Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 07:06:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3212676.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_SRR3212676 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3212676.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 07:06:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3212676.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,771,178
Mapped reads	2,524,094 / 91.08%
Unmapped reads	247,084 / 8.92%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,684 / 0.67%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	129,805 / 4.68%
Duplication rate	4.13%
Clipped reads	1,030,414 / 37.18%

2.2. ACGT Content

Number/percentage of A's	47,023,821 / 27.55%
Number/percentage of C's	32,818,086 / 19.22%
Number/percentage of T's	52,706,331 / 30.87%
Number/percentage of G's	38,165,468 / 22.36%
Number/percentage of N's	1,853 / 0%
GC Percentage	41.58%

2.3. Coverage

Mean	0.0552

Standard Deviation	0.4393

2.4. Mapping Quality

Mean Mapping Quality	46.37

2.5. Mismatches and indels

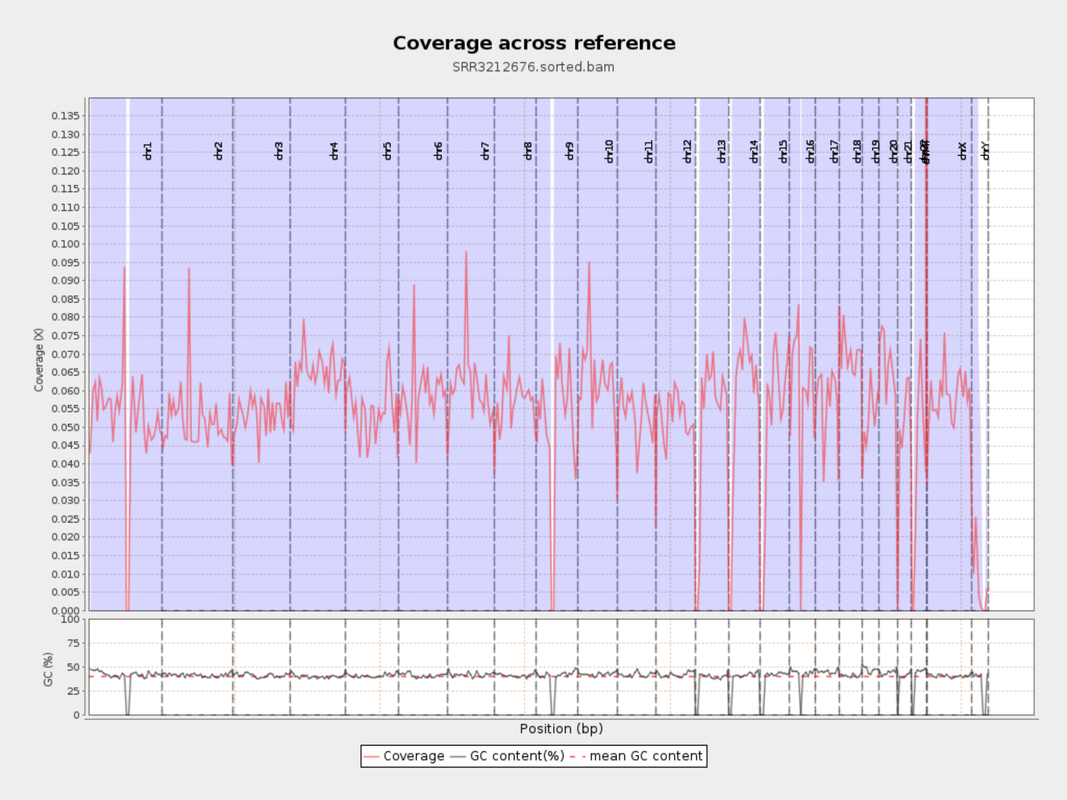
General error rate	0.87%
Mismatches	1,468,200
Insertions	12,155
Mapped reads with at least one insertion	0.48%
Deletions	36,080
Mapped reads with at least one deletion	1.42%
Homopolymer indels	47.37%

2.6. Chromosome stats

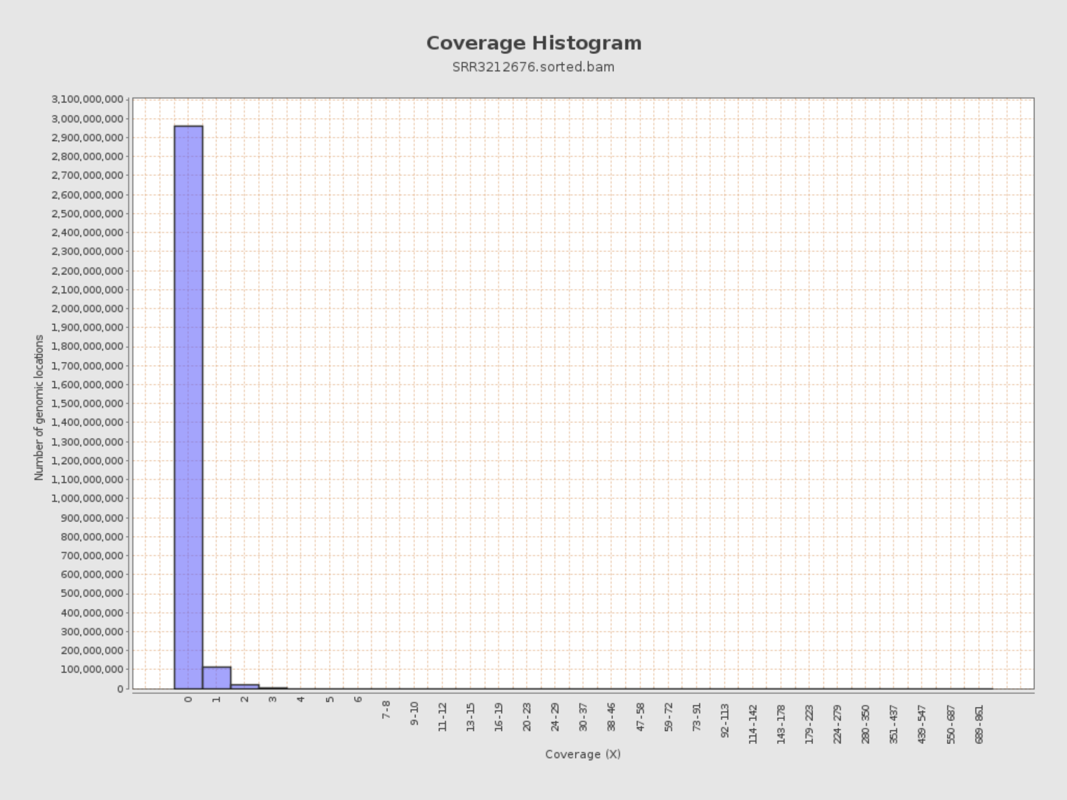
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12977726	0.0521	0.7904
chr2	243199373	12711361	0.0523	0.4998
chr3	198022430	10599210	0.0535	0.2756
chr4	191154276	12400271	0.0649	0.3271
chr5	180915260	9848015	0.0544	0.2798
chr6	171115067	10105829	0.0591	0.3813
chr7	159138663	9868465	0.062	0.5668

chr8	146364022	8400695	0.0574	0.4299
chr9	141213431	7129473	0.0505	0.4222
chr10	135534747	8661271	0.0639	0.432
chr11	135006516	7193661	0.0533	0.3988
chr12	133851895	7117854	0.0532	0.2814
chr13	115169878	5885528	0.0511	0.2686
chr14	107349540	6083036	0.0567	0.3055
chr15	102531392	5173192	0.0505	0.2693
chr16	90354753	5437346	0.0602	0.3386
chr17	81195210	4584248	0.0565	0.3331
chr18	78077248	5506826	0.0705	0.7937
chr19	59128983	3155213	0.0534	0.5636
chr20	63025520	4152219	0.0659	0.3143
chr21	48129895	2314222	0.0481	0.2975
chr22	51304566	1981736	0.0386	0.2342
chrMT	16571	65360	3.9442	3.0496
chrX	155270560	8986496	0.0579	0.3281
chrY	59373566	439988	0.0074	0.1825

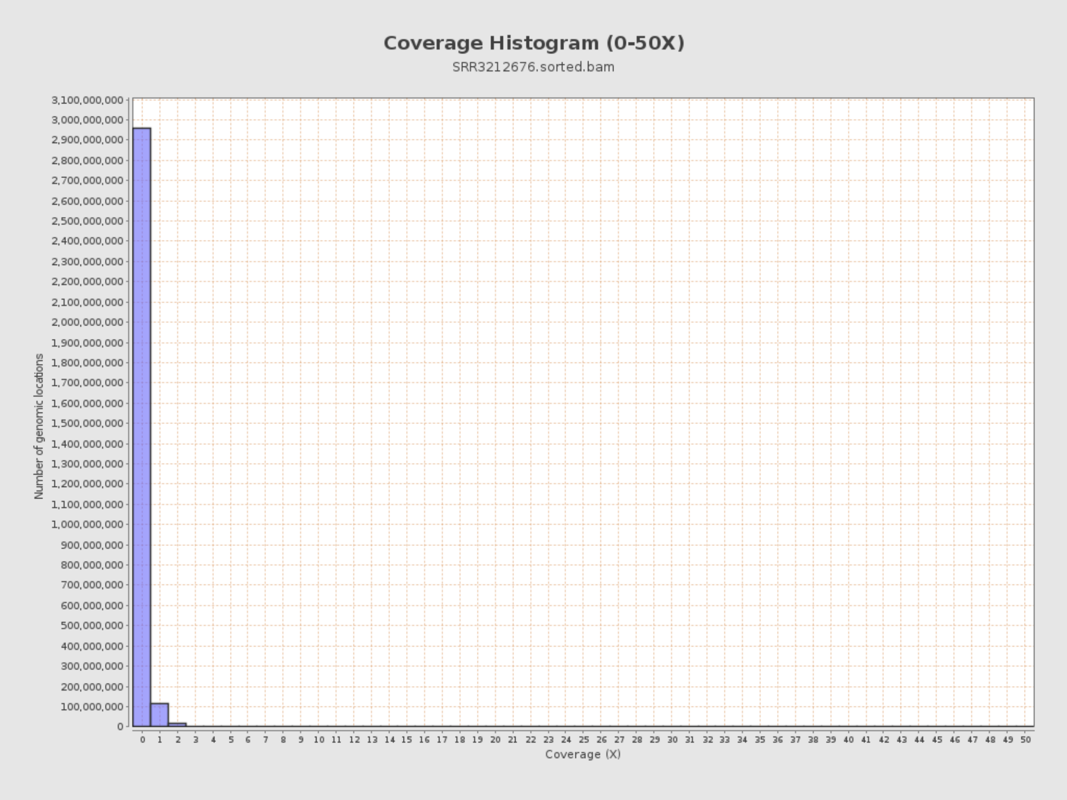
3. Results : Coverage across reference



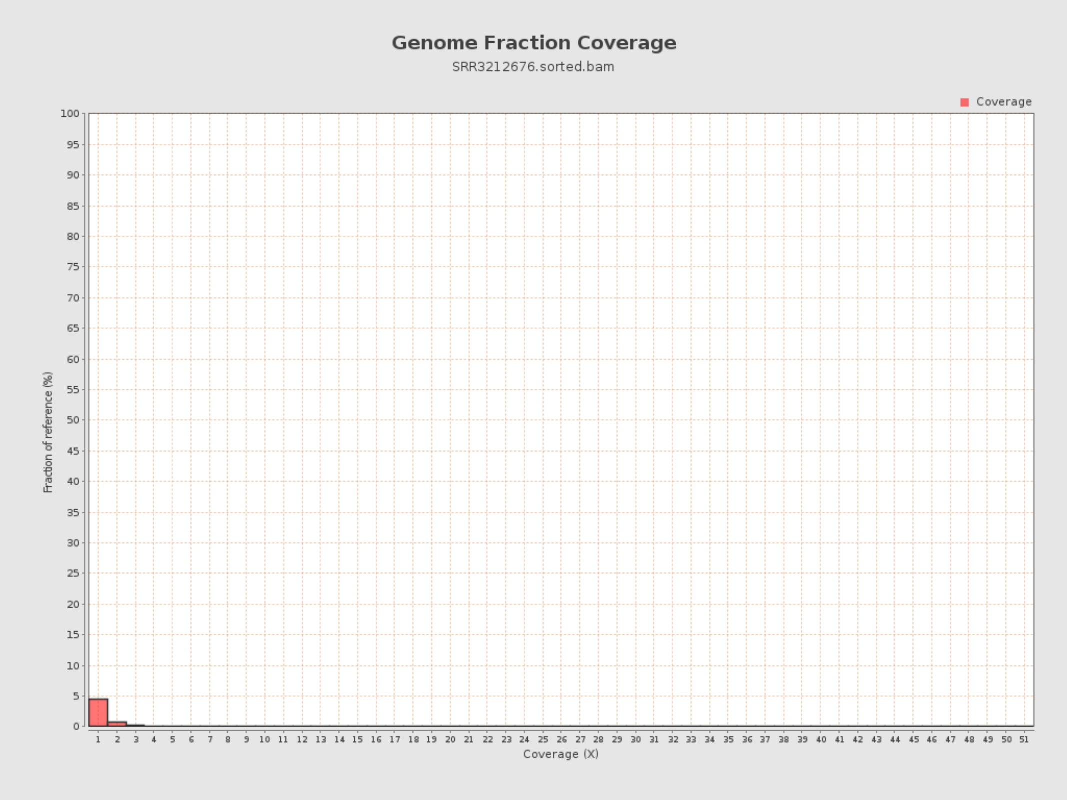
4. Results : Coverage Histogram



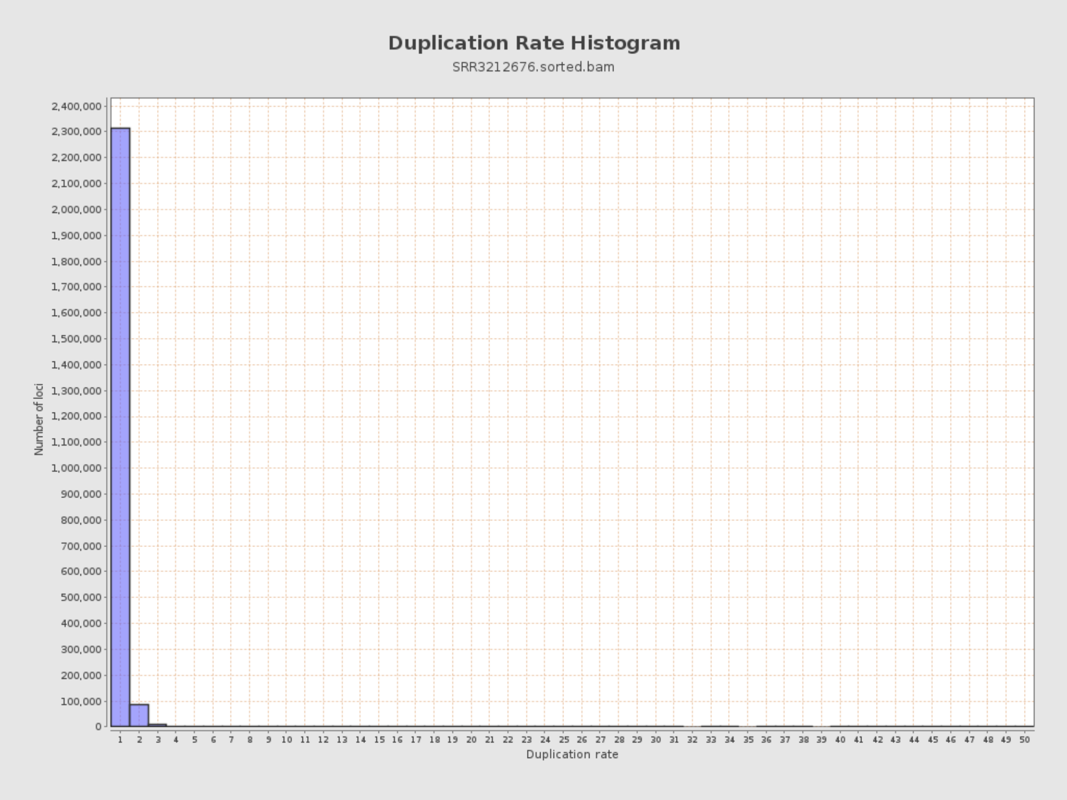
5. Results : Coverage Histogram (0-50X)



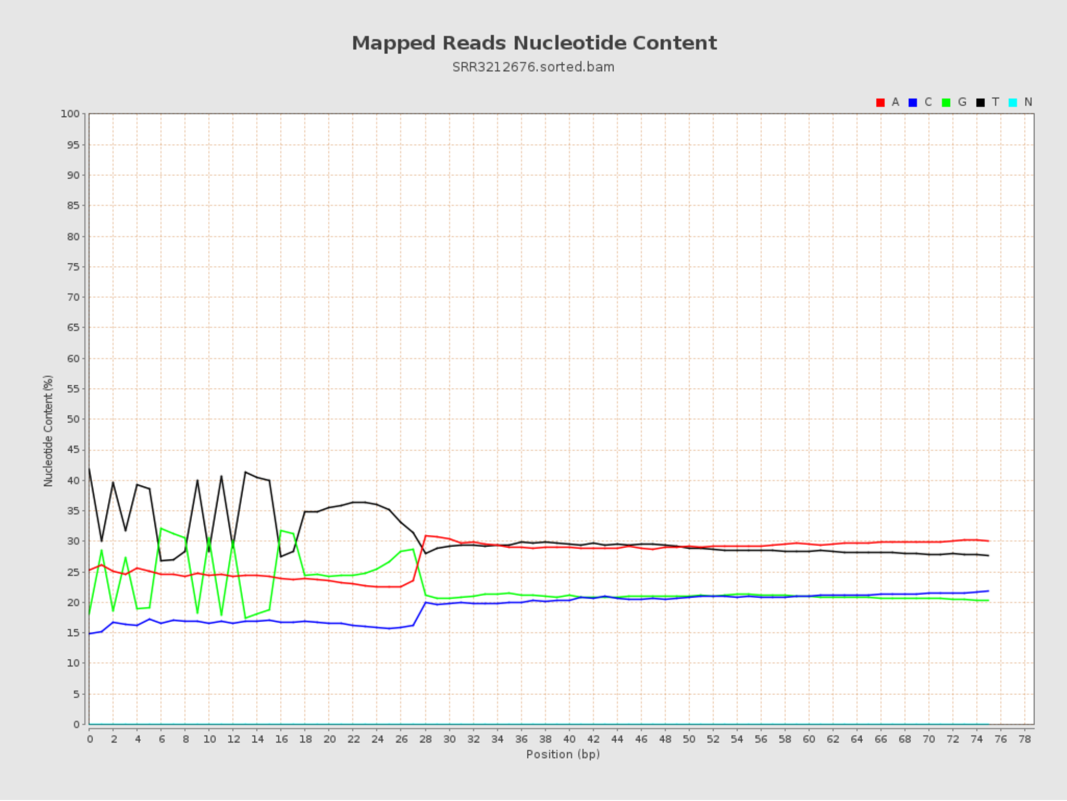
6. Results : Genome Fraction Coverage



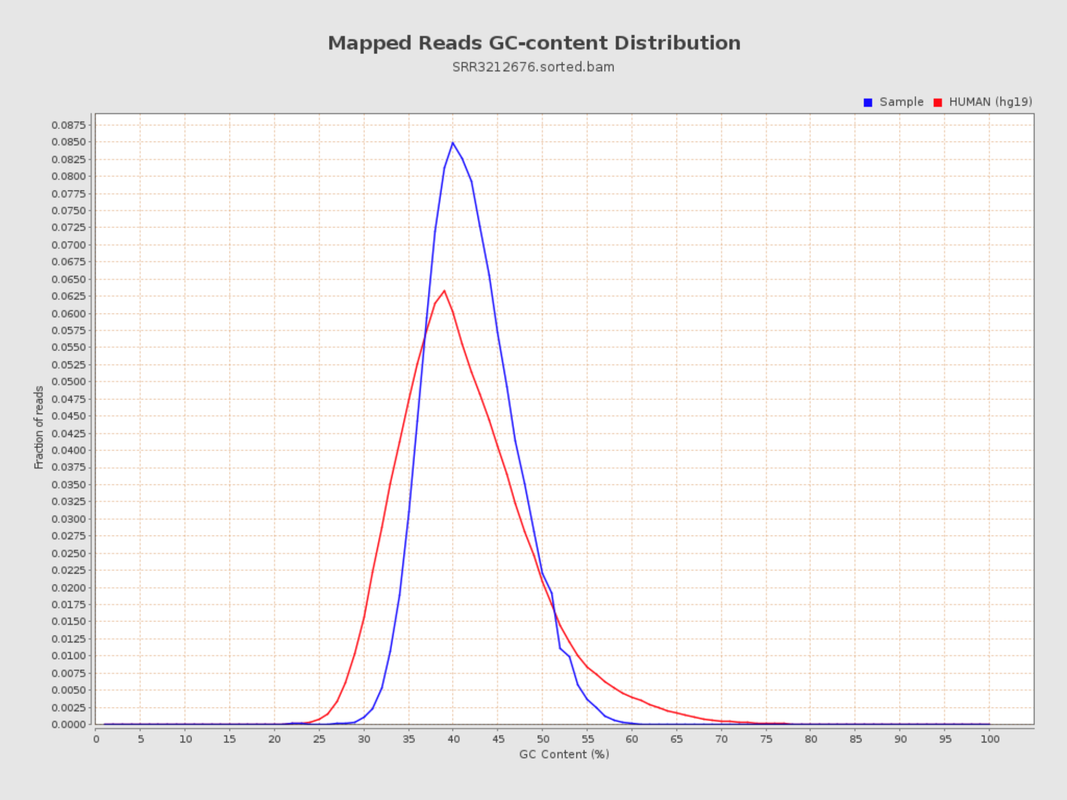
7. Results : Duplication Rate Histogram



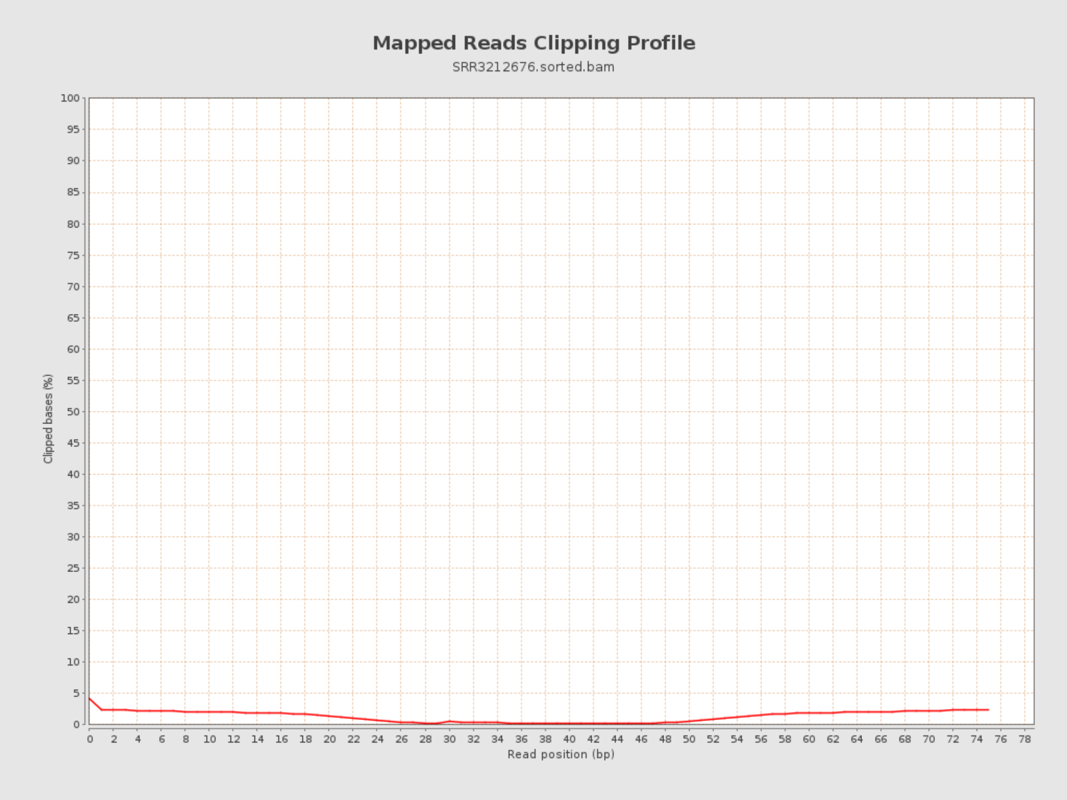
8. Results : Mapped Reads Nucleotide Content



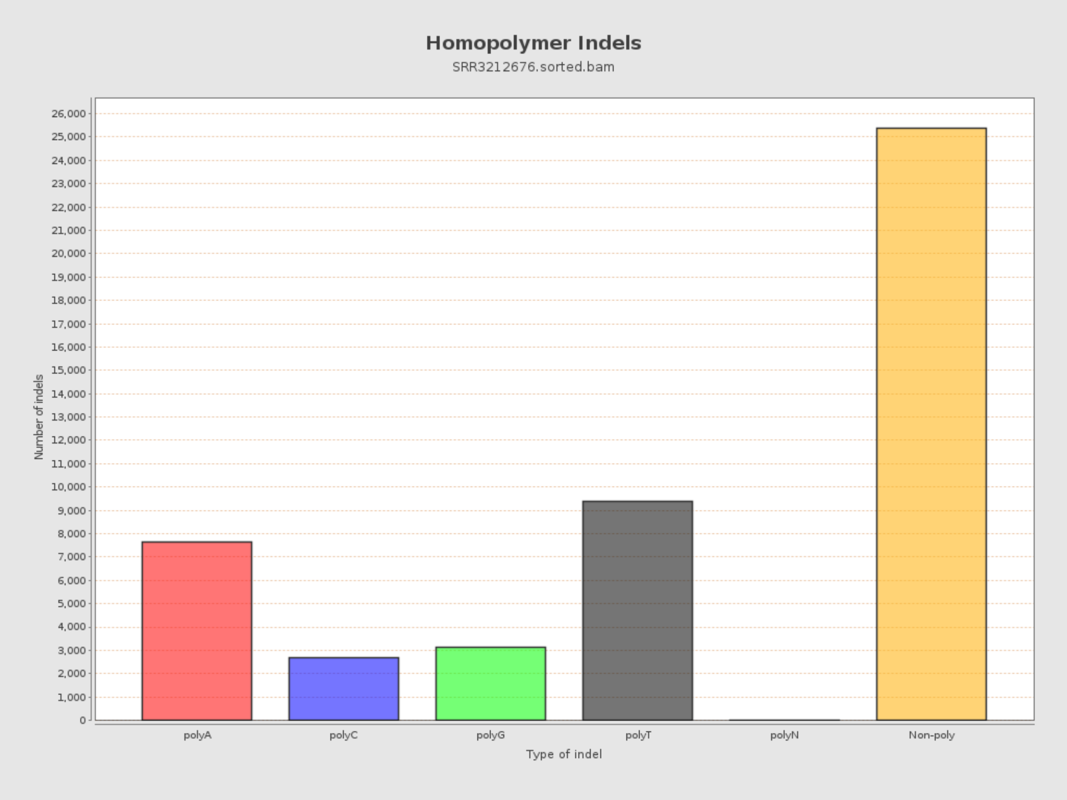
9. Results : Mapped Reads GC-content Distribution



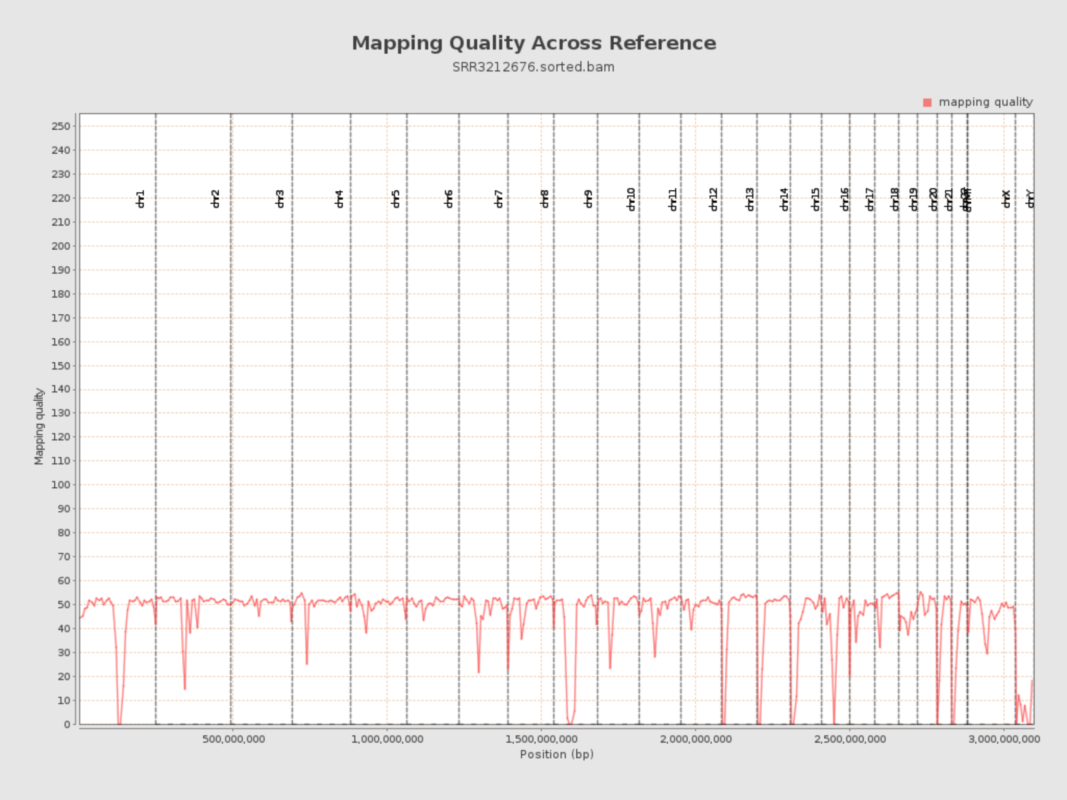
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram