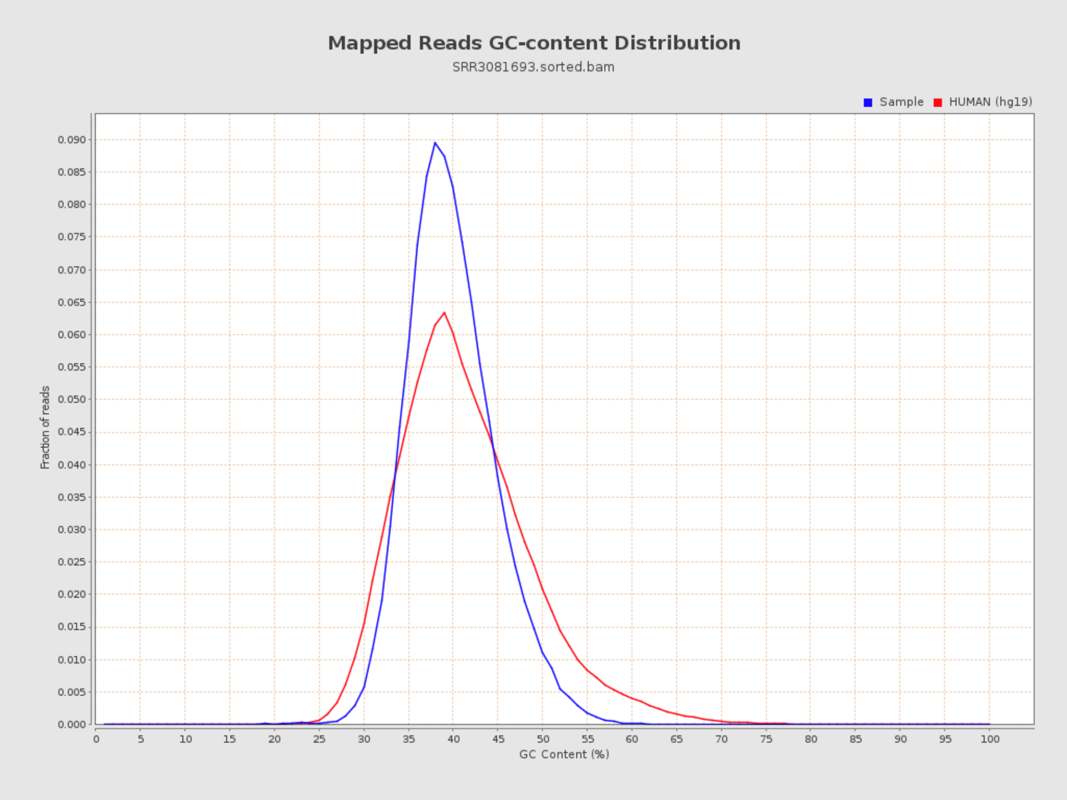
7. Results : Duplication Rate Histogram



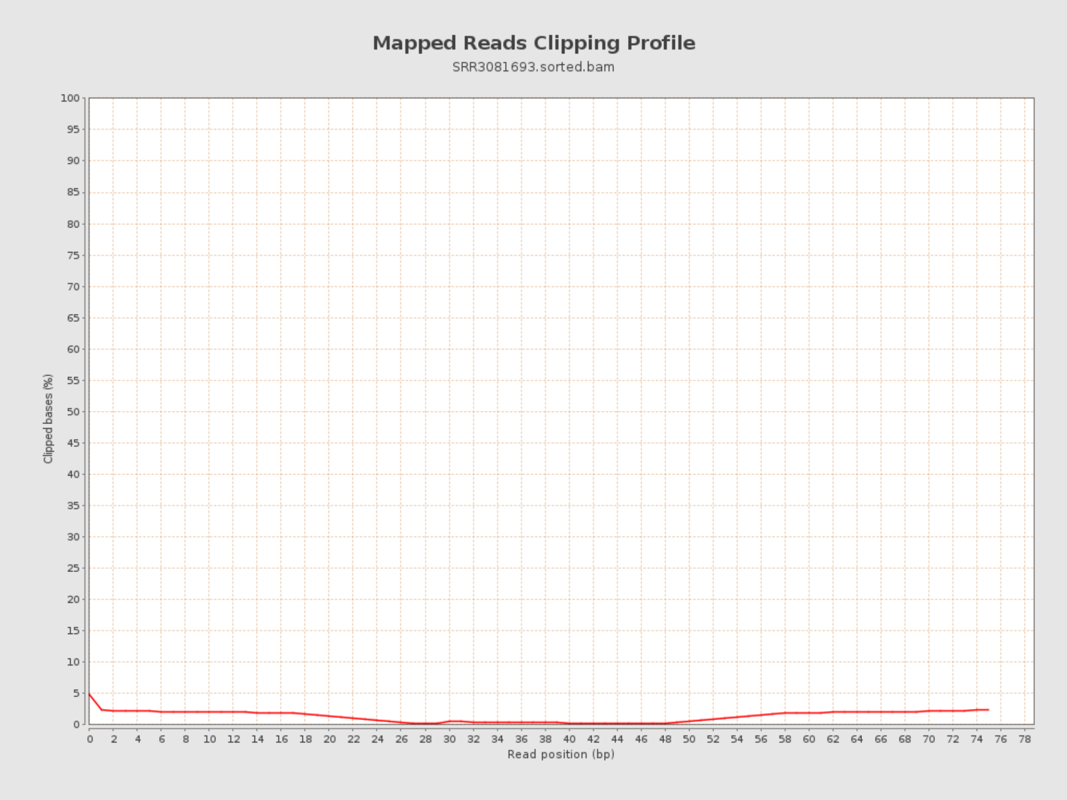
8. Results : Mapped Reads Nucleotide Content



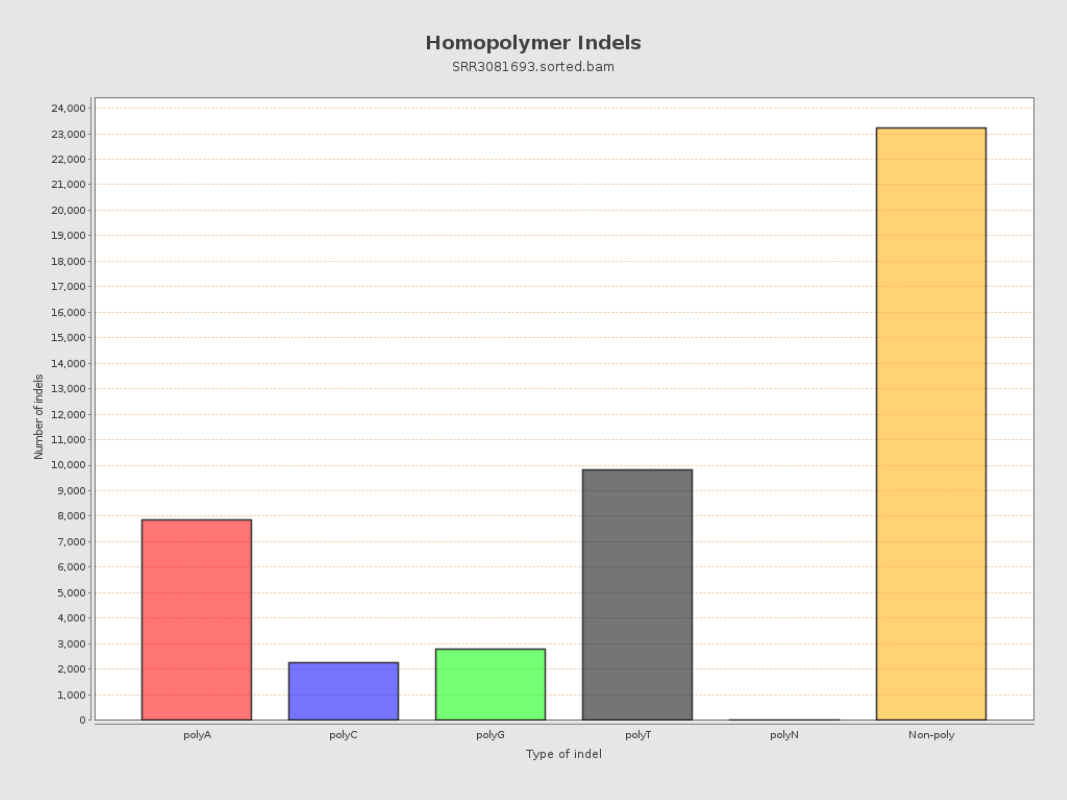
9. Results : Mapped Reads GC-content Distribution



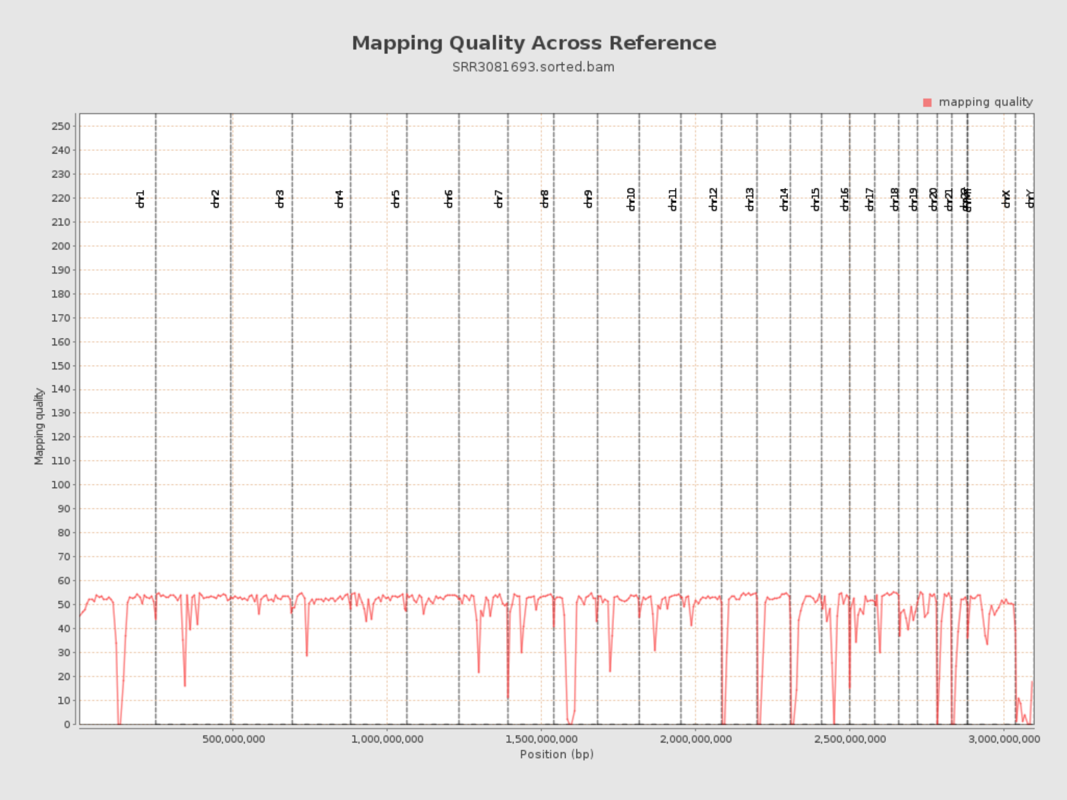
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram