Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 09:38:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081914.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_SRR3081914 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081914.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 09:38:15 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081914.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,772,111
Mapped reads	2,579,429 / 93.05%
Unmapped reads	192,682 / 6.95%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	21,702 / 0.78%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	91,289 / 3.29%
Duplication rate	2.75%
Clipped reads	959,803 / 34.62%

2.2. ACGT Content

Number/percentage of A's	50,606,984 / 28.6%
Number/percentage of C's	33,070,519 / 18.69%
Number/percentage of T's	55,607,155 / 31.43%
Number/percentage of G's	37,662,617 / 21.28%
Number/percentage of N's	2,102 / 0%
GC Percentage	39.97%

2.3. Coverage

Mean	0.0572

Standard Deviation	0.4117

2.4. Mapping Quality

Mean Mapping Quality	46.95

2.5. Mismatches and indels

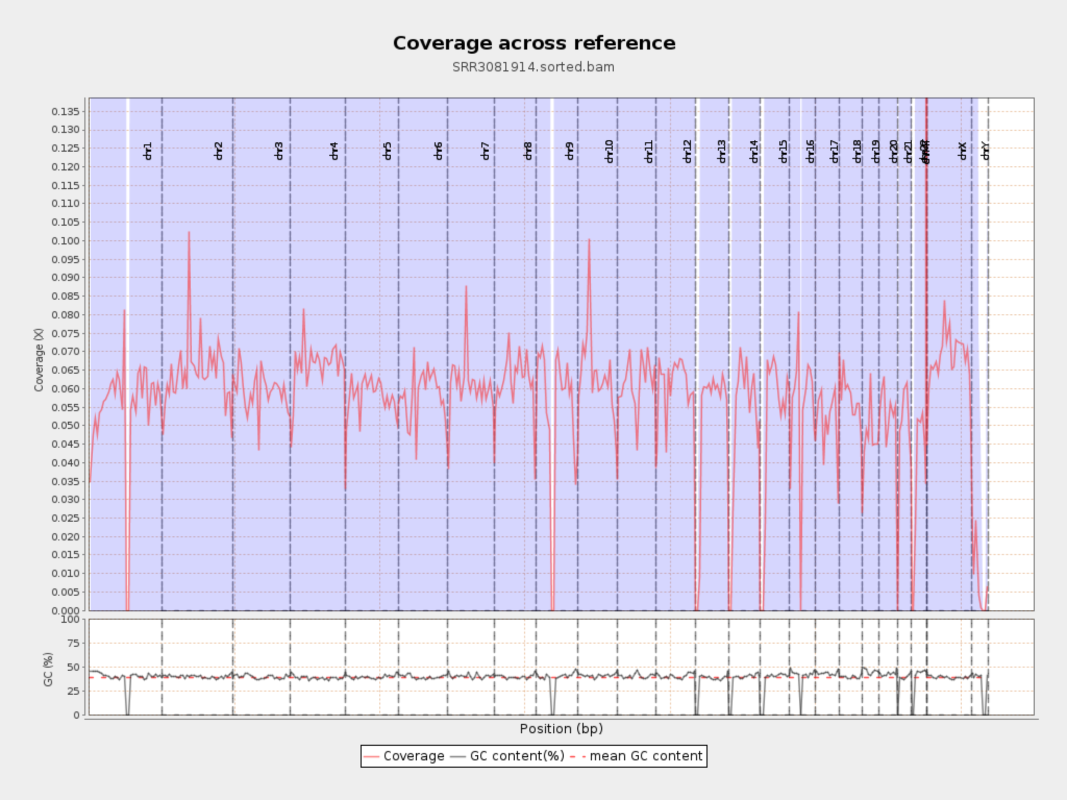
General error rate	0.85%
Mismatches	1,483,618
Insertions	14,229
Mapped reads with at least one insertion	0.55%
Deletions	39,424
Mapped reads with at least one deletion	1.51%
Homopolymer indels	47.86%

2.6. Chromosome stats

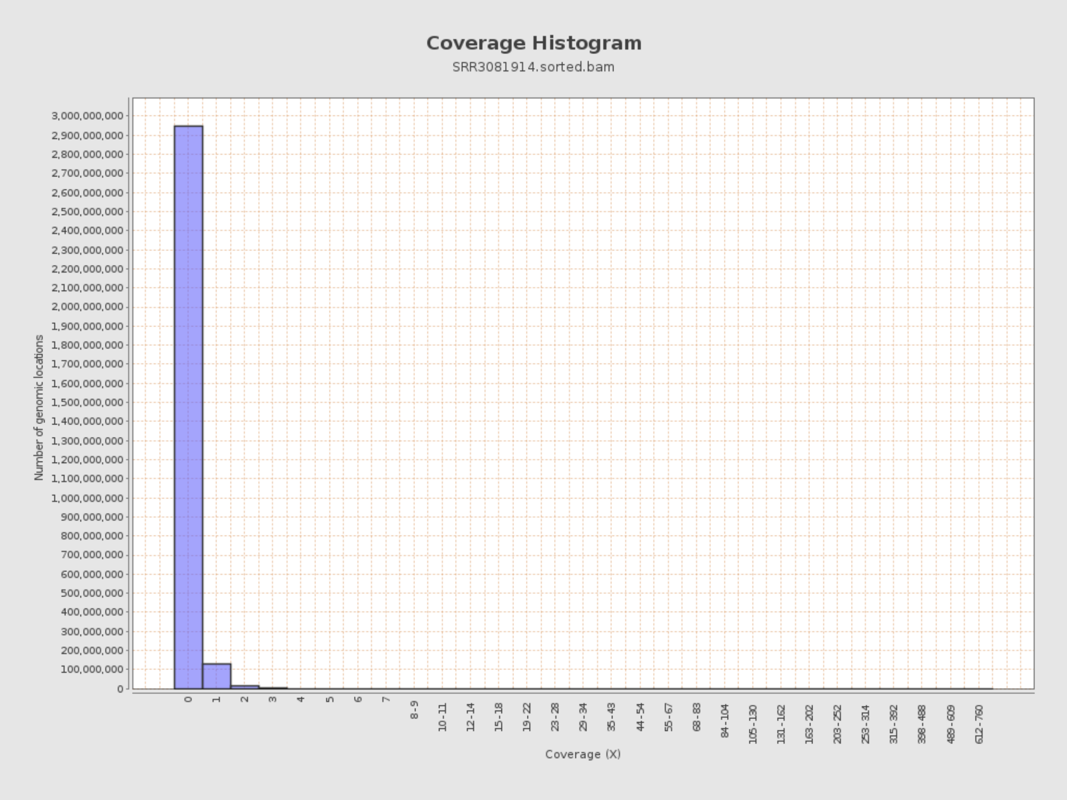
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13563295	0.0544	0.6519
chr2	243199373	15703268	0.0646	0.4967
chr3	198022430	11801865	0.0596	0.2795
chr4	191154276	12695858	0.0664	0.3157
chr5	180915260	10529814	0.0582	0.2747
chr6	171115067	9976521	0.0583	0.3115
chr7	159138663	9794895	0.0615	0.5155

chr8	146364022	9073066	0.062	0.5626
chr9	141213431	7605569	0.0539	0.3936
chr10	135534747	8729292	0.0644	0.4573
chr11	135006516	8285933	0.0614	0.3772
chr12	133851895	8141097	0.0608	0.2824
chr13	115169878	5741989	0.0499	0.2554
chr14	107349540	5384838	0.0502	0.2734
chr15	102531392	5120798	0.0499	0.2568
chr16	90354753	4977770	0.0551	0.304
chr17	81195210	4099948	0.0505	0.279
chr18	78077248	4519625	0.0579	0.7417
chr19	59128983	2785607	0.0471	0.5201
chr20	63025520	3346837	0.0531	0.2724
chr21	48129895	2274430	0.0473	0.2688
chr22	51304566	1789094	0.0349	0.2092
chrMT	16571	11493	0.6936	0.9878
chrX	155270560	10609139	0.0683	0.3281
chrY	59373566	452585	0.0076	0.1801

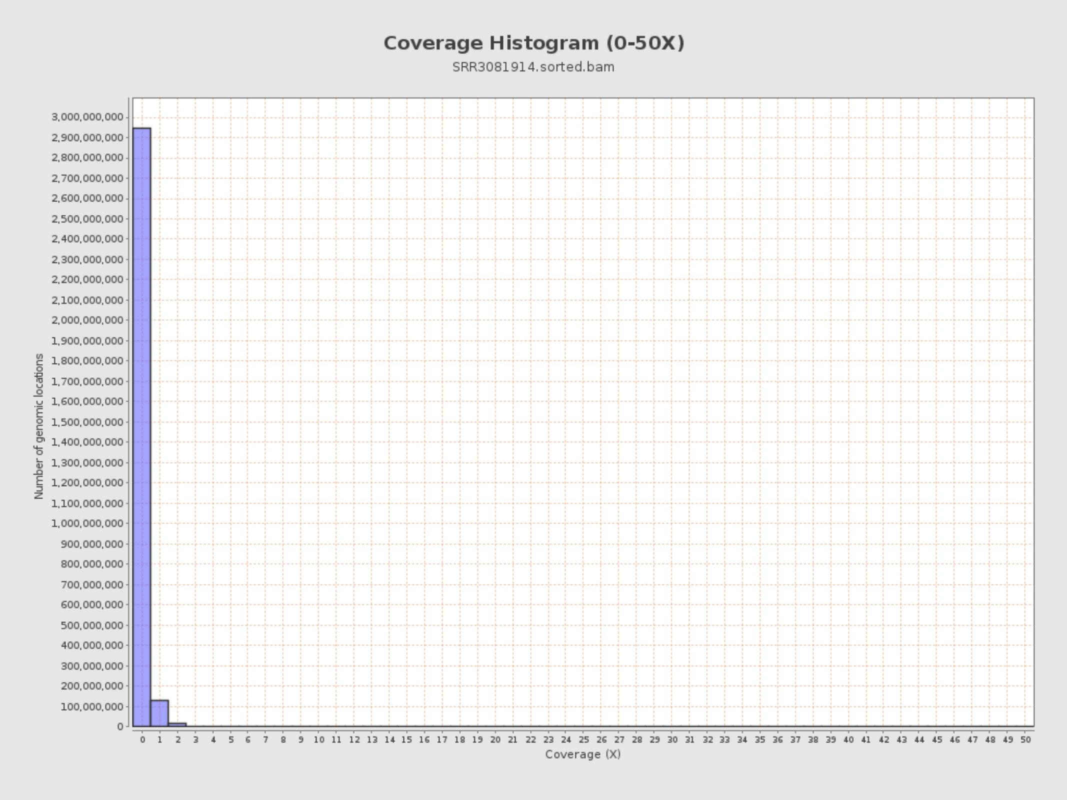
3. Results : Coverage across reference



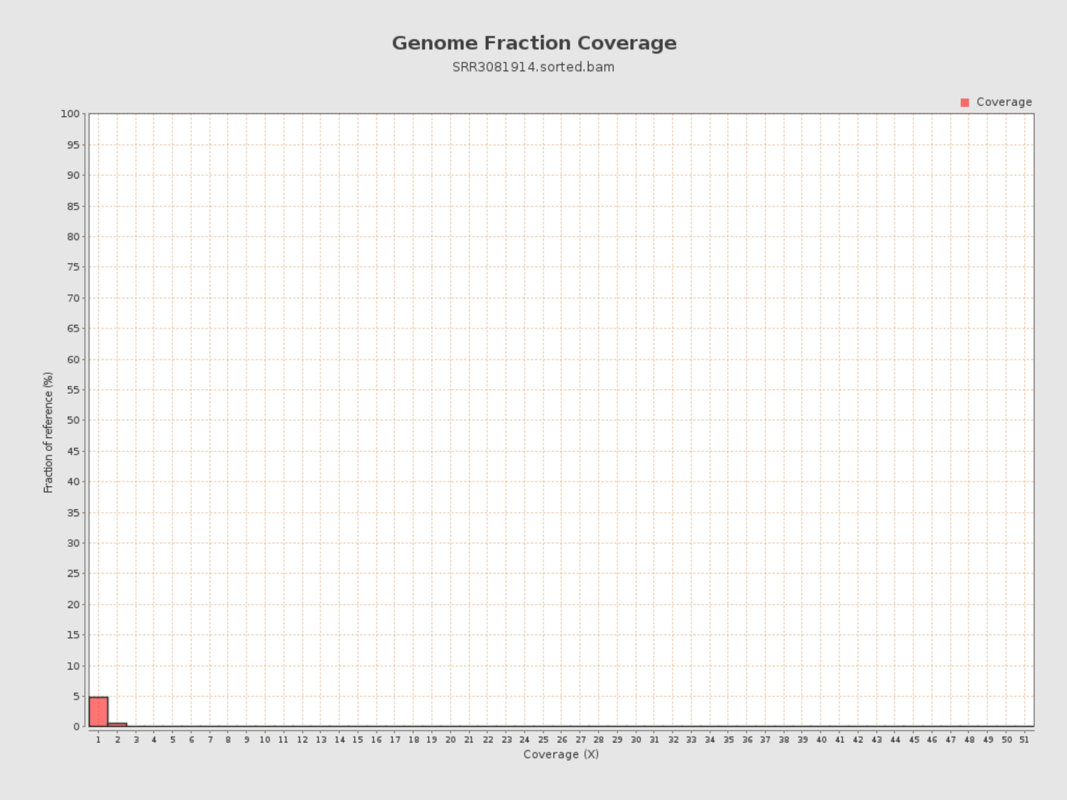
4. Results : Coverage Histogram



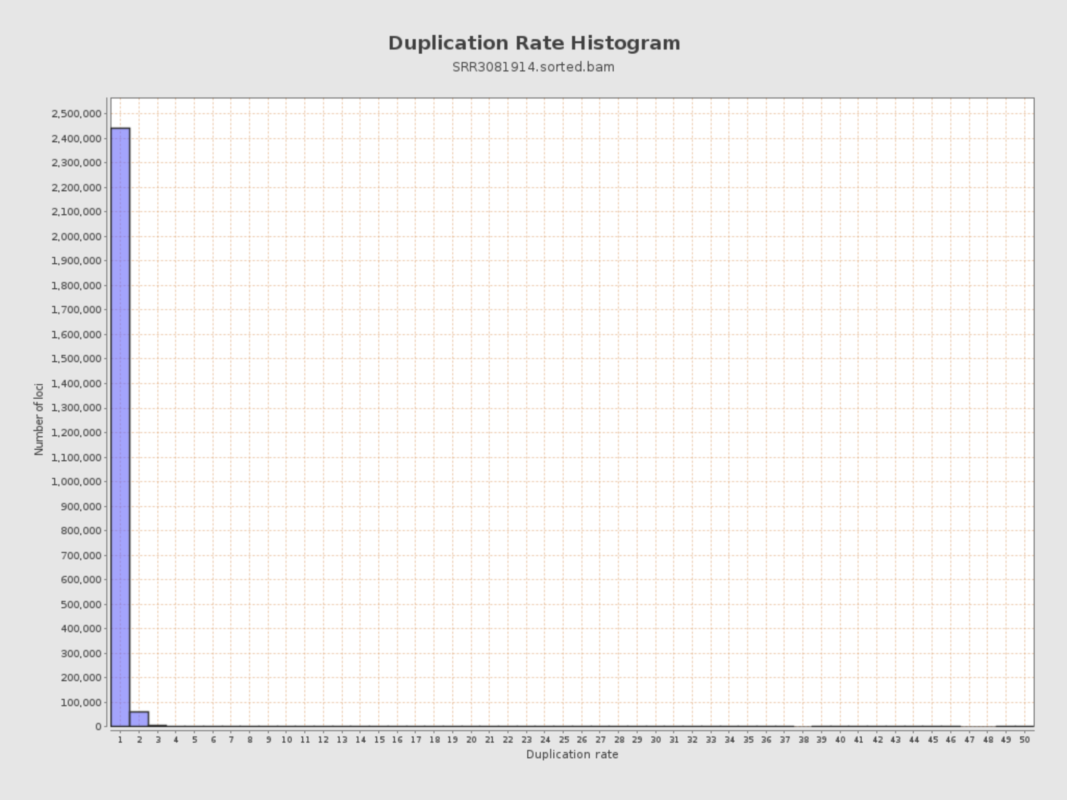
5. Results : Coverage Histogram (0-50X)



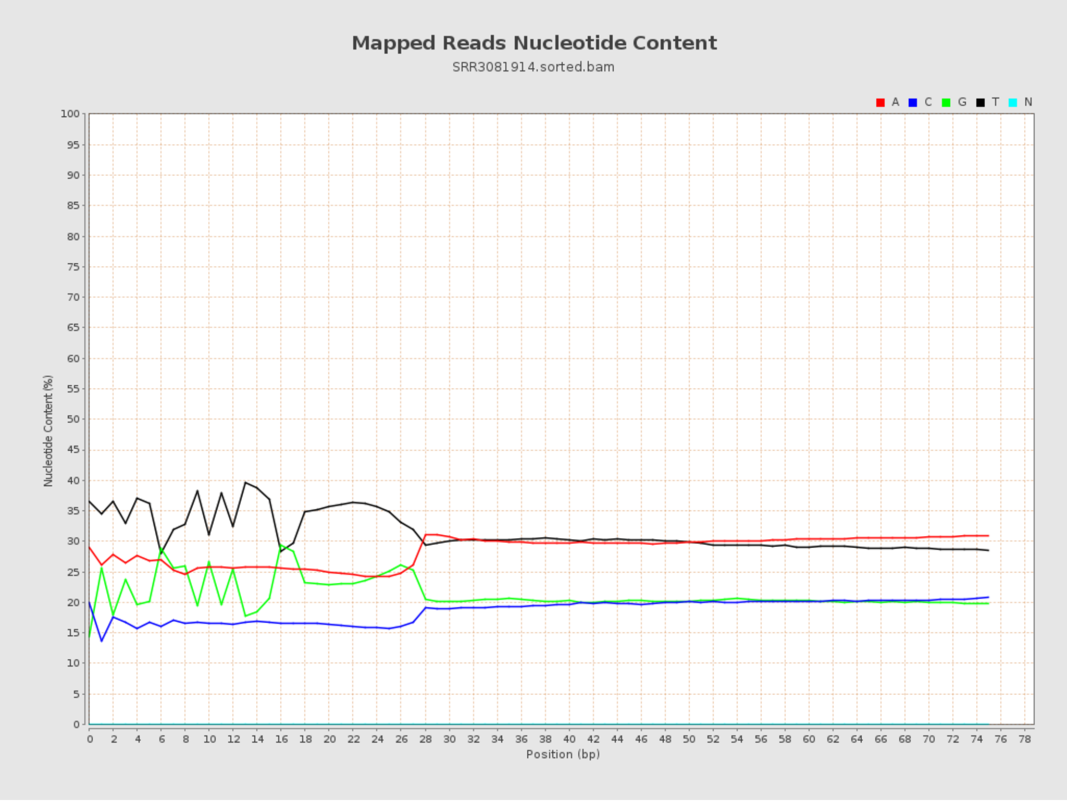
6. Results : Genome Fraction Coverage



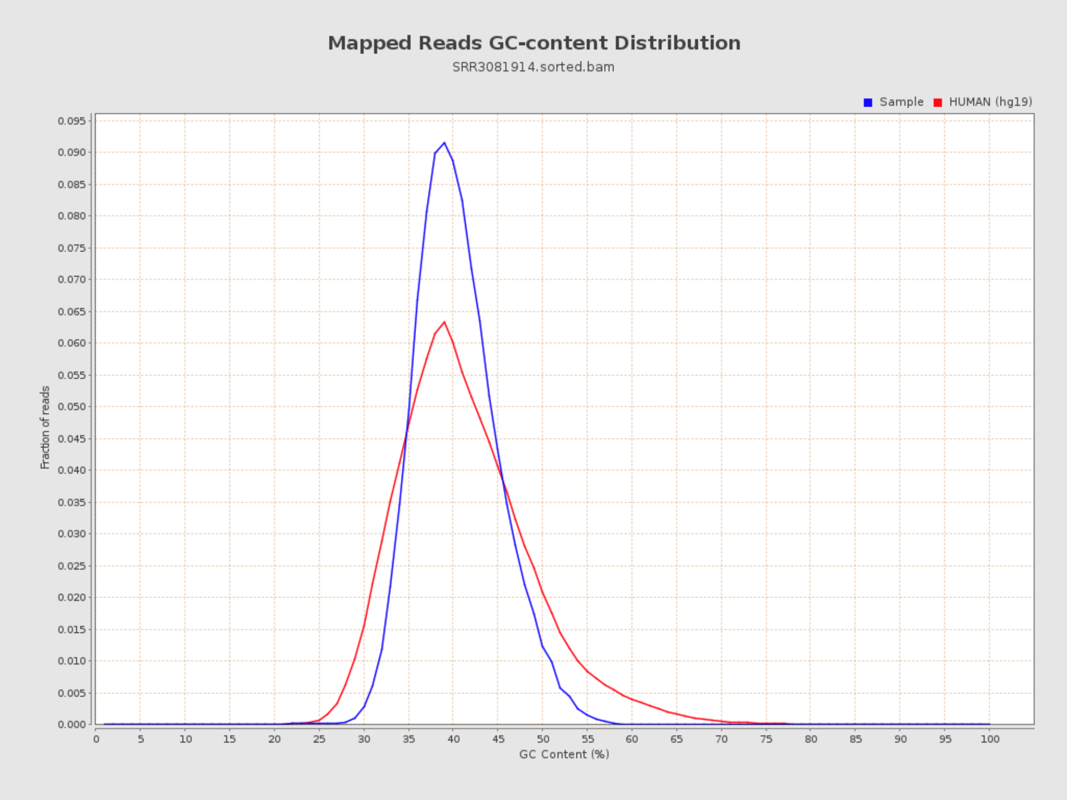
7. Results : Duplication Rate Histogram



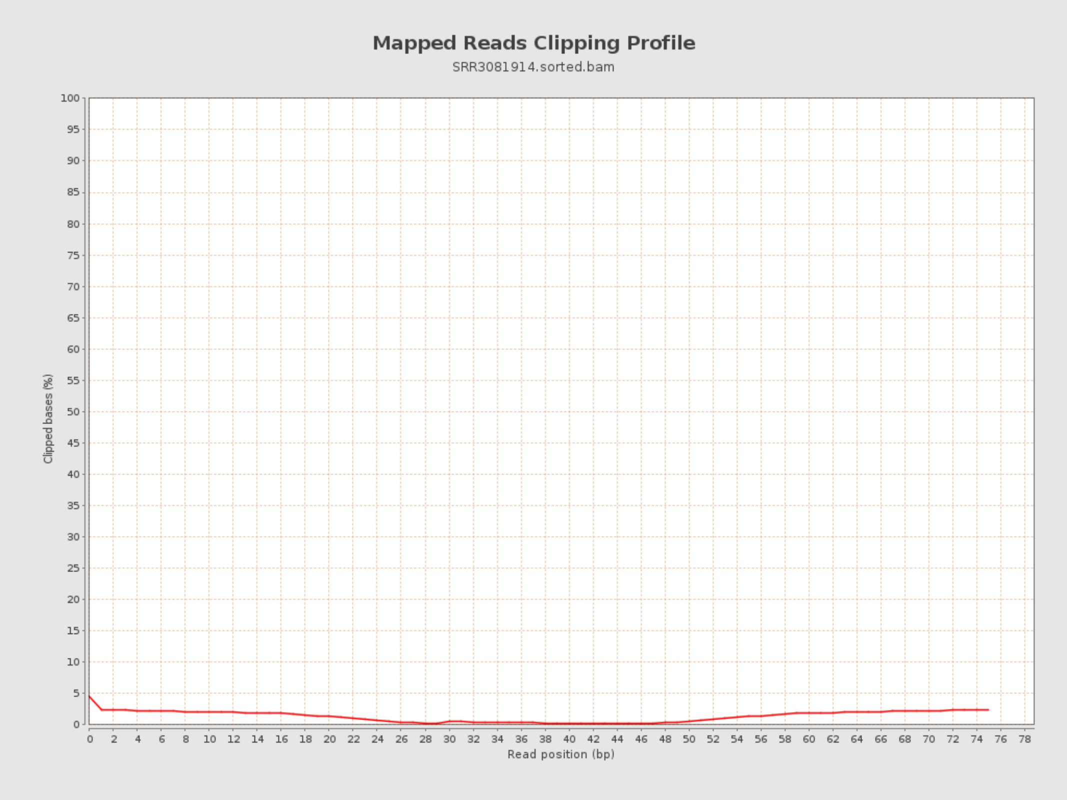
8. Results : Mapped Reads Nucleotide Content



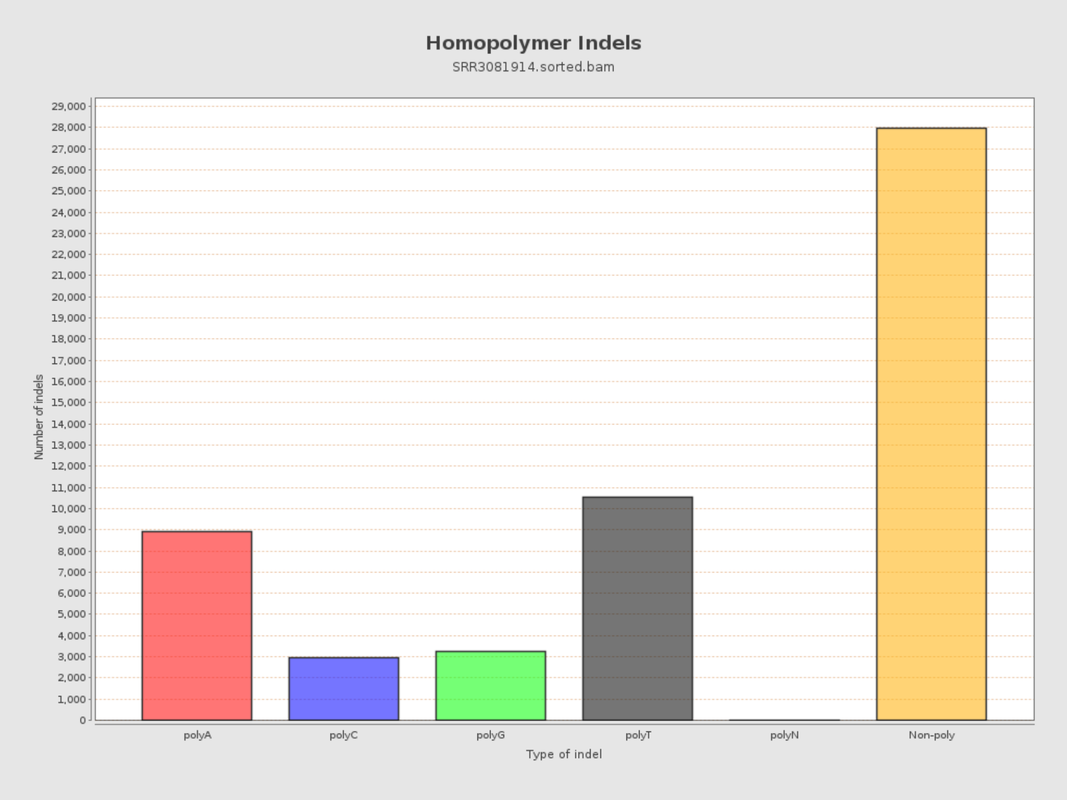
9. Results : Mapped Reads GC-content Distribution



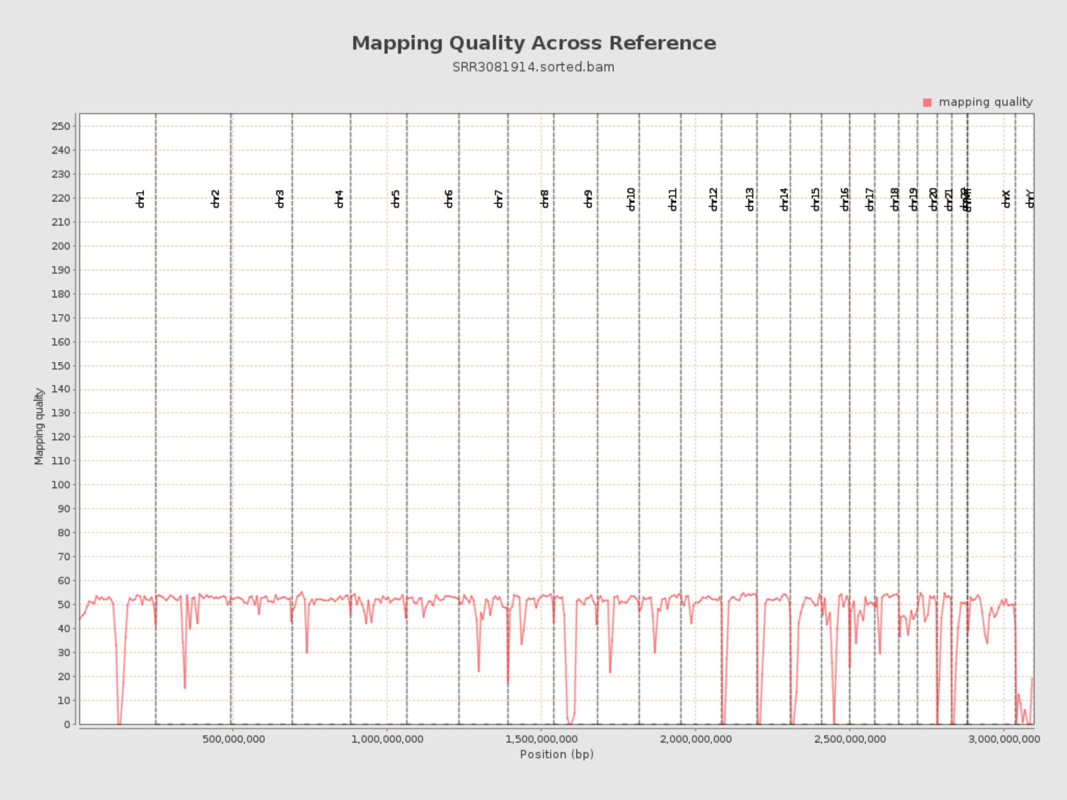
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram