Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/01 08:29:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472822.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_SRR3472822 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472822.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 01 08:29:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472822.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,246,015
Mapped reads	1,562,468 / 69.57%
Unmapped reads	683,547 / 30.43%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,878 / 0.53%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	132,860 / 5.92%
Duplication rate	6.08%
Clipped reads	1,004,034 / 44.7%

2.2. ACGT Content

Number/percentage of A's	25,744,525 / 26.68%
Number/percentage of C's	19,186,204 / 19.89%
Number/percentage of T's	28,501,824 / 29.54%
Number/percentage of G's	23,050,522 / 23.89%
Number/percentage of N's	2,190 / 0%
GC Percentage	43.78%

2.3. Coverage

Mean	0.0312

Standard Deviation	0.3032

2.4. Mapping Quality

Mean Mapping Quality	42.41

2.5. Mismatches and indels

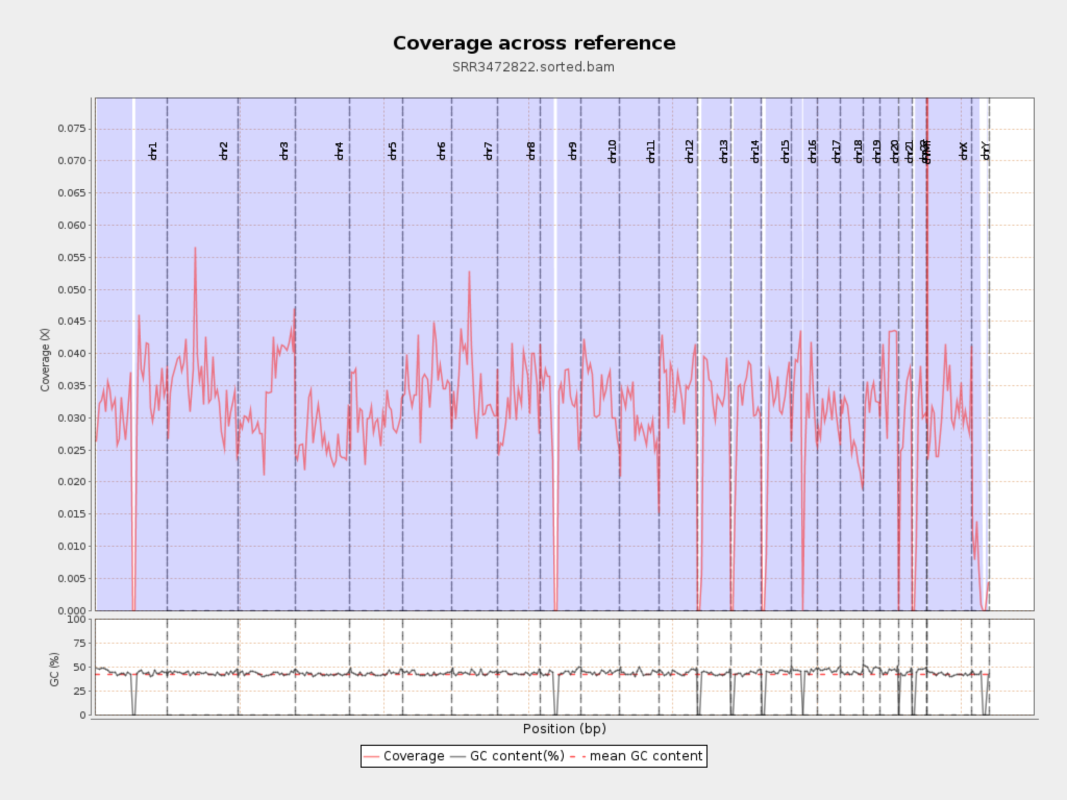
General error rate	0.93%
Mismatches	880,502
Insertions	7,128
Mapped reads with at least one insertion	0.45%
Deletions	25,871
Mapped reads with at least one deletion	1.64%
Homopolymer indels	45.9%

2.6. Chromosome stats

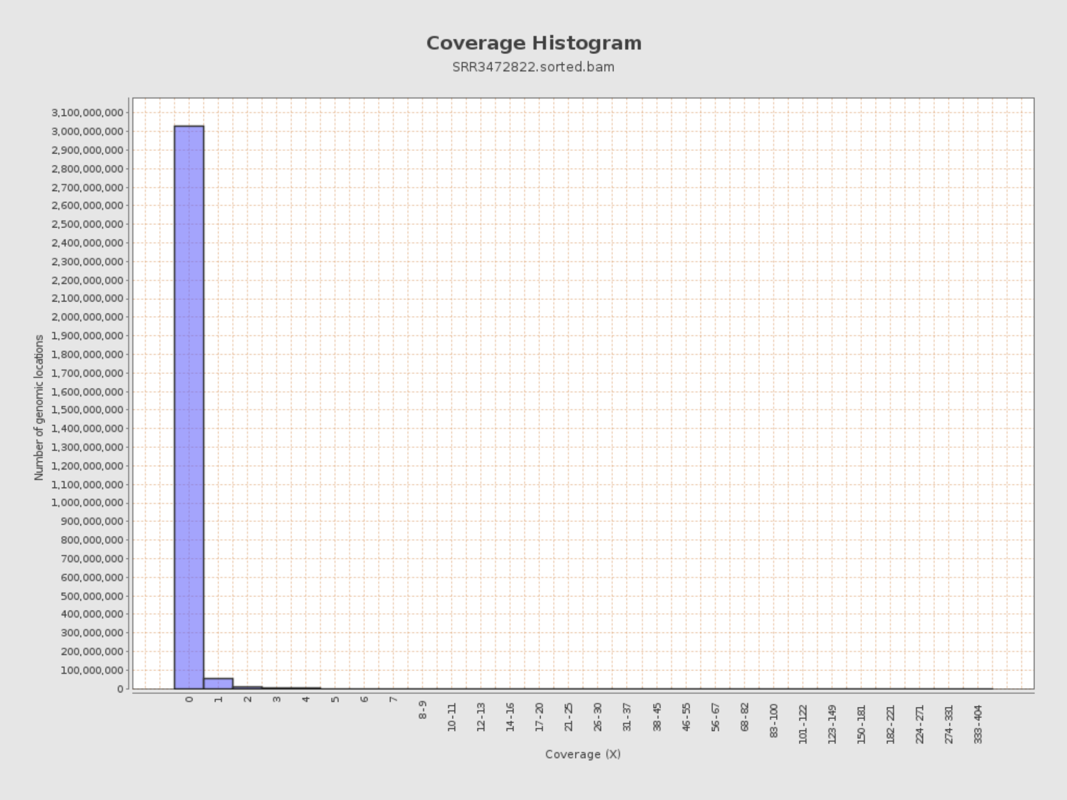
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7775339	0.0312	0.3525
chr2	243199373	8572715	0.0352	0.3656
chr3	198022430	6731556	0.034	0.2611
chr4	191154276	5056517	0.0265	0.2412
chr5	180915260	5506773	0.0304	0.2549
chr6	171115067	6108922	0.0357	0.2936
chr7	159138663	5563774	0.035	0.4417

chr8	146364022	4858079	0.0332	0.2939
chr9	141213431	4233425	0.03	0.3062
chr10	135534747	4610328	0.034	0.2968
chr11	135006516	3997365	0.0296	0.2957
chr12	133851895	4783058	0.0357	0.2752
chr13	115169878	3322043	0.0288	0.2485
chr14	107349540	3043256	0.0283	0.2711
chr15	102531392	2830136	0.0276	0.2576
chr16	90354753	2799006	0.031	0.2635
chr17	81195210	2461532	0.0303	0.2699
chr18	78077248	2110479	0.027	0.4166
chr19	59128983	1925598	0.0326	0.3064
chr20	63025520	2426459	0.0385	0.2899
chr21	48129895	1370356	0.0285	0.2533
chr22	51304566	1163221	0.0227	0.225
chrMT	16571	168186	10.1494	7.6624
chrX	155270560	4792112	0.0309	0.2737
chrY	59373566	321388	0.0054	0.1081

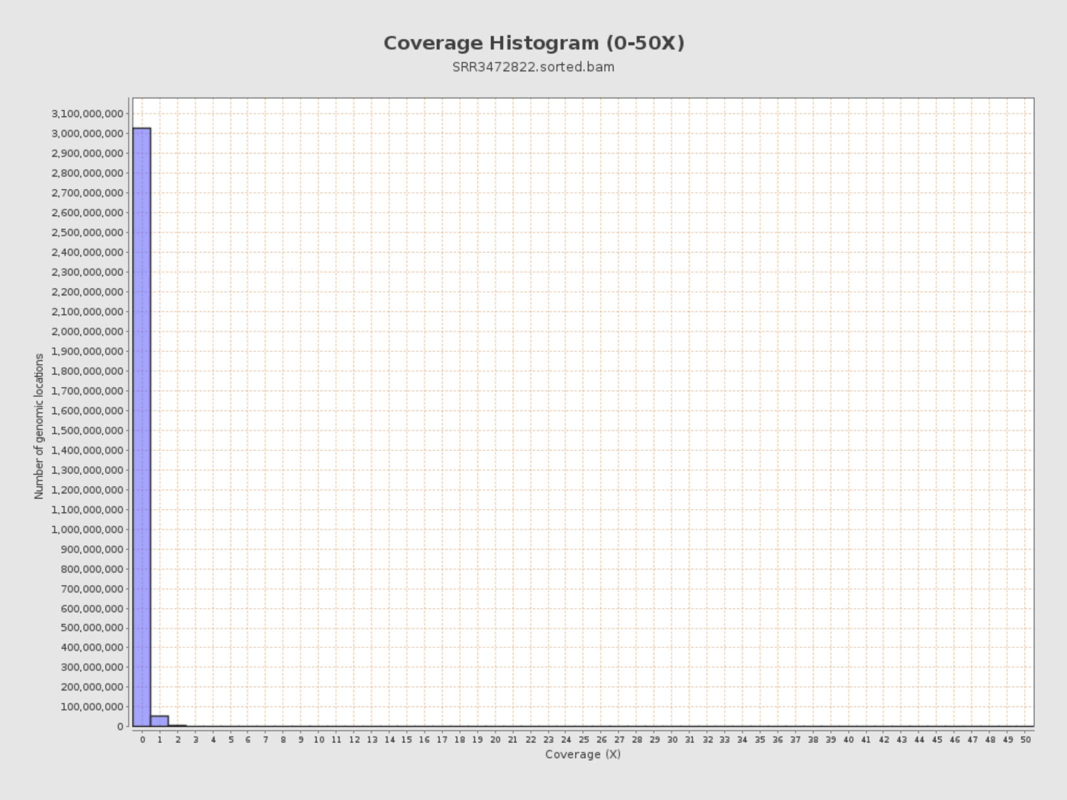
3. Results : Coverage across reference



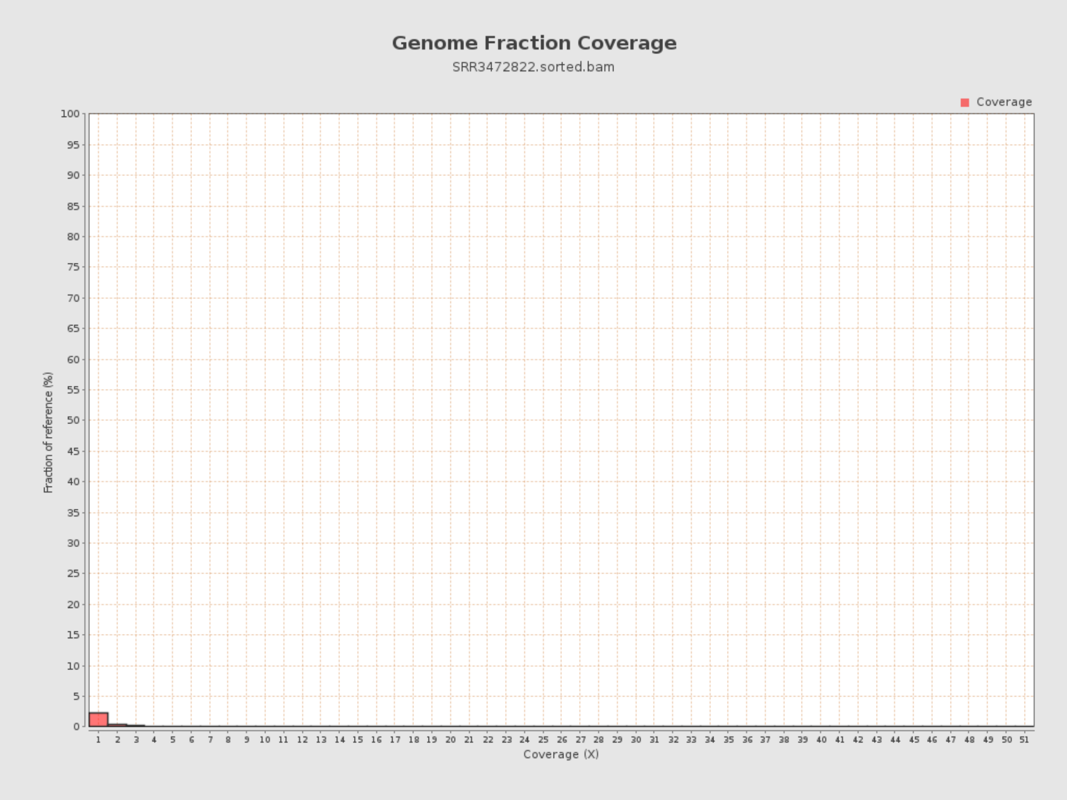
4. Results : Coverage Histogram



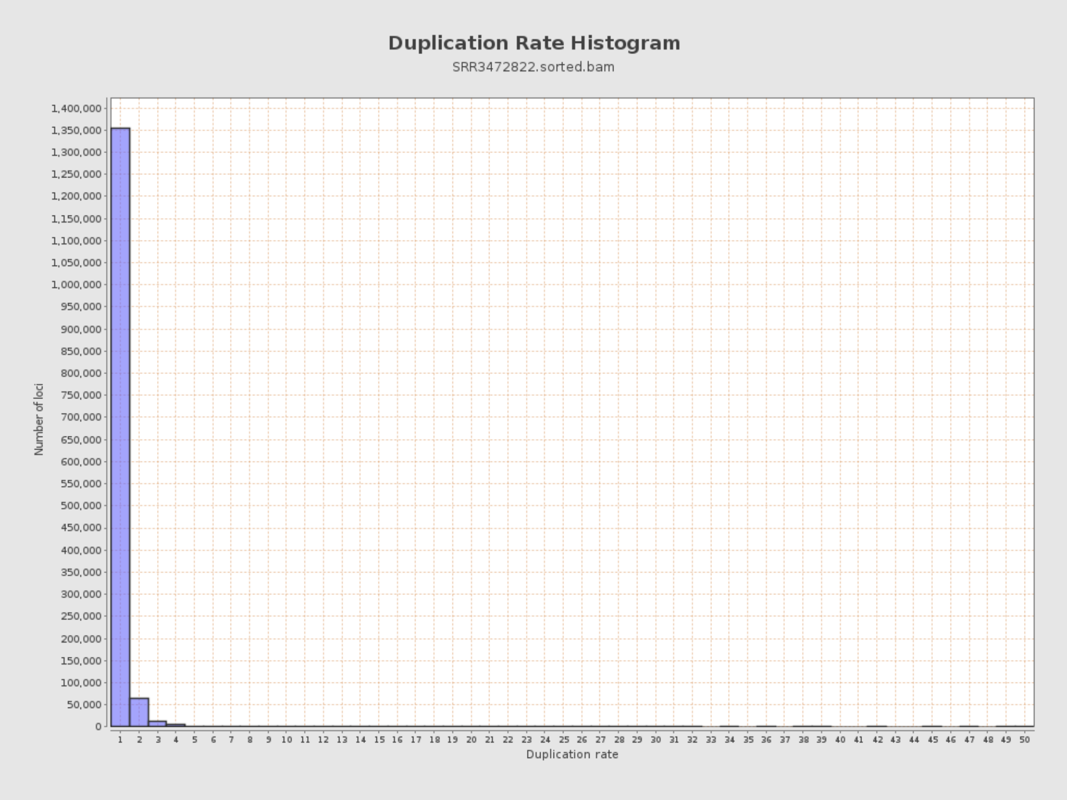
5. Results : Coverage Histogram (0-50X)



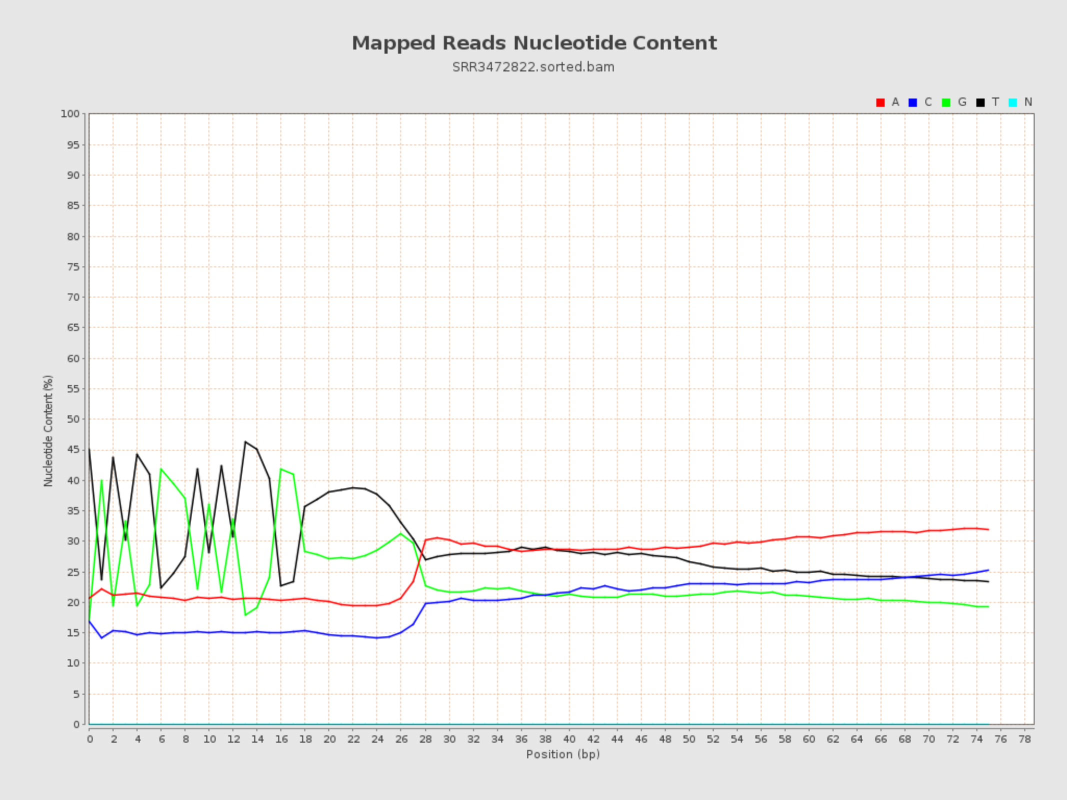
6. Results : Genome Fraction Coverage



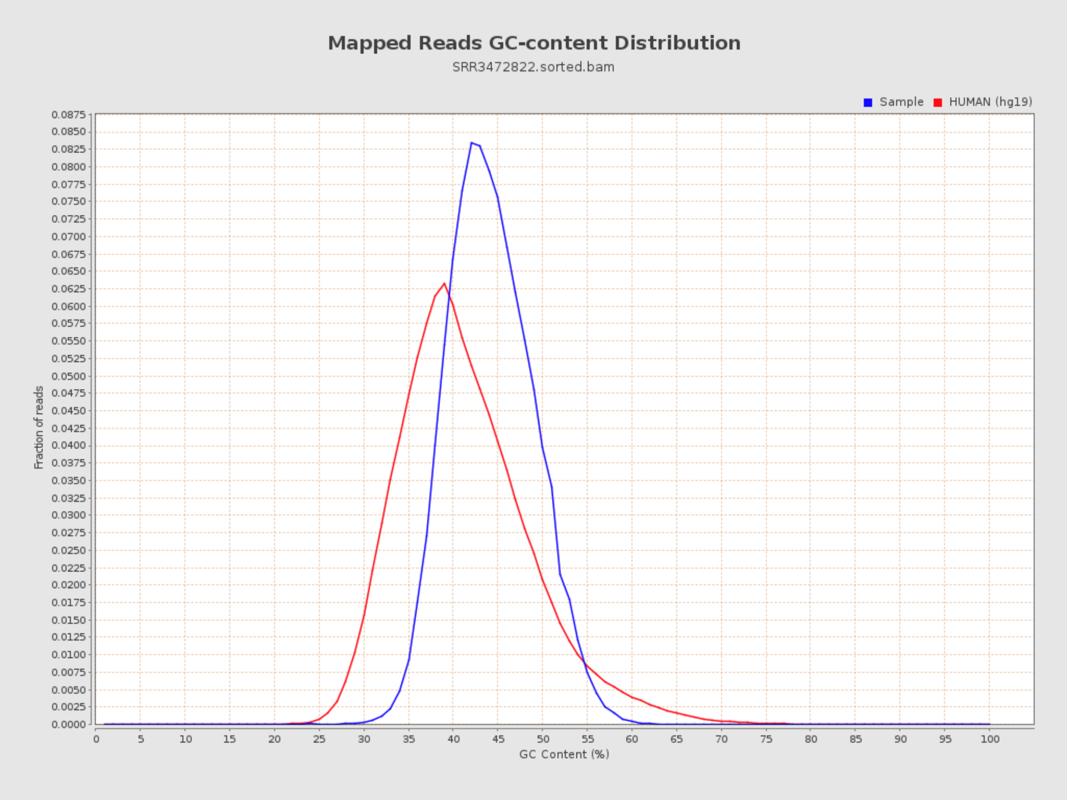
7. Results : Duplication Rate Histogram



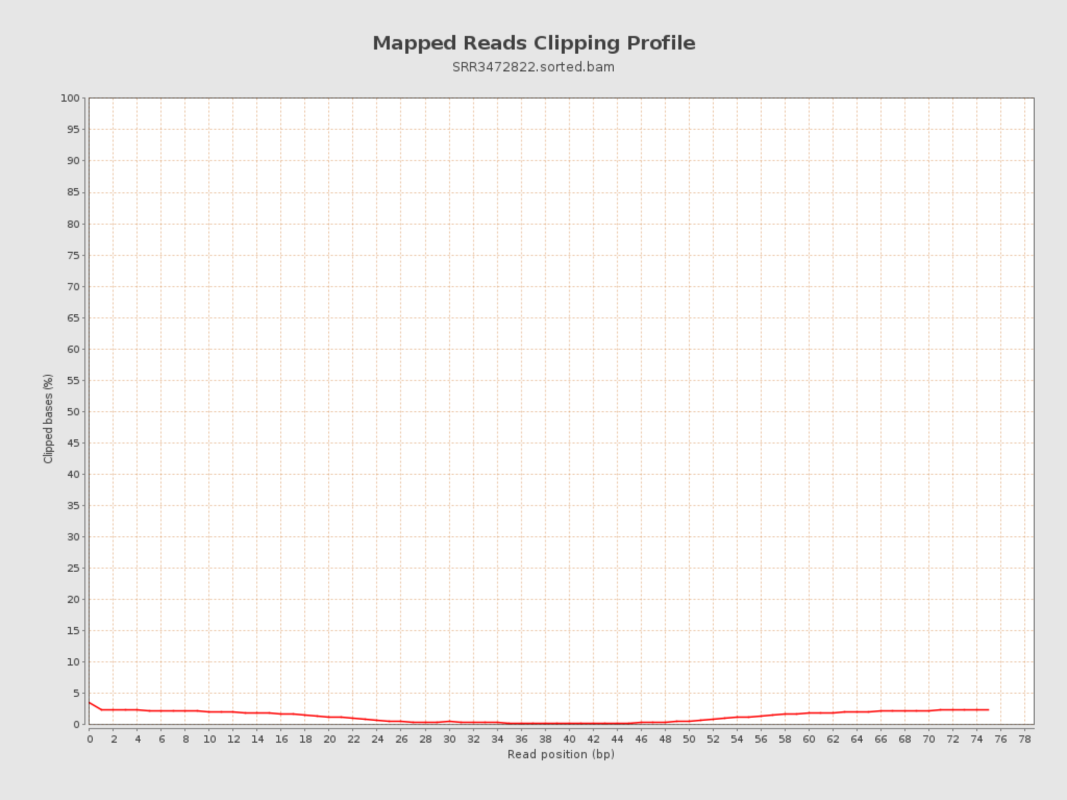
8. Results : Mapped Reads Nucleotide Content



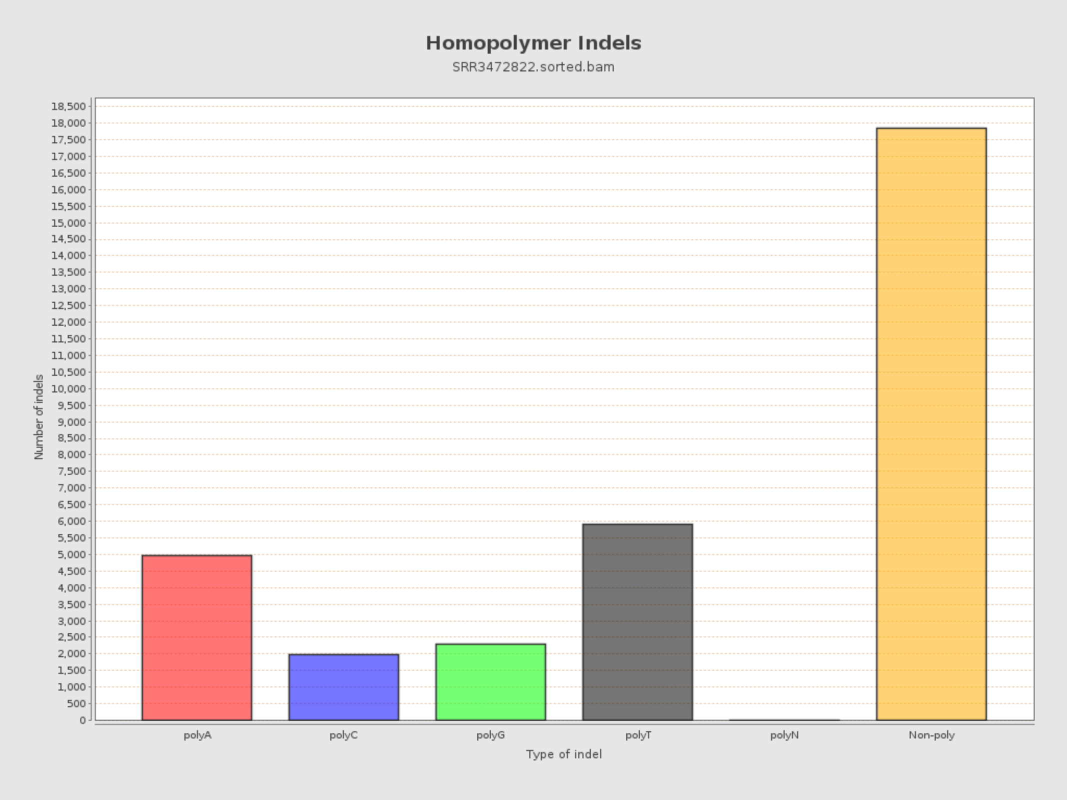
9. Results : Mapped Reads GC-content Distribution



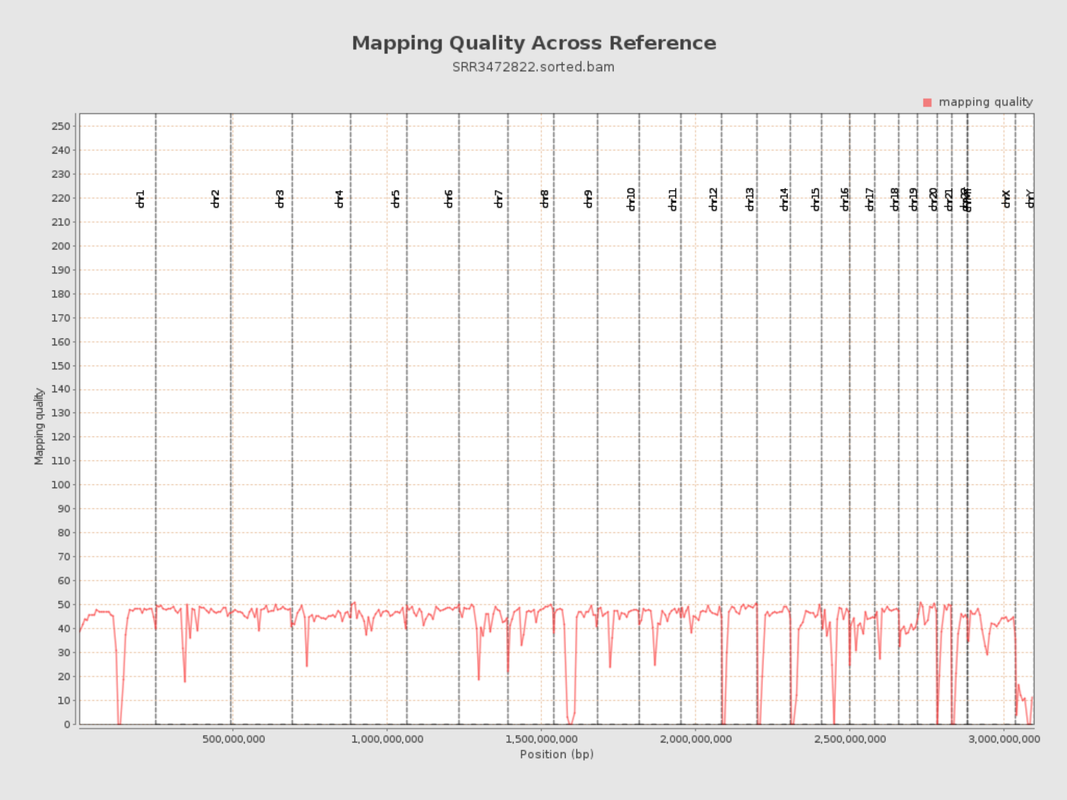
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram