Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 14:36:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013181.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_SRR6013181 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013181.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 14:36:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013181.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,767,734
Mapped reads	2,505,237 / 90.52%
Unmapped reads	262,497 / 9.48%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,838 / 0.43%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	88,469 / 3.2%
Duplication rate	2.67%
Clipped reads	1,162,422 / 42%

2.2. ACGT Content

Number/percentage of A's	45,408,829 / 27.39%
Number/percentage of C's	31,399,930 / 18.94%
Number/percentage of T's	51,001,185 / 30.77%
Number/percentage of G's	37,914,357 / 22.87%
Number/percentage of N's	39,913 / 0.02%
GC Percentage	41.81%

2.3. Coverage

Mean	0.0536

Standard Deviation	0.4077

2.4. Mapping Quality

Mean Mapping Quality	44.64

2.5. Mismatches and indels

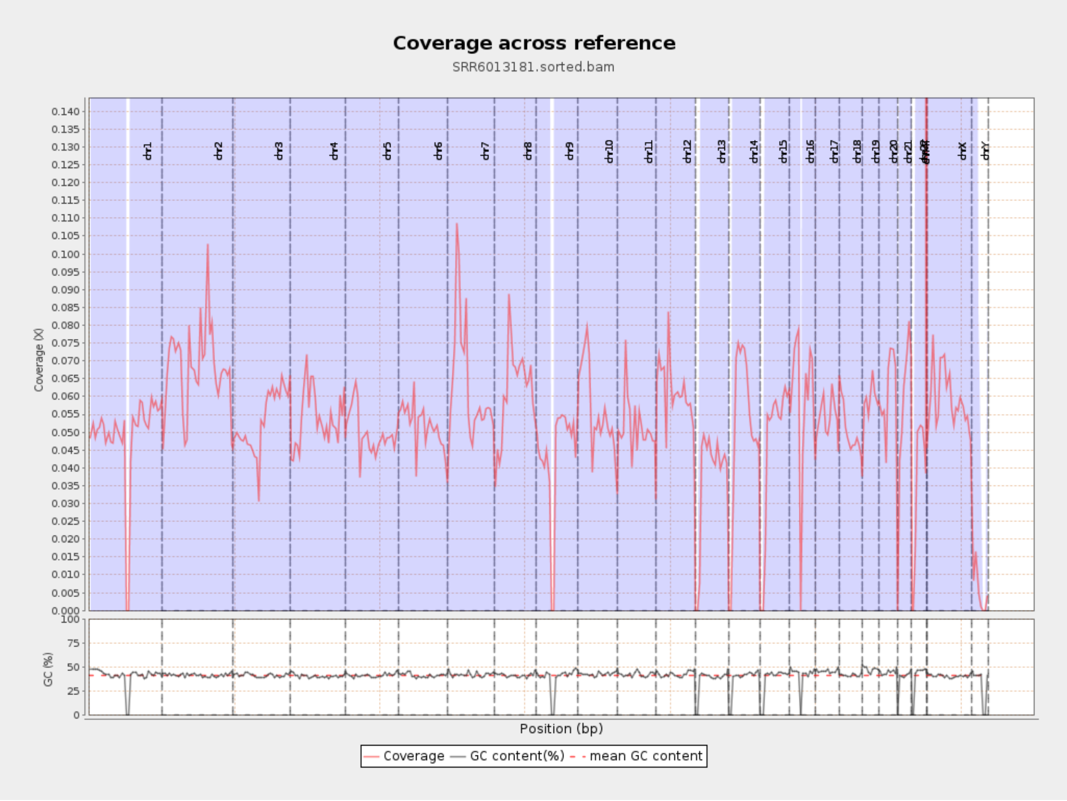
General error rate	0.77%
Mismatches	1,258,141
Insertions	11,861
Mapped reads with at least one insertion	0.47%
Deletions	37,552
Mapped reads with at least one deletion	1.48%
Homopolymer indels	46.92%

2.6. Chromosome stats

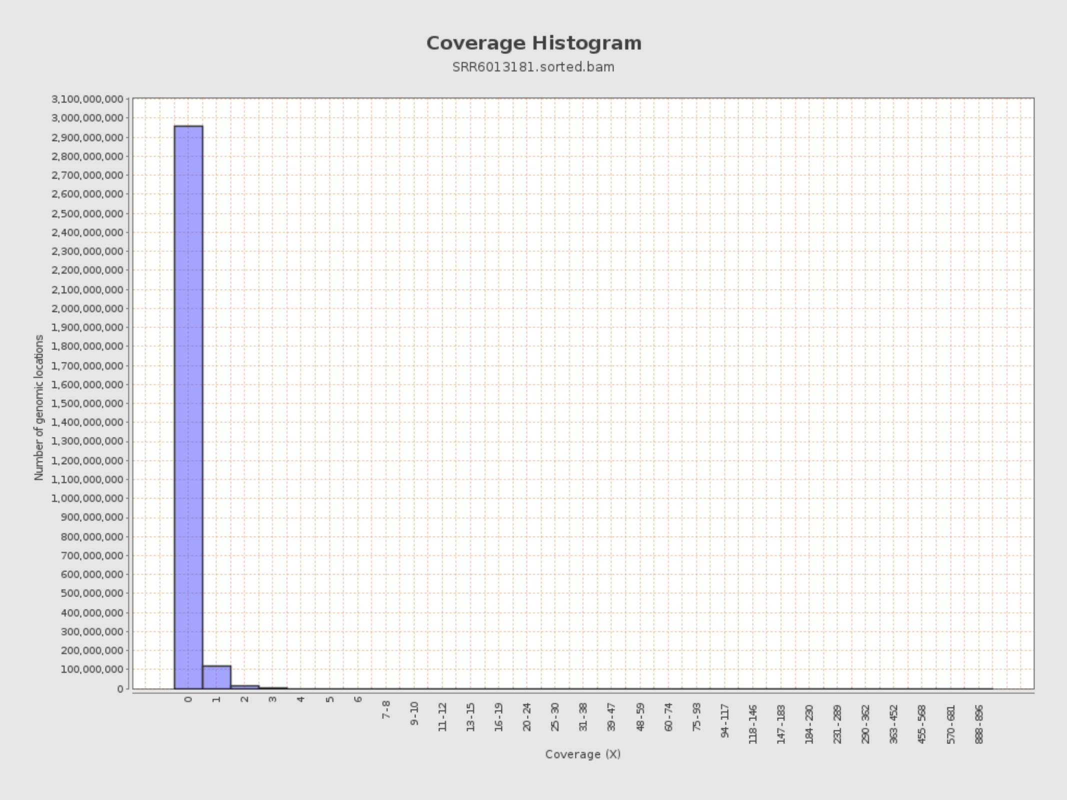
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12203442	0.049	0.4483
chr2	243199373	16592862	0.0682	0.5396
chr3	198022430	10511308	0.0531	0.2639
chr4	191154276	10300307	0.0539	0.2782
chr5	180915260	9028505	0.0499	0.2576
chr6	171115067	8853590	0.0517	0.314
chr7	159138663	10118683	0.0636	0.6959

chr8	146364022	9016680	0.0616	0.4498
chr9	141213431	6042865	0.0428	0.3339
chr10	135534747	7728809	0.057	0.3755
chr11	135006516	6946735	0.0515	0.3168
chr12	133851895	8252598	0.0617	0.291
chr13	115169878	4218852	0.0366	0.2446
chr14	107349540	5529272	0.0515	0.2751
chr15	102531392	4717093	0.046	0.2586
chr16	90354753	5363806	0.0594	0.3116
chr17	81195210	4391493	0.0541	0.2866
chr18	78077248	3952029	0.0506	0.5374
chr19	59128983	3476515	0.0588	0.4057
chr20	63025520	3833213	0.0608	0.2887
chr21	48129895	2738050	0.0569	0.2915
chr22	51304566	1746957	0.0341	0.2106
chrMT	16571	713401	43.0512	50.8845
chrX	155270560	9176906	0.0591	0.2966
chrY	59373566	375741	0.0063	0.1278

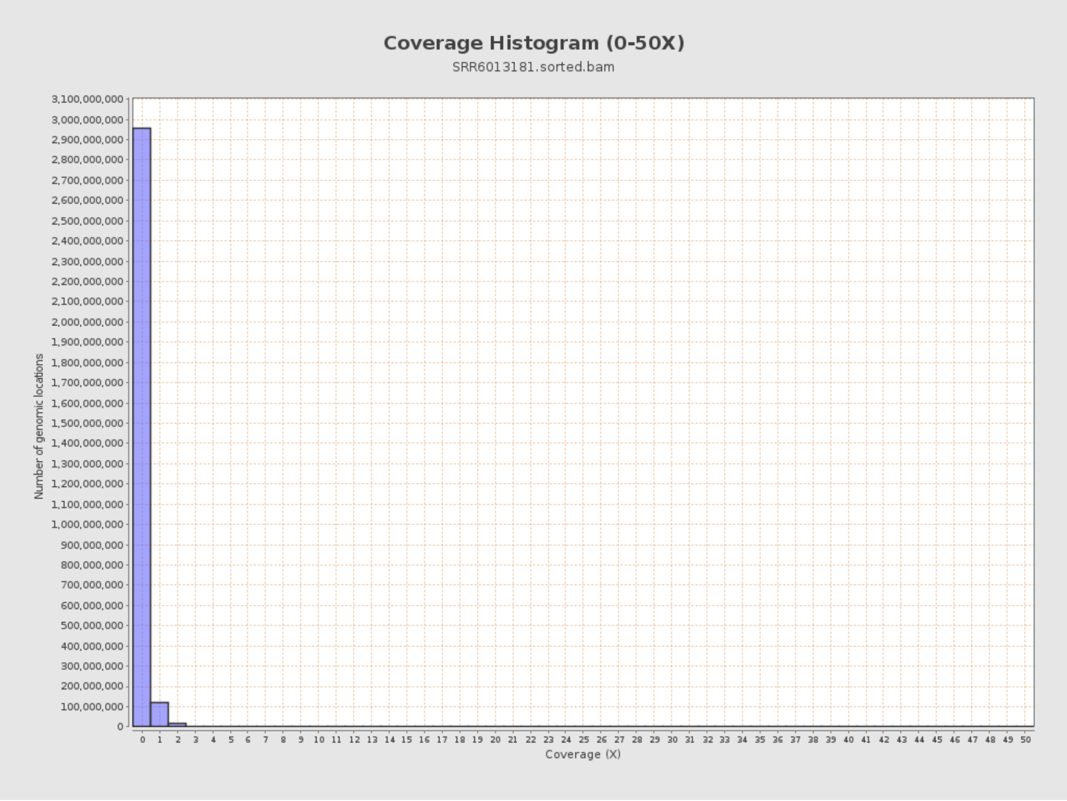
3. Results : Coverage across reference



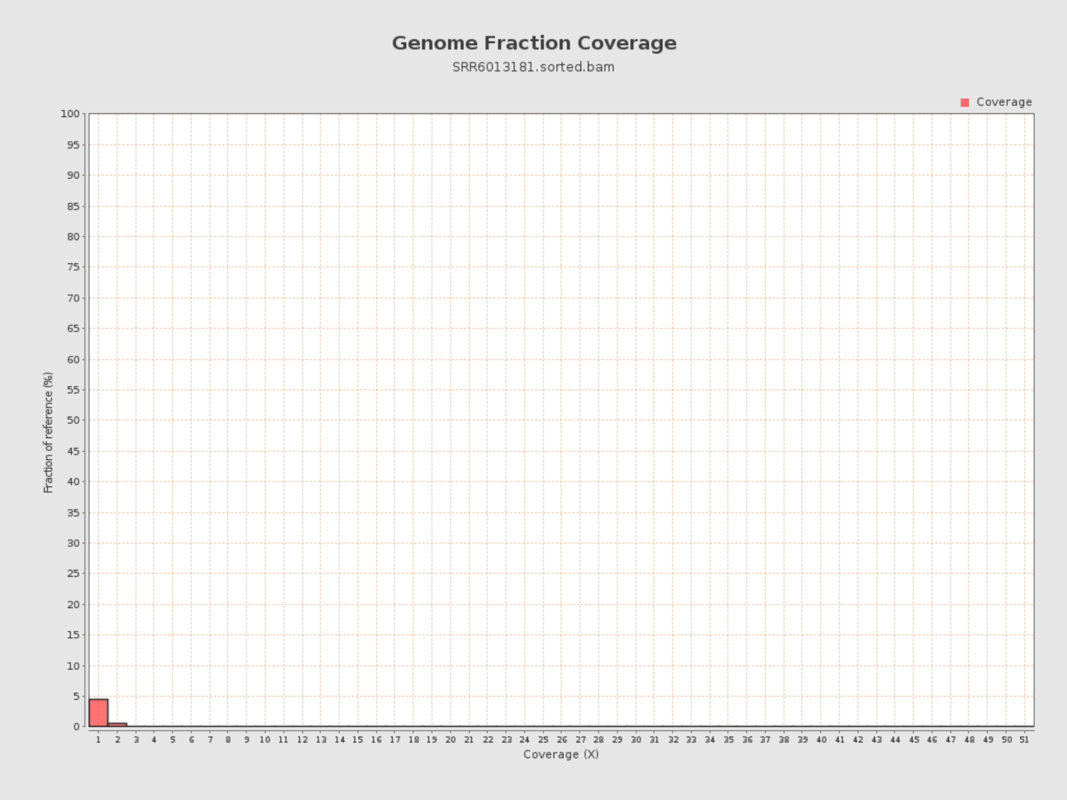
4. Results : Coverage Histogram



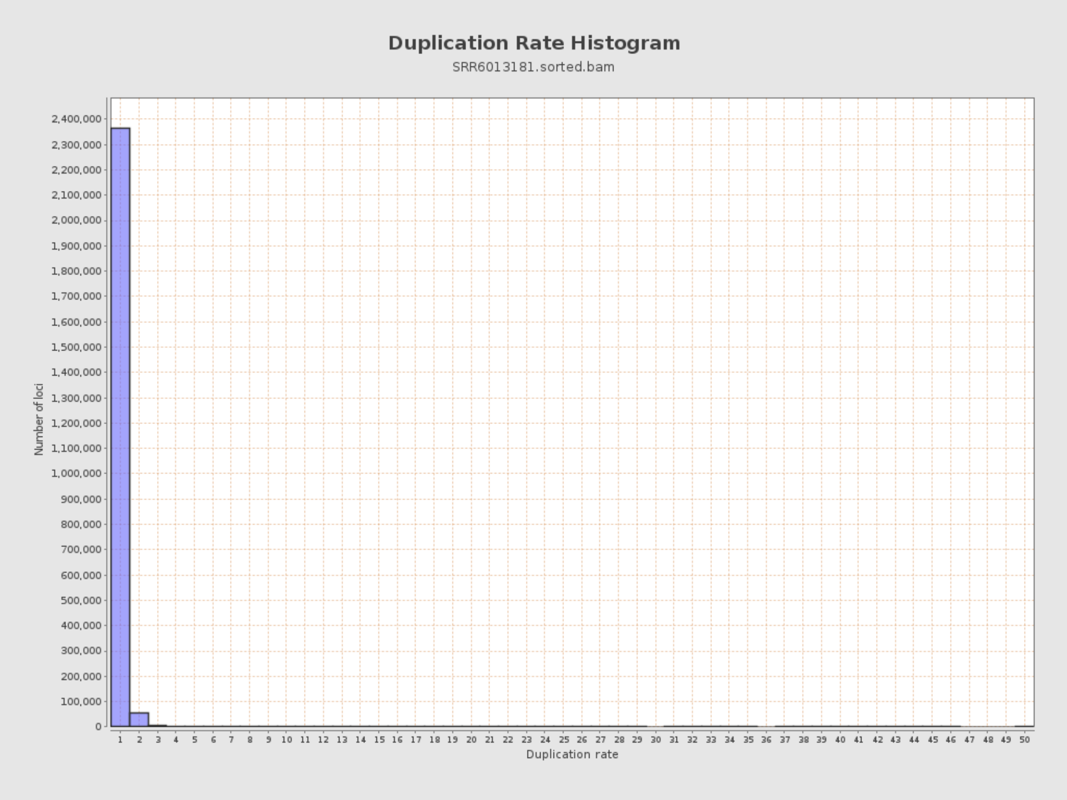
5. Results : Coverage Histogram (0-50X)



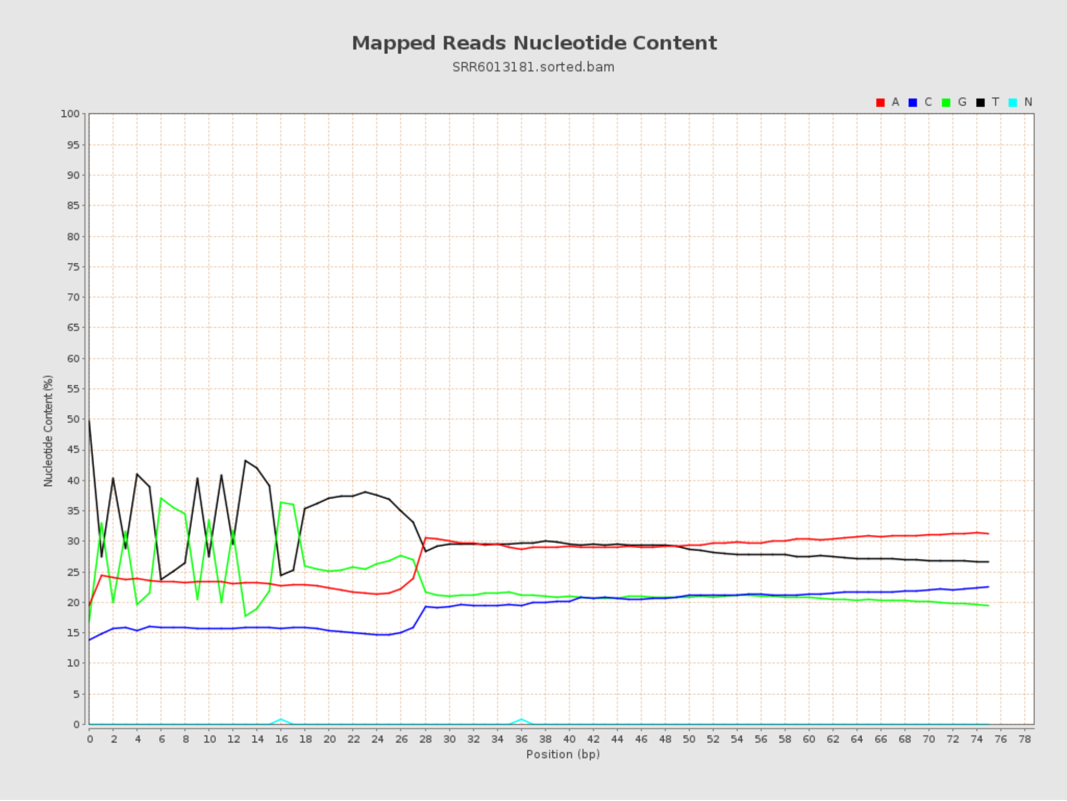
6. Results : Genome Fraction Coverage



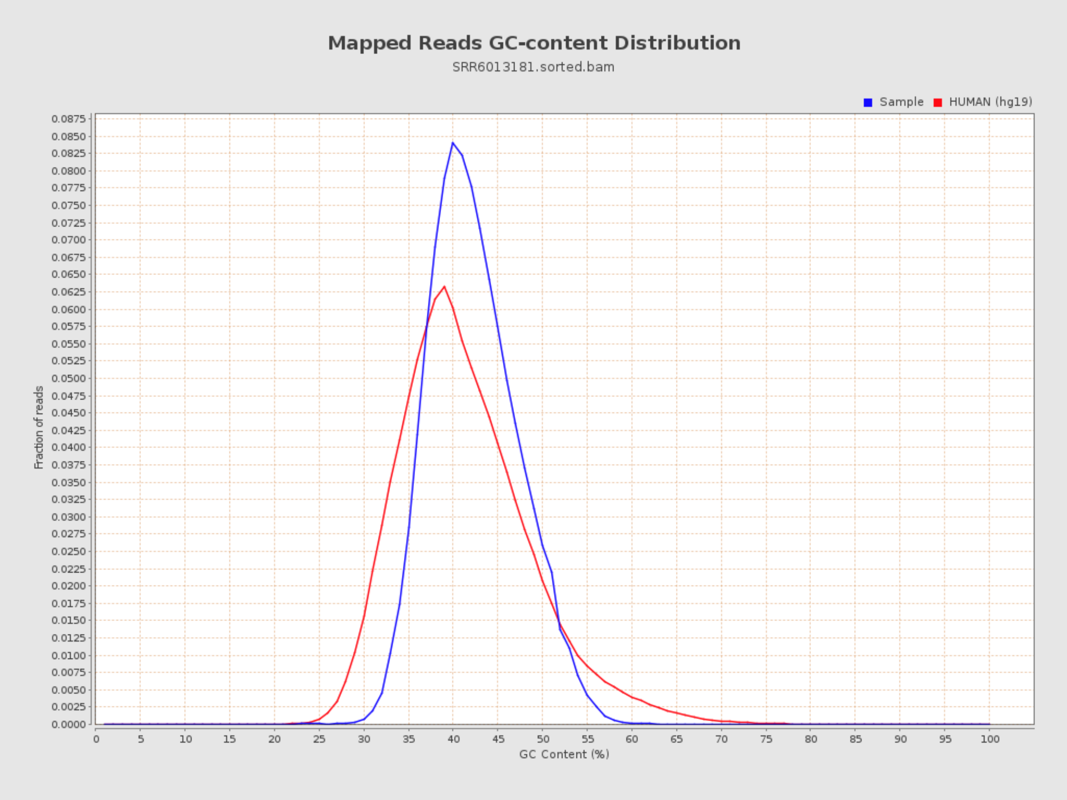
7. Results : Duplication Rate Histogram



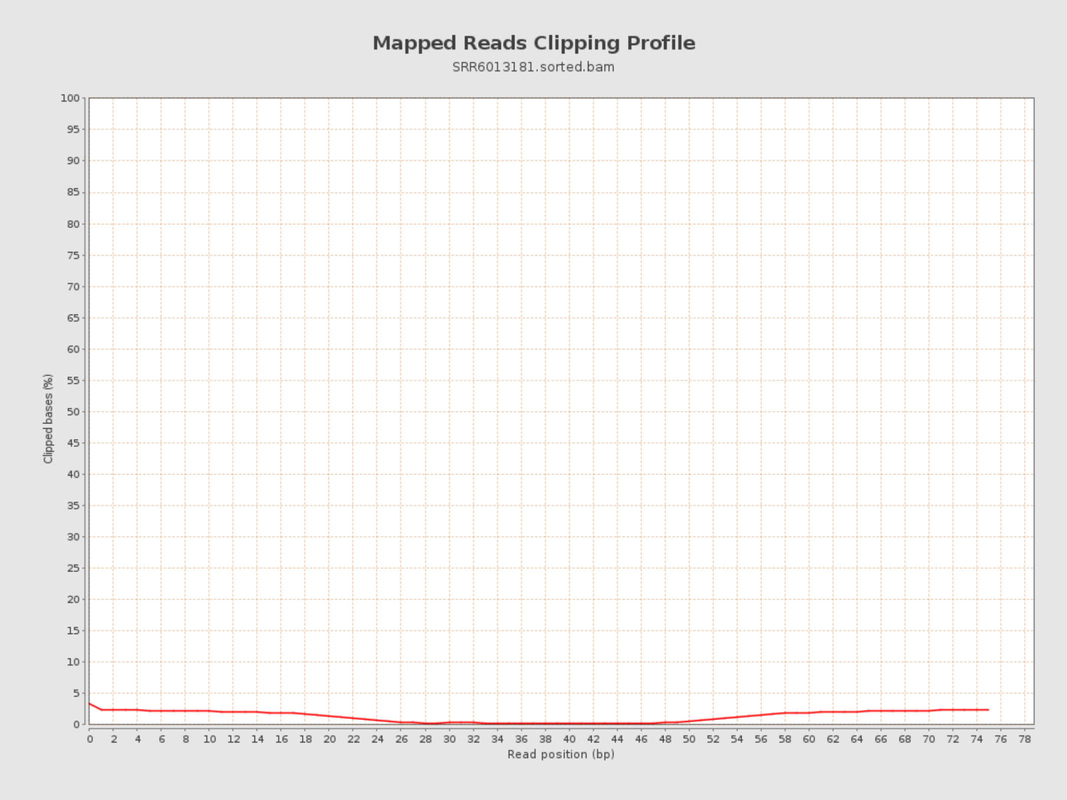
8. Results : Mapped Reads Nucleotide Content



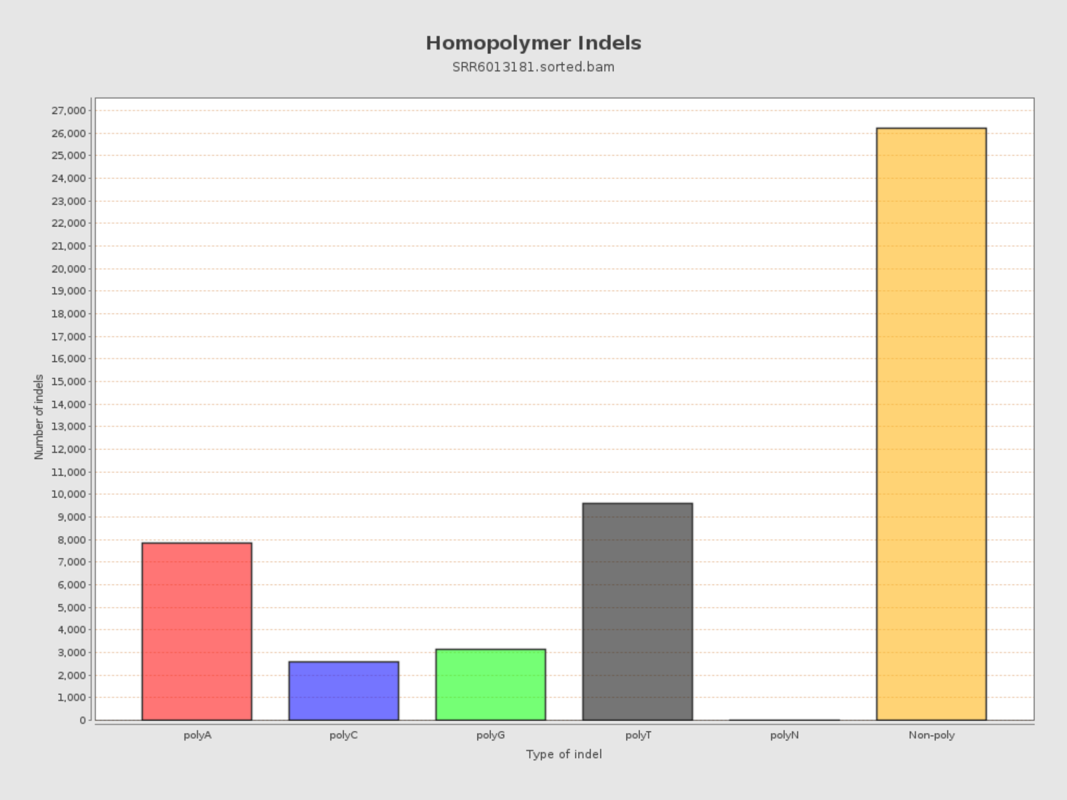
9. Results : Mapped Reads GC-content Distribution



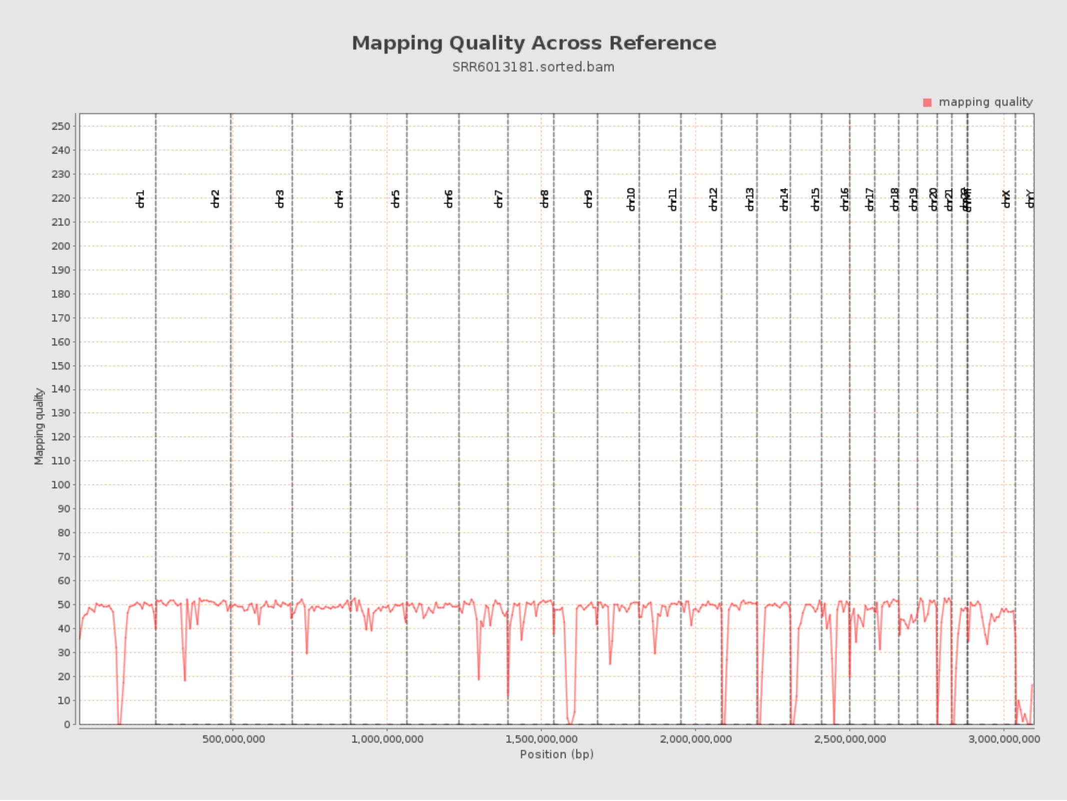
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram