Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/01 07:52:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472814.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_SRR3472814 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472814.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 01 07:52:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472814.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,514,610
Mapped reads	1,990,488 / 79.16%
Unmapped reads	524,122 / 20.84%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,568 / 0.74%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	117,578 / 4.68%
Duplication rate	4.23%
Clipped reads	1,197,470 / 47.62%

2.2. ACGT Content

Number/percentage of A's	34,018,061 / 27.23%
Number/percentage of C's	24,298,252 / 19.45%
Number/percentage of T's	37,445,456 / 29.98%
Number/percentage of G's	29,141,443 / 23.33%
Number/percentage of N's	2,746 / 0%
GC Percentage	42.78%

2.3. Coverage

Mean	0.0404

Standard Deviation	0.3366

2.4. Mapping Quality

Mean Mapping Quality	43.22

2.5. Mismatches and indels

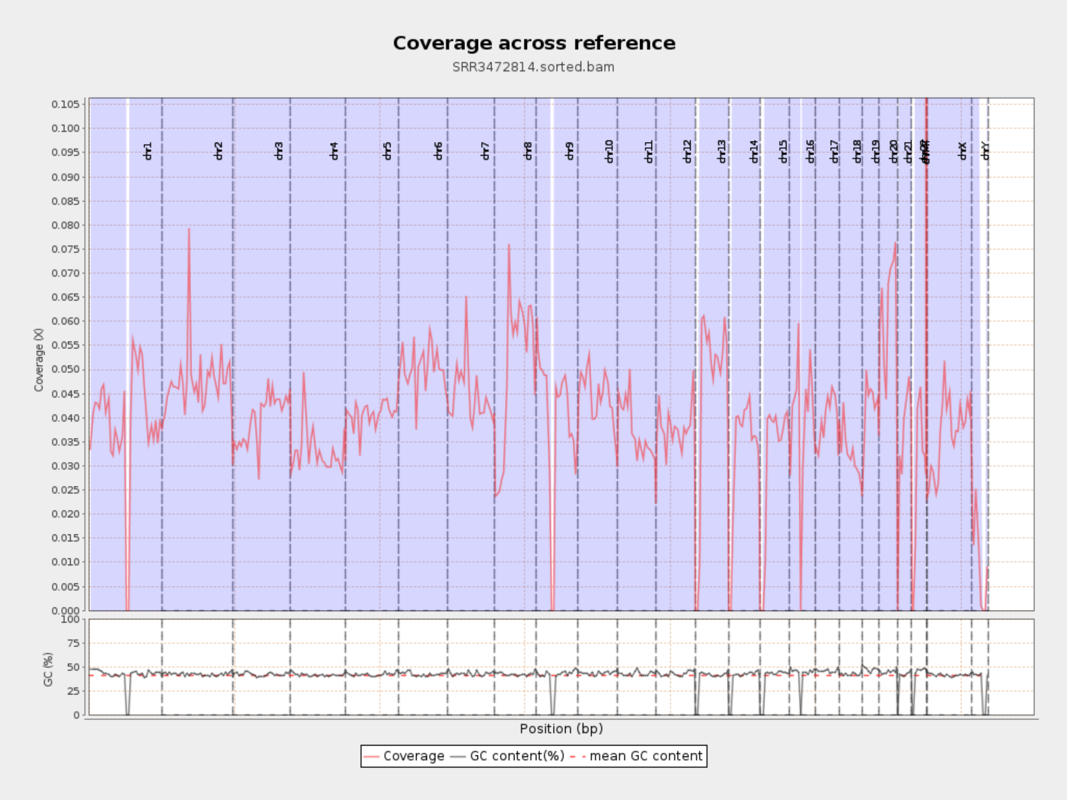
General error rate	0.91%
Mismatches	1,121,146
Insertions	9,685
Mapped reads with at least one insertion	0.48%
Deletions	32,113
Mapped reads with at least one deletion	1.59%
Homopolymer indels	46.11%

2.6. Chromosome stats

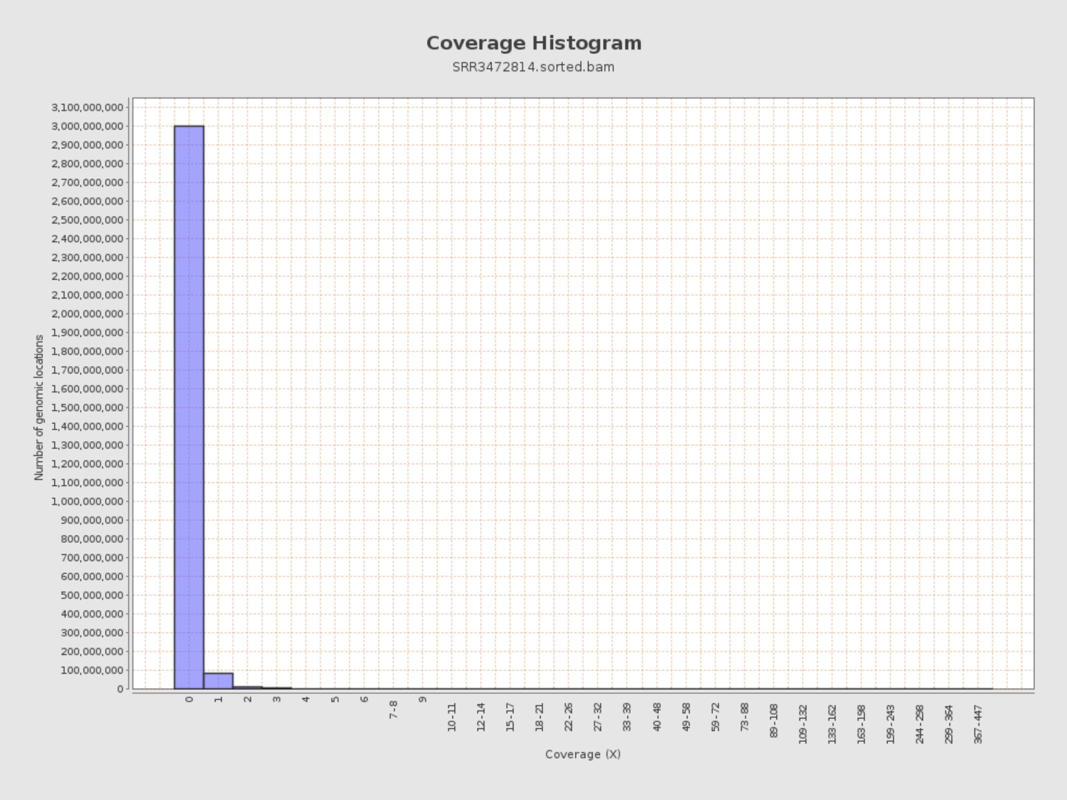
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9737627	0.0391	0.4034
chr2	243199373	11632409	0.0478	0.4482
chr3	198022430	7862388	0.0397	0.2528
chr4	191154276	6296935	0.0329	0.2501
chr5	180915260	7383037	0.0408	0.2591
chr6	171115067	8633996	0.0505	0.309
chr7	159138663	7144409	0.0449	0.4624

chr8	146364022	7373561	0.0504	0.3539
chr9	141213431	5463006	0.0387	0.3538
chr10	135534747	6050871	0.0446	0.318
chr11	135006516	5022366	0.0372	0.3664
chr12	133851895	5089394	0.038	0.2613
chr13	115169878	5249065	0.0456	0.2724
chr14	107349540	3483099	0.0324	0.2699
chr15	102531392	3194853	0.0312	0.2549
chr16	90354753	3592586	0.0398	0.2718
chr17	81195210	3227564	0.0398	0.2748
chr18	78077248	2564108	0.0328	0.5716
chr19	59128983	2520536	0.0426	0.3508
chr20	63025520	3977164	0.0631	0.3271
chr21	48129895	1704757	0.0354	0.2619
chr22	51304566	1348927	0.0263	0.2131
chrMT	16571	167236	10.0921	7.3663
chrX	155270560	5681418	0.0366	0.282
chrY	59373566	561624	0.0095	0.1441

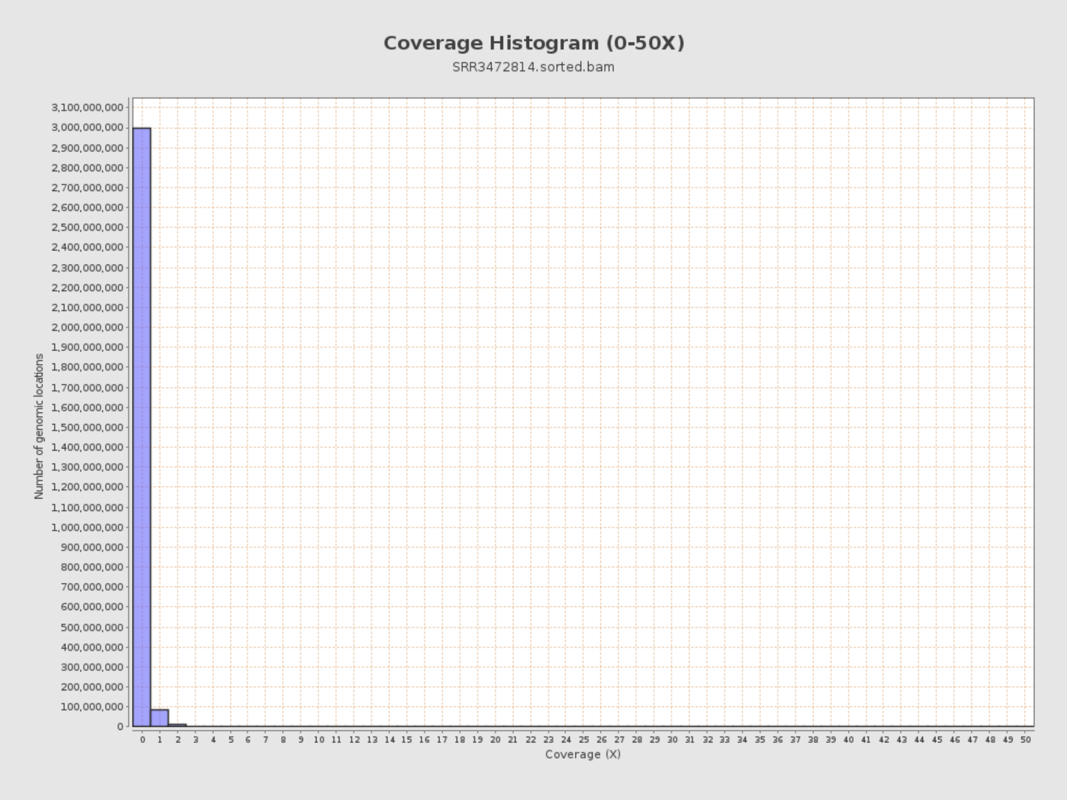
3. Results : Coverage across reference



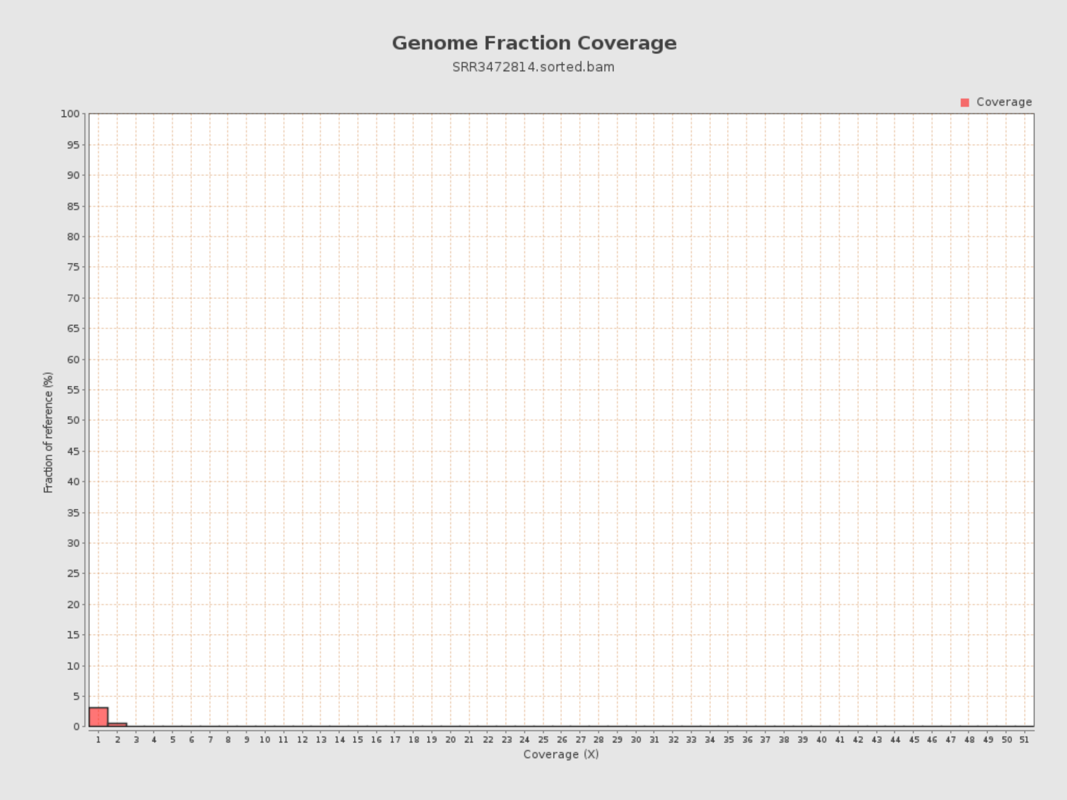
4. Results : Coverage Histogram



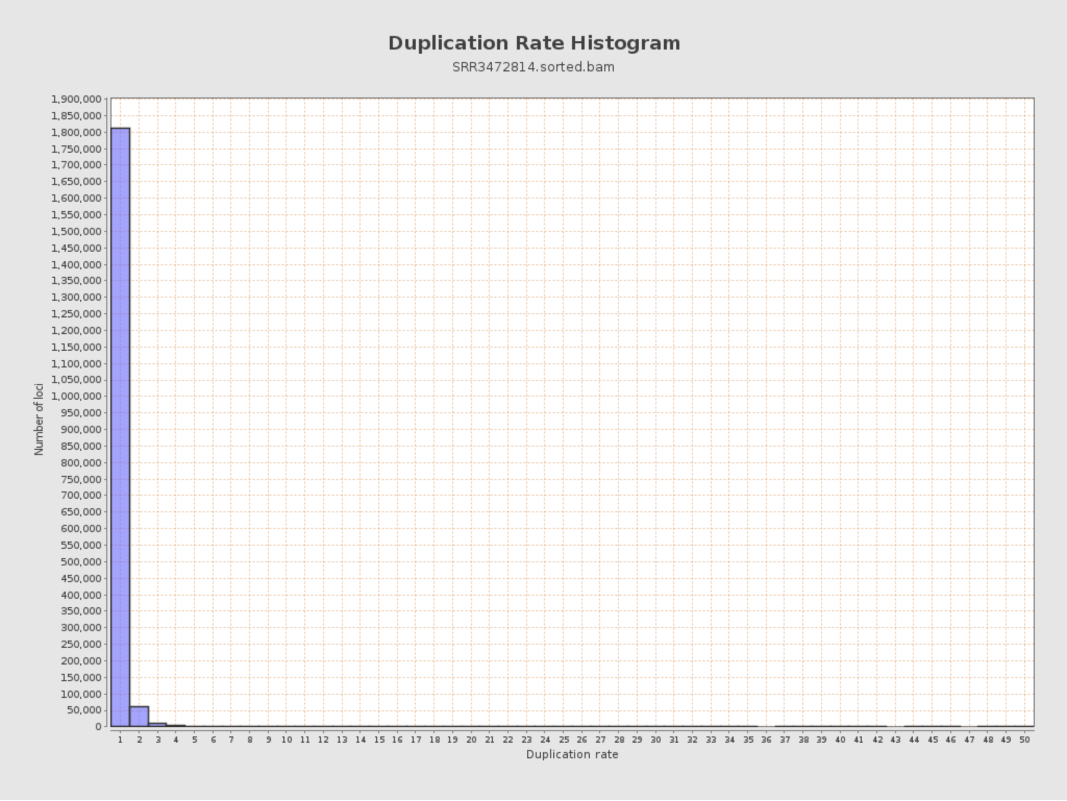
5. Results : Coverage Histogram (0-50X)



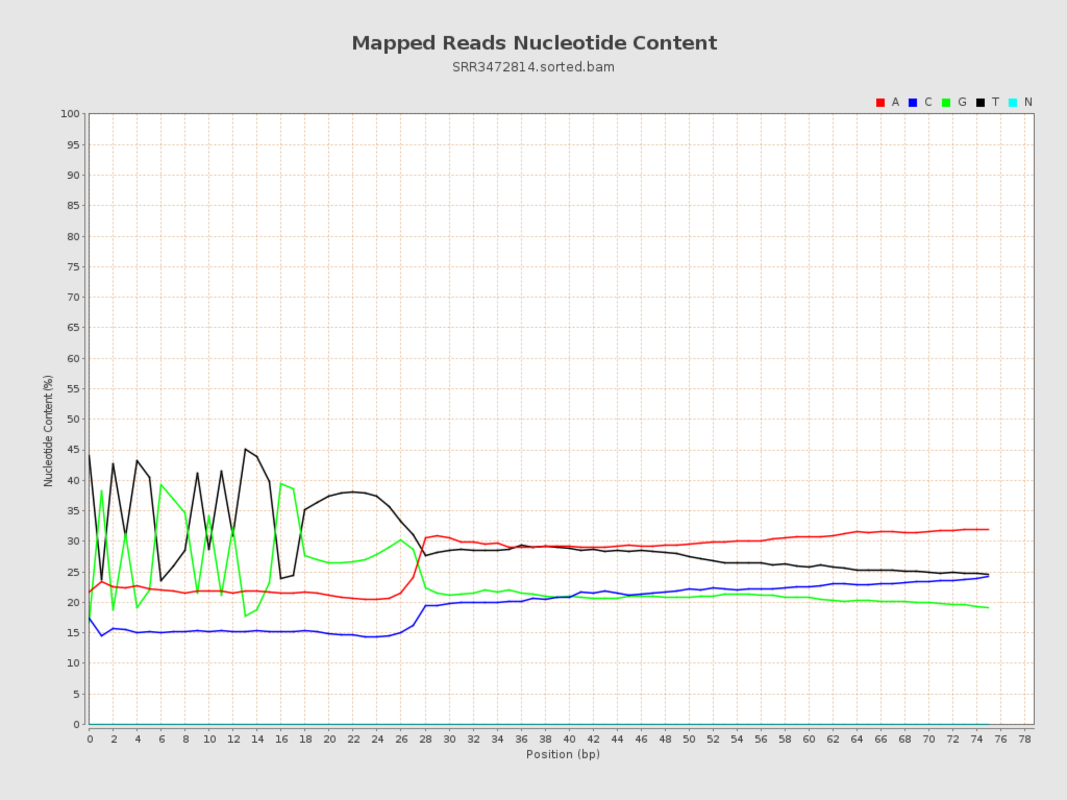
6. Results : Genome Fraction Coverage



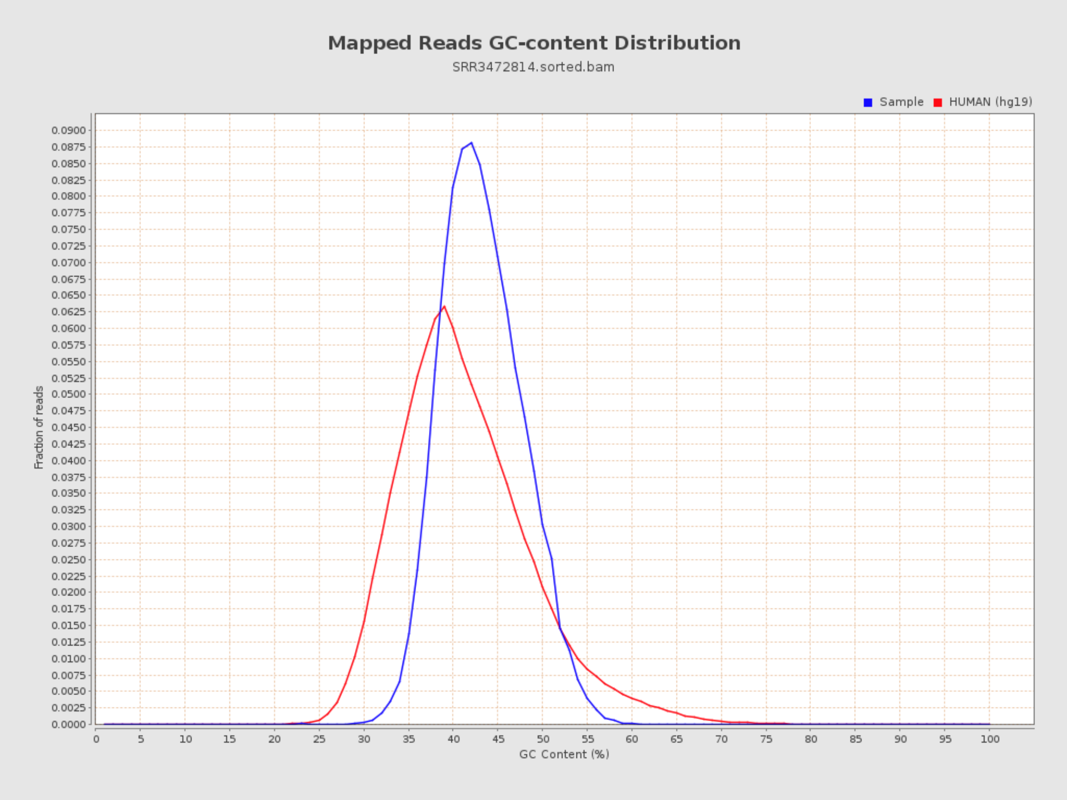
7. Results : Duplication Rate Histogram



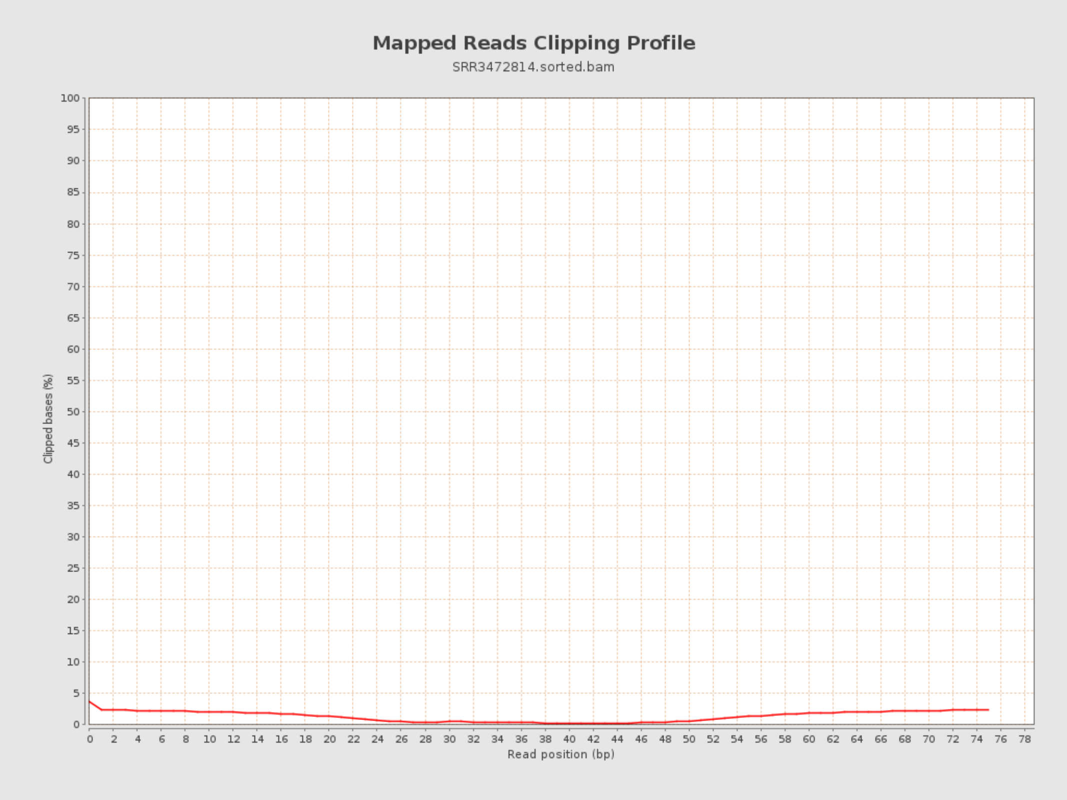
8. Results : Mapped Reads Nucleotide Content



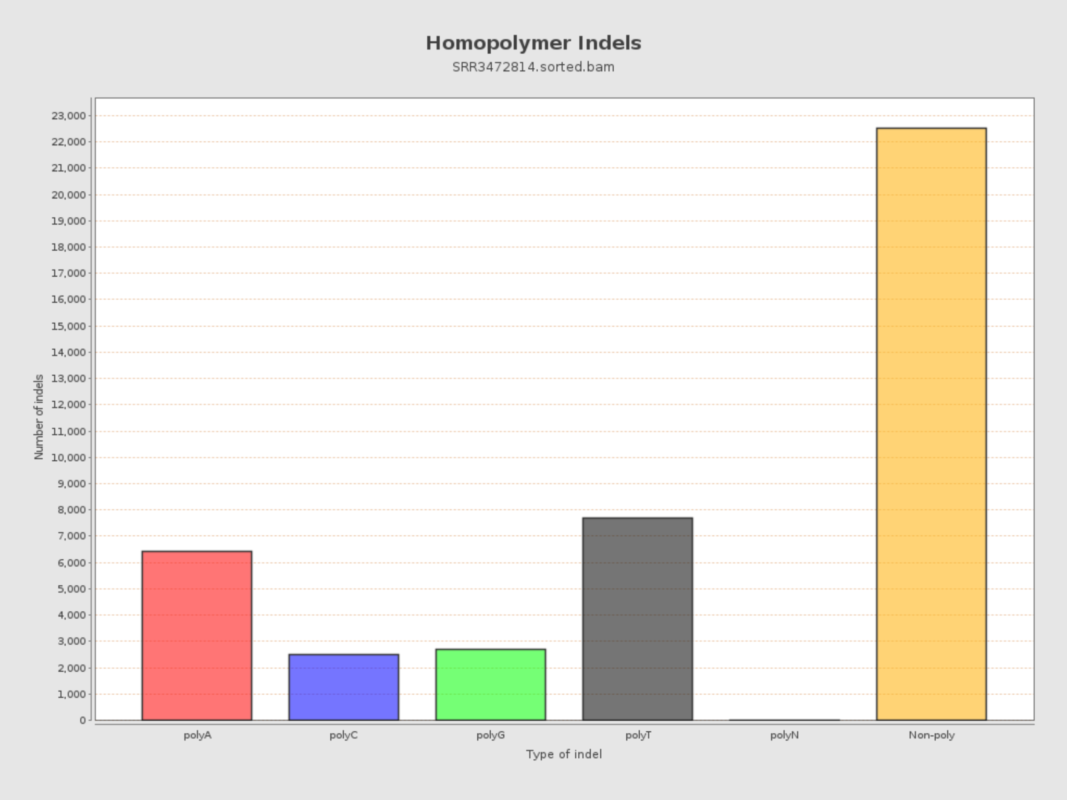
9. Results : Mapped Reads GC-content Distribution



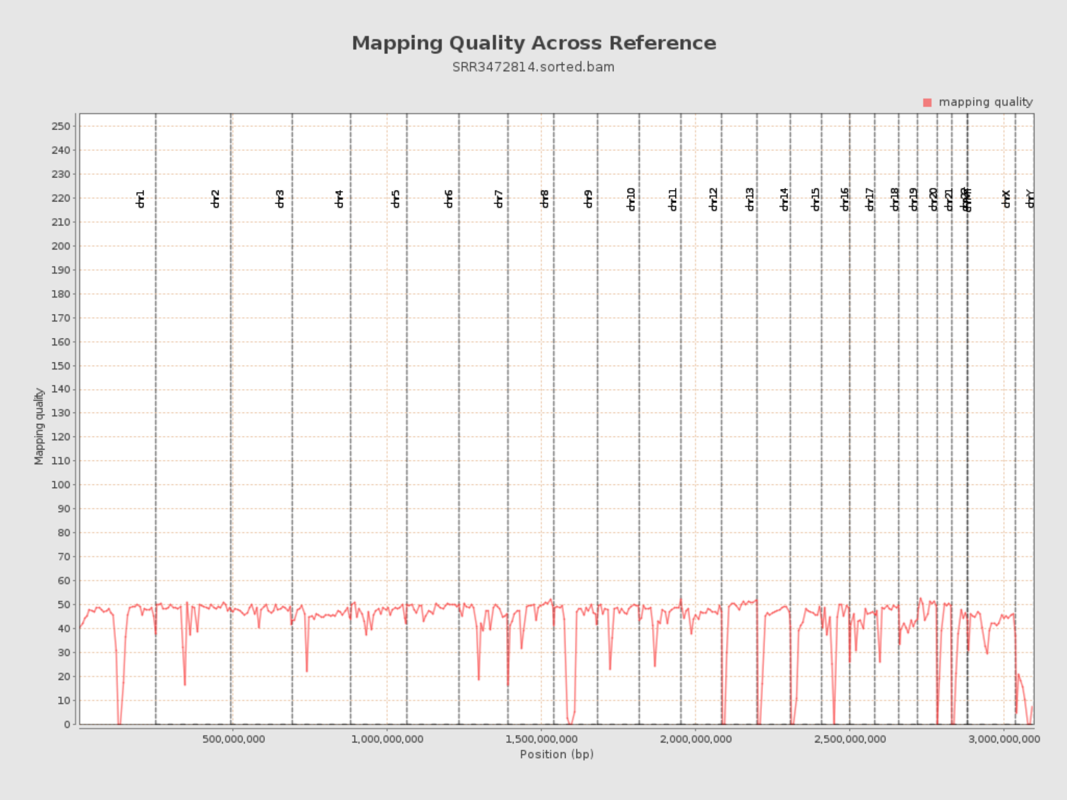
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram