Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/01 08:55:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472828.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_SRR3472828 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472828.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 01 08:55:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472828.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,833,343
Mapped reads	2,351,561 / 83%
Unmapped reads	481,782 / 17%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,221 / 0.57%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	75,570 / 2.67%
Duplication rate	2.44%
Clipped reads	1,209,056 / 42.67%

2.2. ACGT Content

Number/percentage of A's	41,499,616 / 27.22%
Number/percentage of C's	29,350,272 / 19.25%
Number/percentage of T's	46,390,294 / 30.43%
Number/percentage of G's	35,221,788 / 23.1%
Number/percentage of N's	3,639 / 0%
GC Percentage	42.35%

2.3. Coverage

Mean	0.0493

Standard Deviation	0.3504

2.4. Mapping Quality

Mean Mapping Quality	44.72

2.5. Mismatches and indels

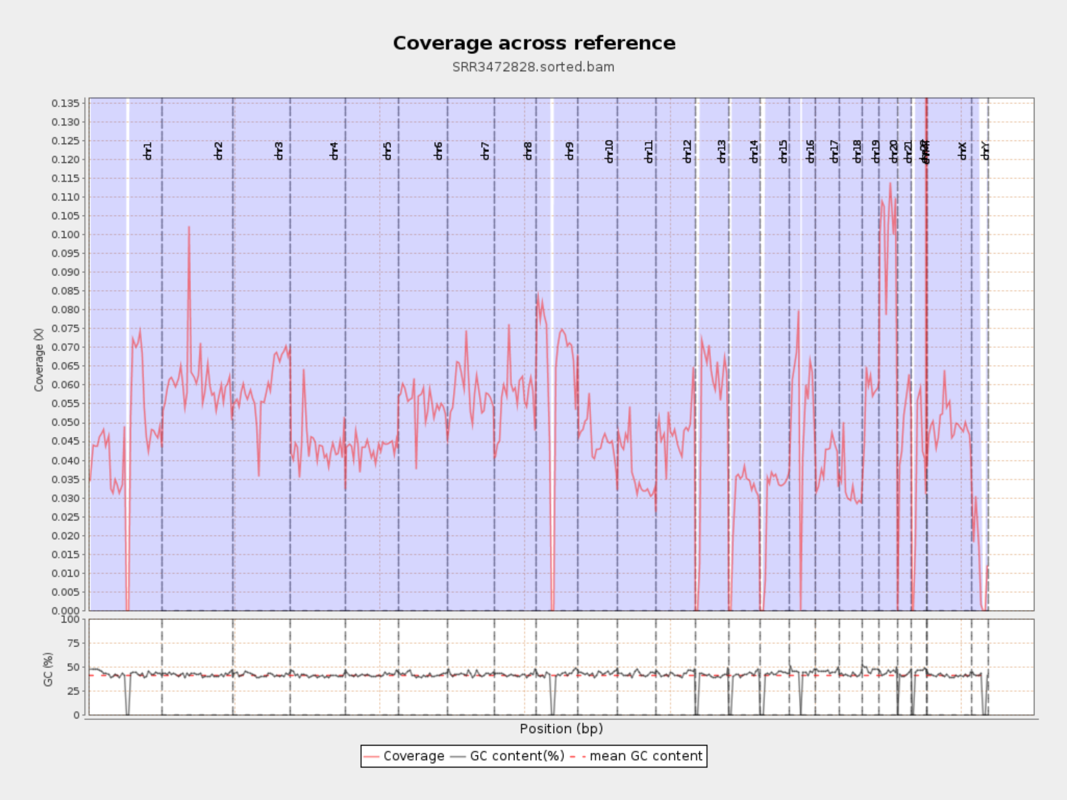
General error rate	0.88%
Mismatches	1,312,473
Insertions	12,214
Mapped reads with at least one insertion	0.51%
Deletions	35,575
Mapped reads with at least one deletion	1.5%
Homopolymer indels	46.21%

2.6. Chromosome stats

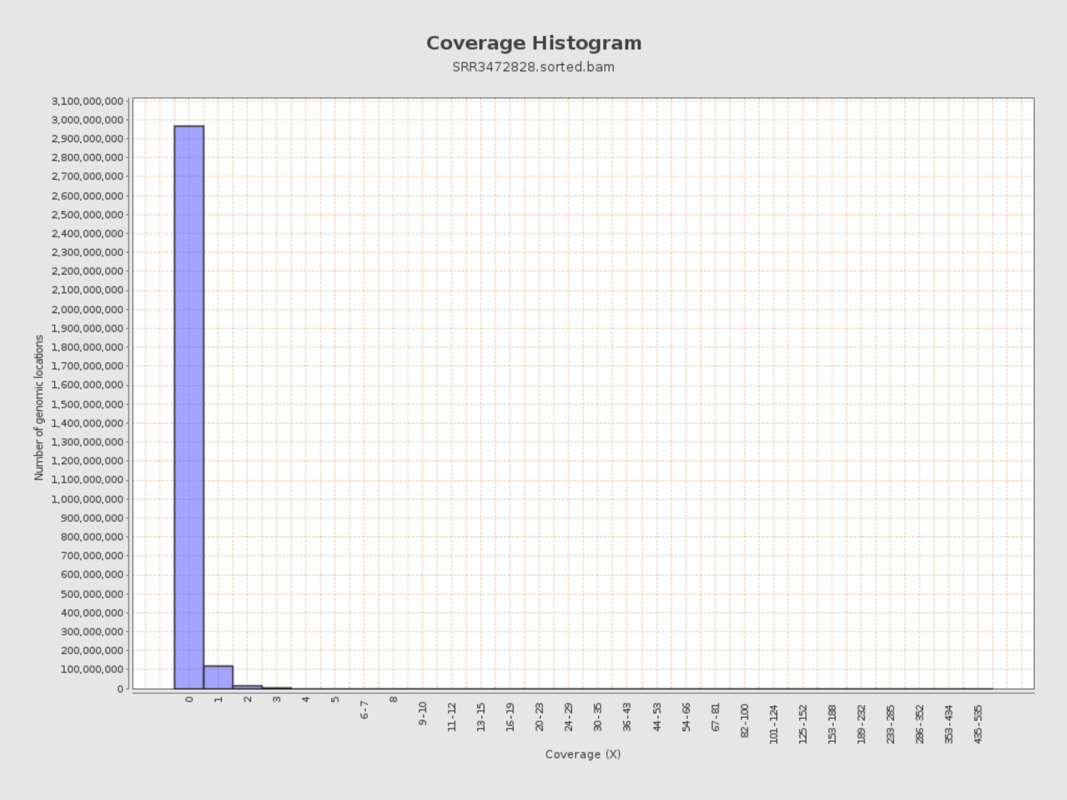
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11160219	0.0448	0.4296
chr2	243199373	14825692	0.061	0.5147
chr3	198022430	11747649	0.0593	0.2717
chr4	191154276	8373559	0.0438	0.255
chr5	180915260	7821699	0.0432	0.2332
chr6	171115067	9417391	0.055	0.2886
chr7	159138663	9270829	0.0583	0.4575

chr8	146364022	8286491	0.0566	0.3699
chr9	141213431	8908774	0.0631	0.432
chr10	135534747	6179730	0.0456	0.2975
chr11	135006516	5053356	0.0374	0.3387
chr12	133851895	6381254	0.0477	0.2514
chr13	115169878	6190428	0.0538	0.2678
chr14	107349540	3118208	0.029	0.2344
chr15	102531392	2856268	0.0279	0.2031
chr16	90354753	4964645	0.0549	0.2906
chr17	81195210	3221748	0.0397	0.2436
chr18	78077248	2560549	0.0328	0.6568
chr19	59128983	3362531	0.0569	0.3567
chr20	63025520	6383854	0.1013	0.3835
chr21	48129895	2226596	0.0463	0.2781
chr22	51304566	1728337	0.0337	0.2172
chrMT	16571	85441	5.1561	4.5475
chrX	155270560	7656381	0.0493	0.2836
chrY	59373566	746777	0.0126	0.1619

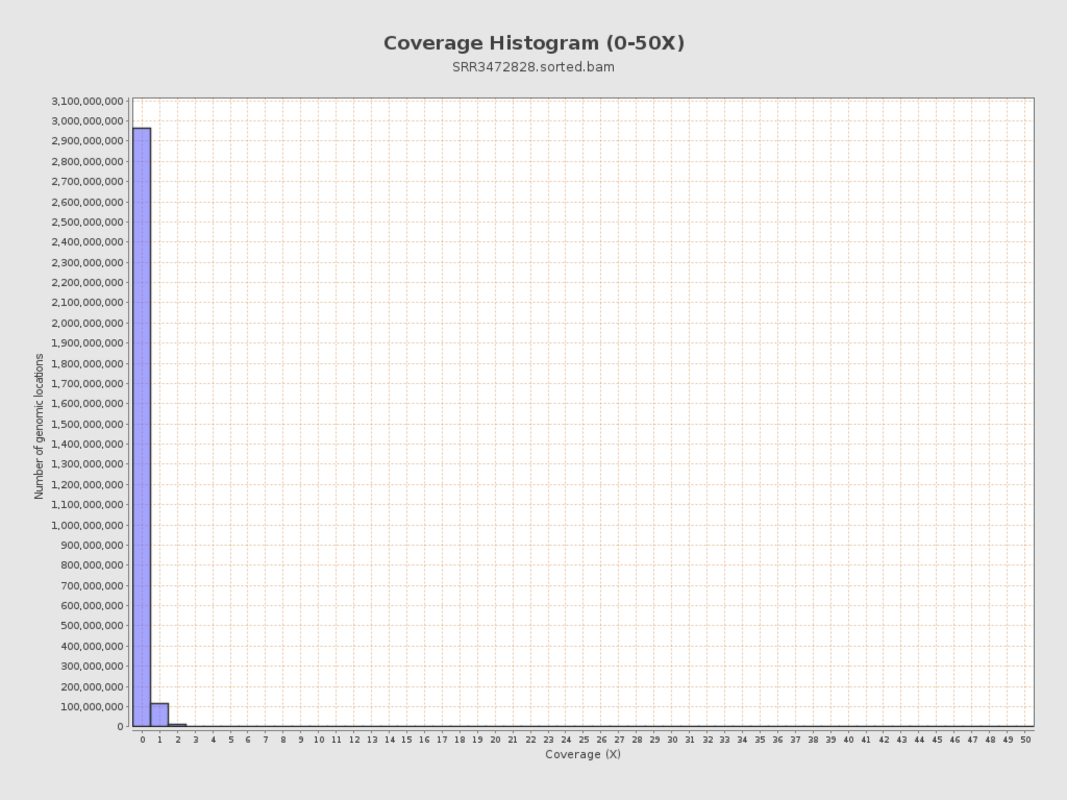
3. Results : Coverage across reference



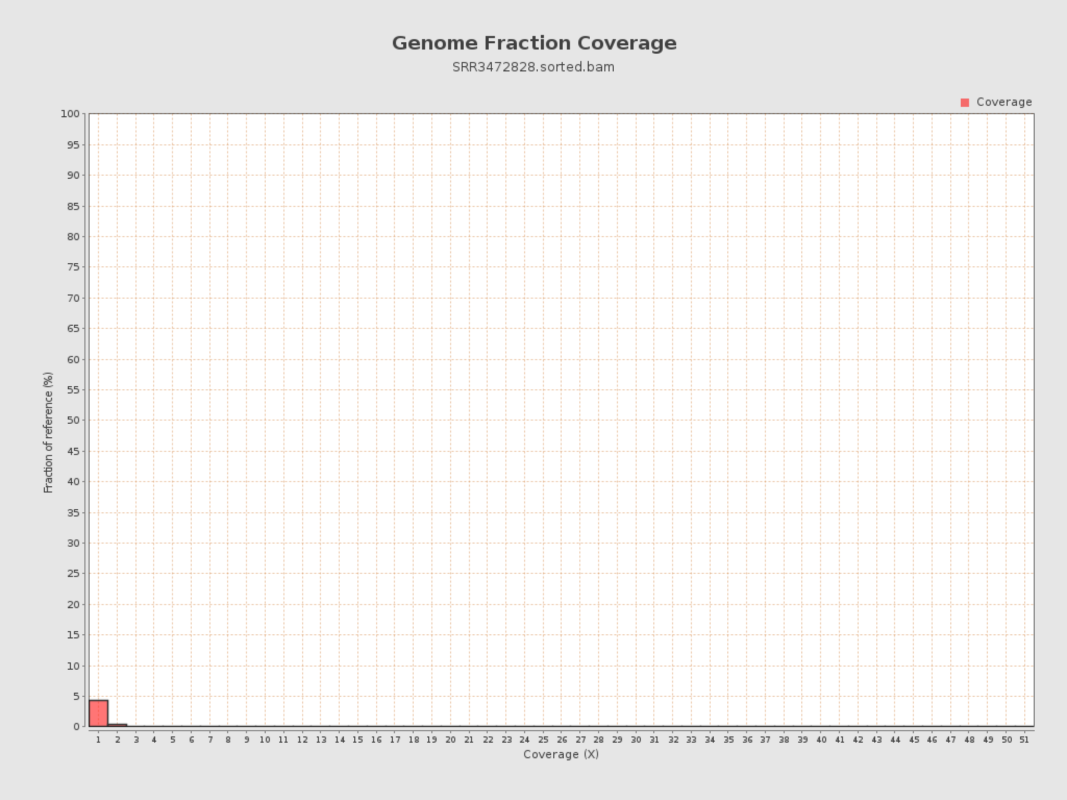
4. Results : Coverage Histogram



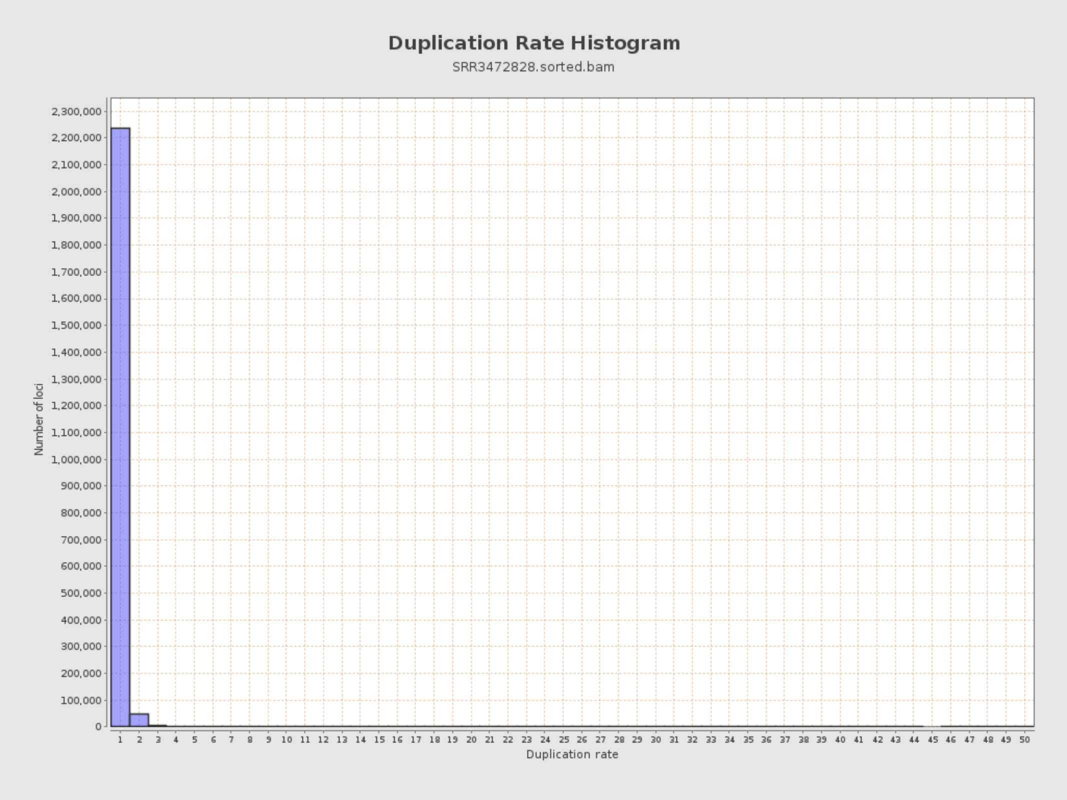
5. Results : Coverage Histogram (0-50X)



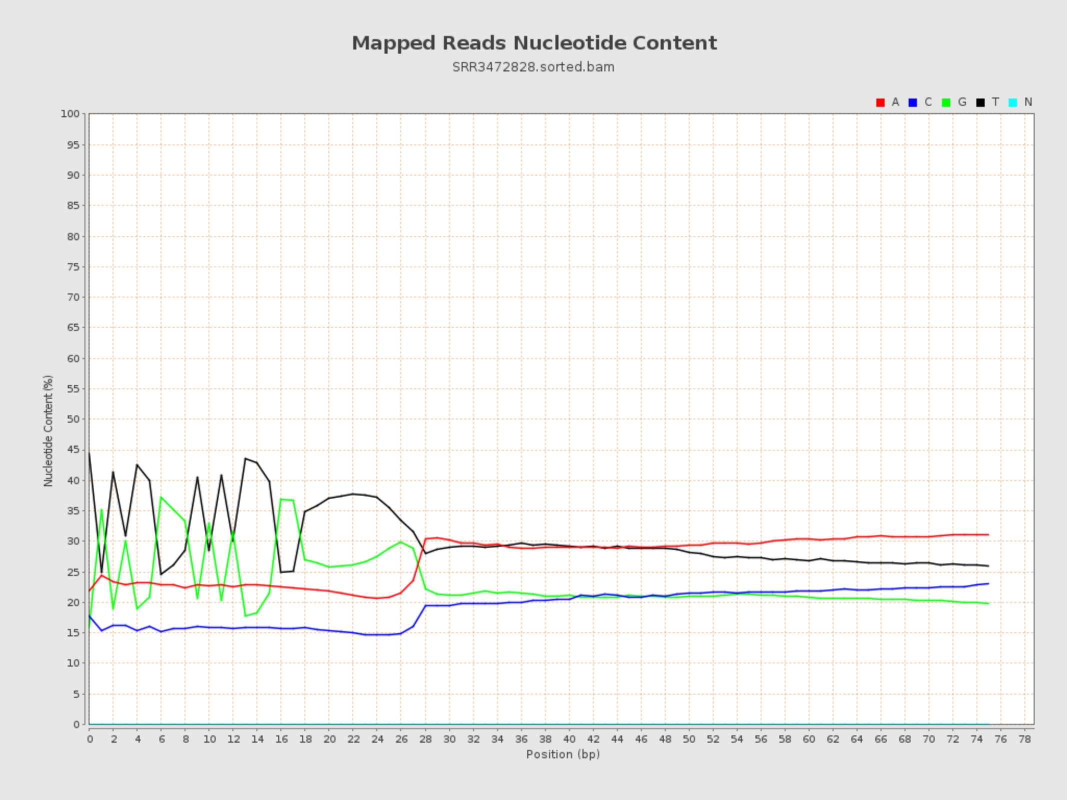
6. Results : Genome Fraction Coverage



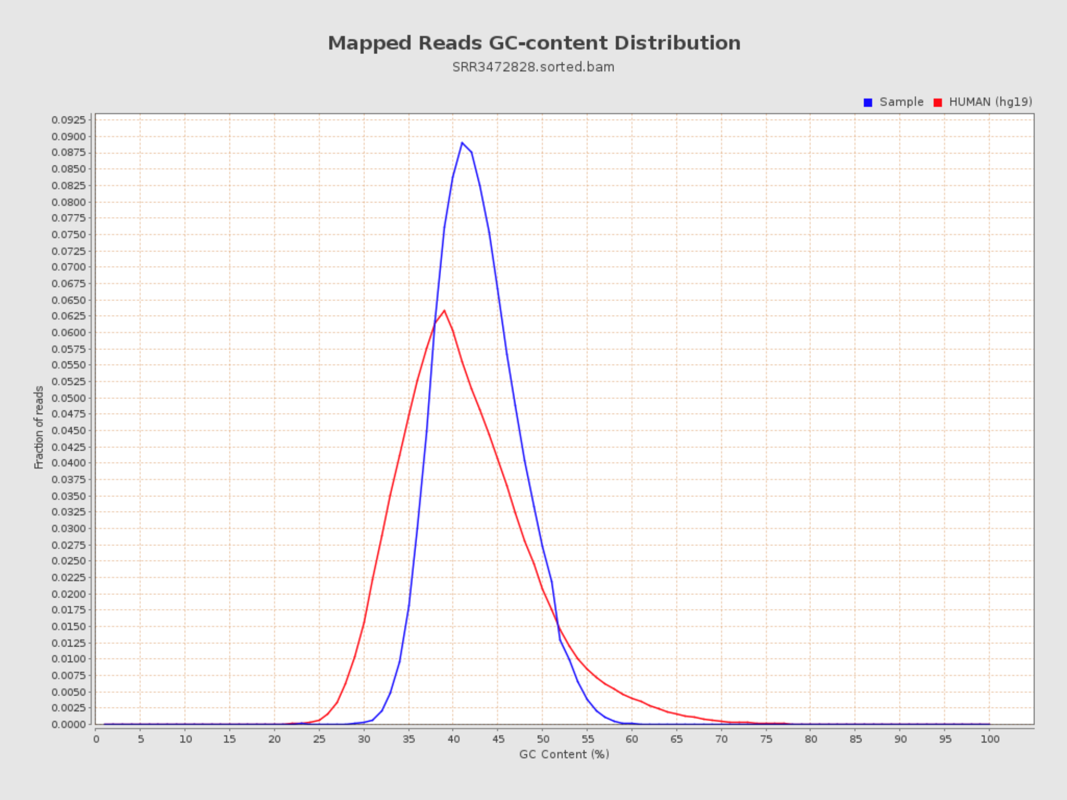
7. Results : Duplication Rate Histogram



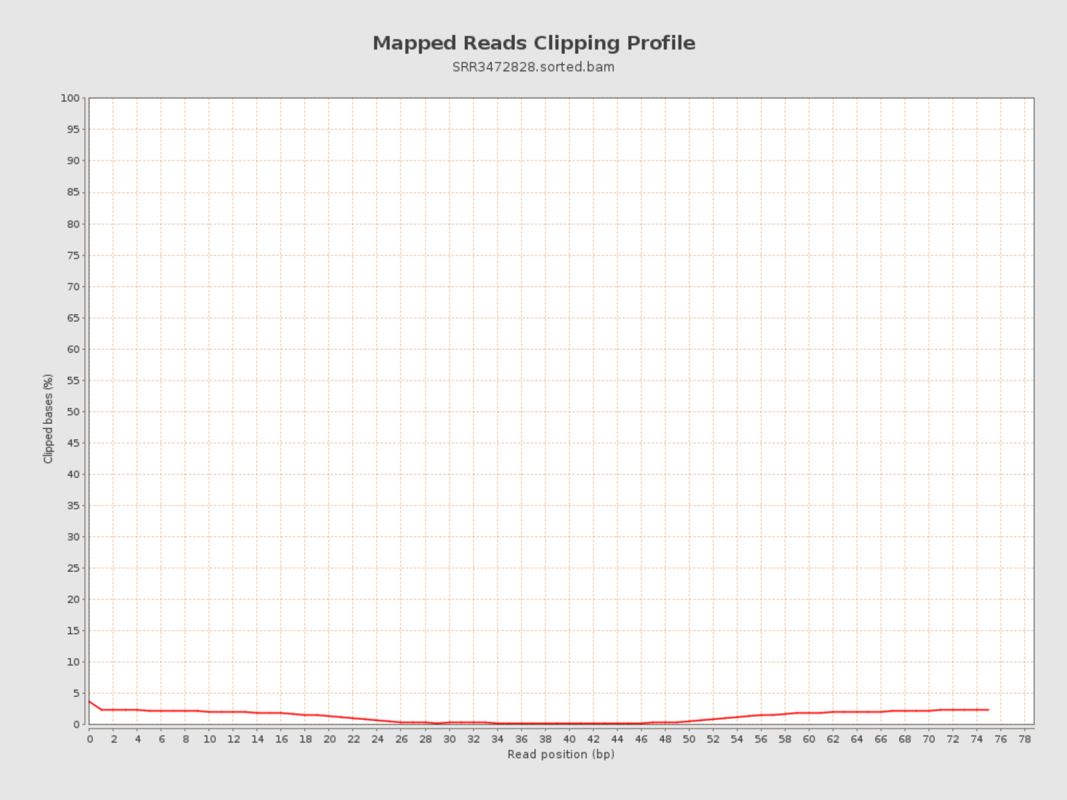
8. Results : Mapped Reads Nucleotide Content



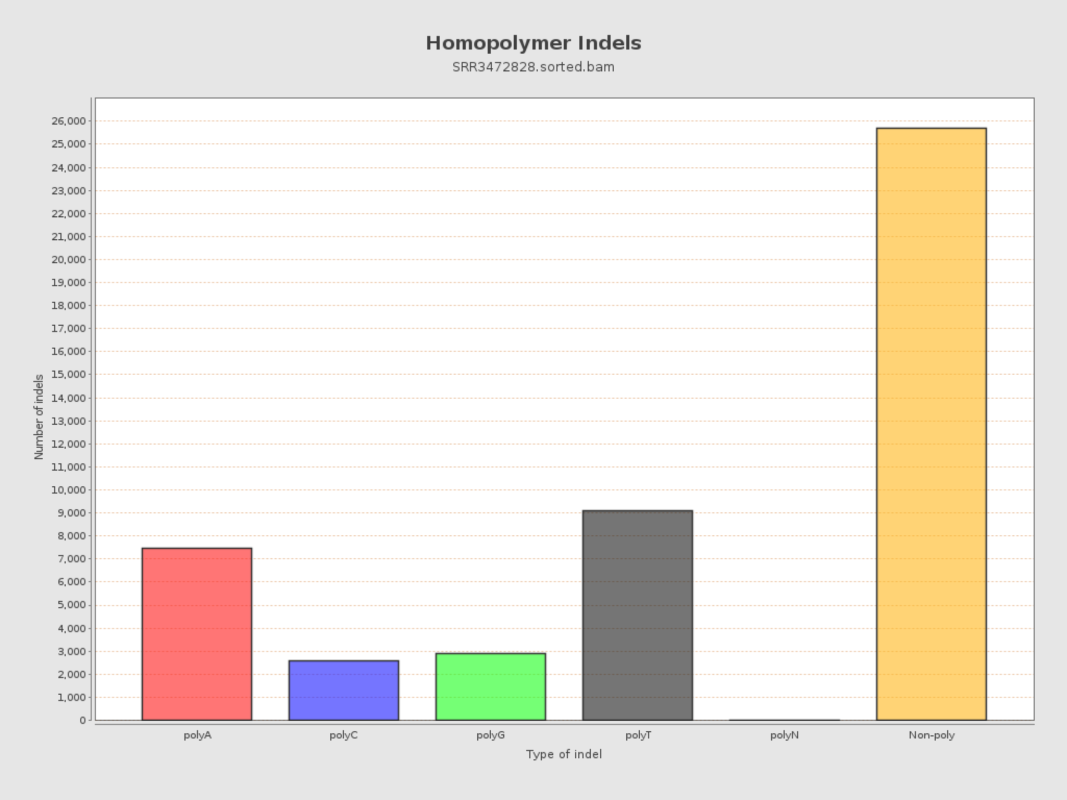
9. Results : Mapped Reads GC-content Distribution



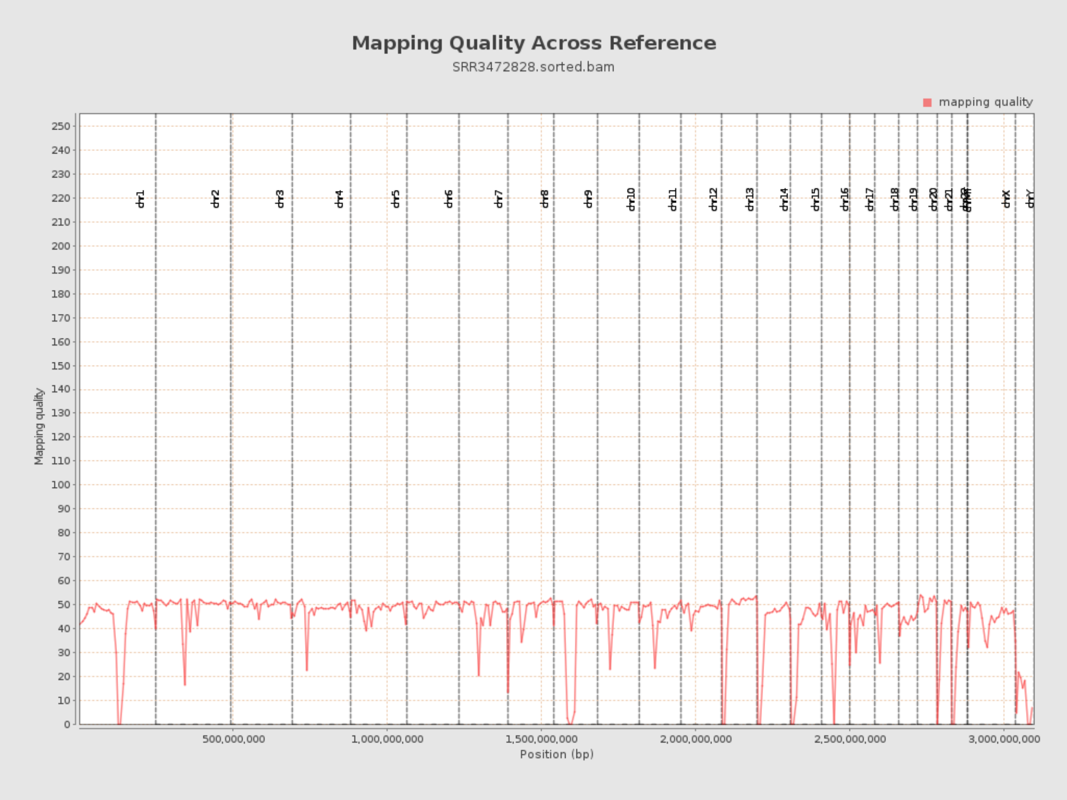
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram