Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/01 08:01:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472816.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_SRR3472816 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472816.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 01 08:01:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472816.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,955,275
Mapped reads	2,205,283 / 74.62%
Unmapped reads	749,992 / 25.38%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	22,755 / 0.77%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	114,389 / 3.87%
Duplication rate	3.72%
Clipped reads	1,325,199 / 44.84%

2.2. ACGT Content

Number/percentage of A's	36,852,369 / 26.61%
Number/percentage of C's	28,223,701 / 20.38%
Number/percentage of T's	40,417,933 / 29.18%
Number/percentage of G's	32,996,774 / 23.83%
Number/percentage of N's	3,027 / 0%
GC Percentage	44.2%

2.3. Coverage

Mean	0.0448

Standard Deviation	0.3469

2.4. Mapping Quality

Mean Mapping Quality	42.46

2.5. Mismatches and indels

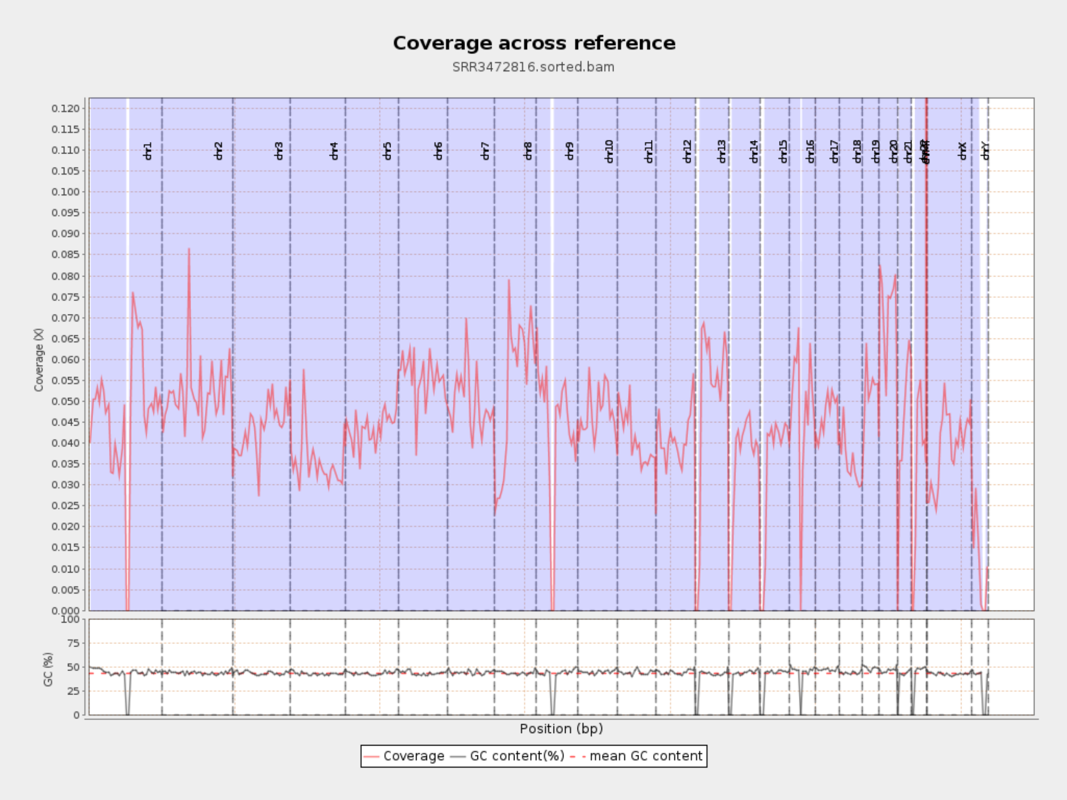
General error rate	0.91%
Mismatches	1,245,555
Insertions	10,871
Mapped reads with at least one insertion	0.49%
Deletions	34,135
Mapped reads with at least one deletion	1.53%
Homopolymer indels	44.35%

2.6. Chromosome stats

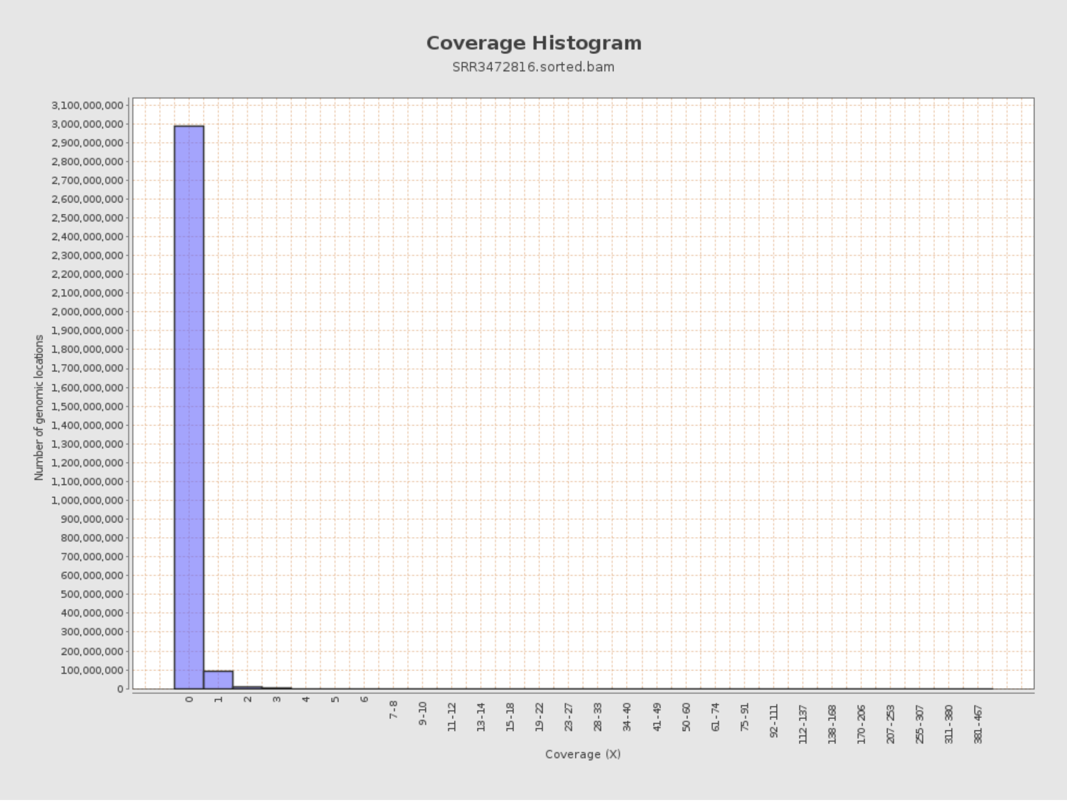
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11673695	0.0468	0.4106
chr2	243199373	12726308	0.0523	0.4721
chr3	198022430	8644728	0.0437	0.2635
chr4	191154276	6744506	0.0353	0.2636
chr5	180915260	7888898	0.0436	0.2626
chr6	171115067	9509990	0.0556	0.3163
chr7	159138663	7935749	0.0499	0.4711

chr8	146364022	7860954	0.0537	0.348
chr9	141213431	6011991	0.0426	0.3688
chr10	135534747	6380393	0.0471	0.3373
chr11	135006516	5512117	0.0408	0.3613
chr12	133851895	5540661	0.0414	0.2677
chr13	115169878	5751163	0.0499	0.2868
chr14	107349540	3726036	0.0347	0.2729
chr15	102531392	3492737	0.0341	0.2615
chr16	90354753	4344802	0.0481	0.2965
chr17	81195210	3800066	0.0468	0.2948
chr18	78077248	2789675	0.0357	0.5887
chr19	59128983	3082789	0.0521	0.3626
chr20	63025520	4550480	0.0722	0.3465
chr21	48129895	2157049	0.0448	0.2957
chr22	51304566	1631763	0.0318	0.2349
chrMT	16571	127819	7.7134	6.0708
chrX	155270560	6031586	0.0388	0.2841
chrY	59373566	639779	0.0108	0.1606

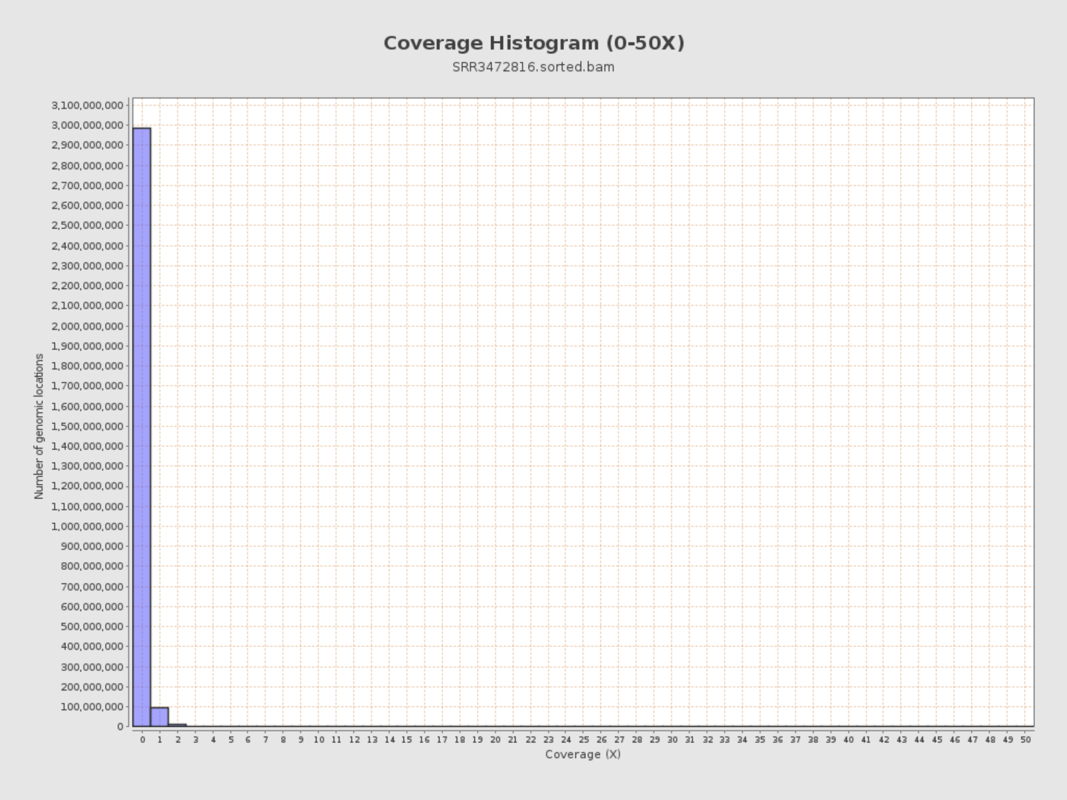
3. Results : Coverage across reference



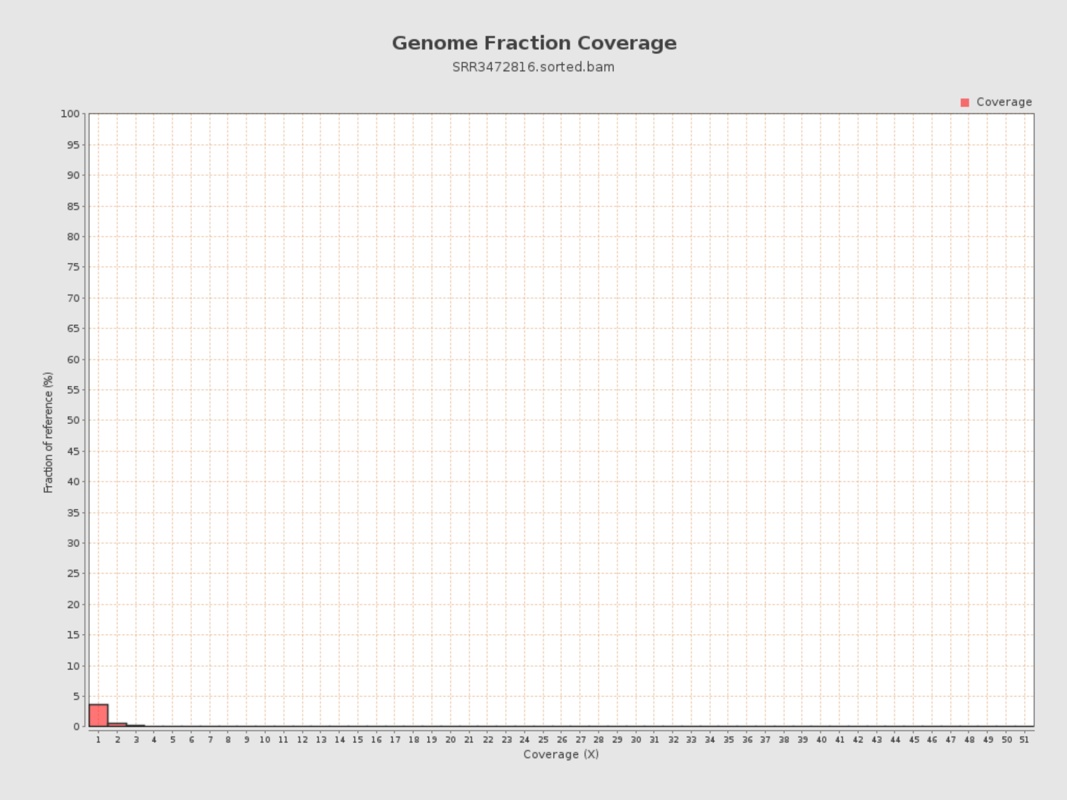
4. Results : Coverage Histogram



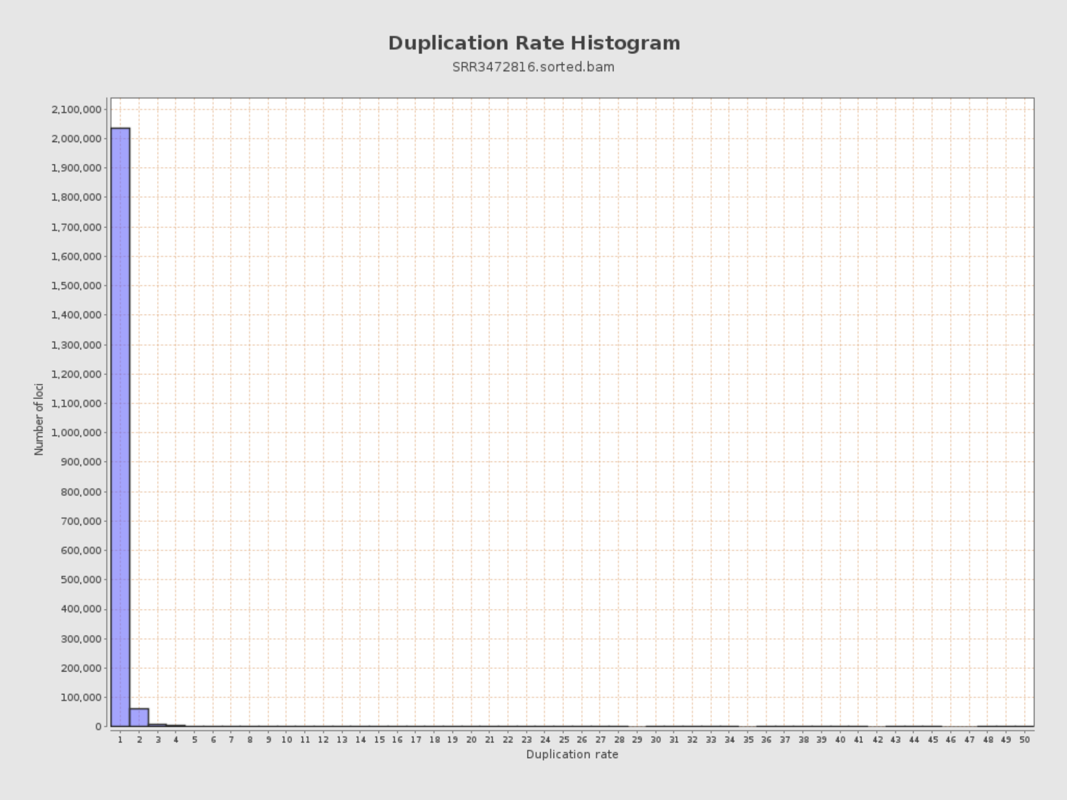
5. Results : Coverage Histogram (0-50X)



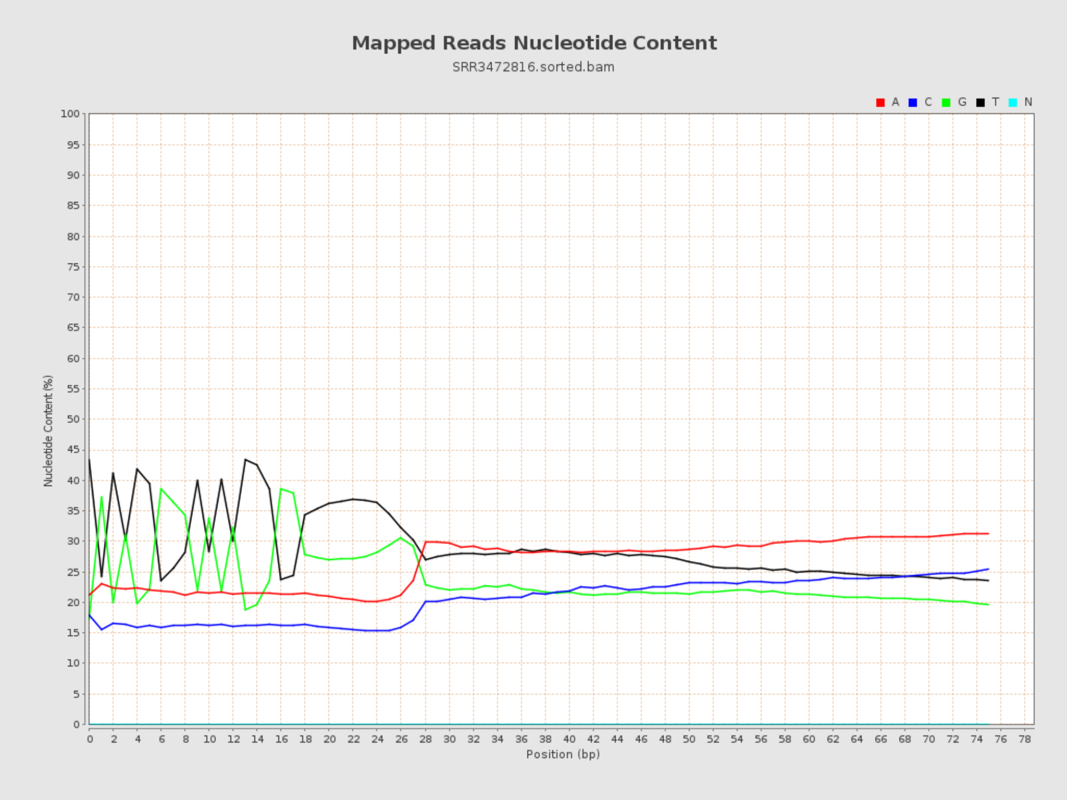
6. Results : Genome Fraction Coverage



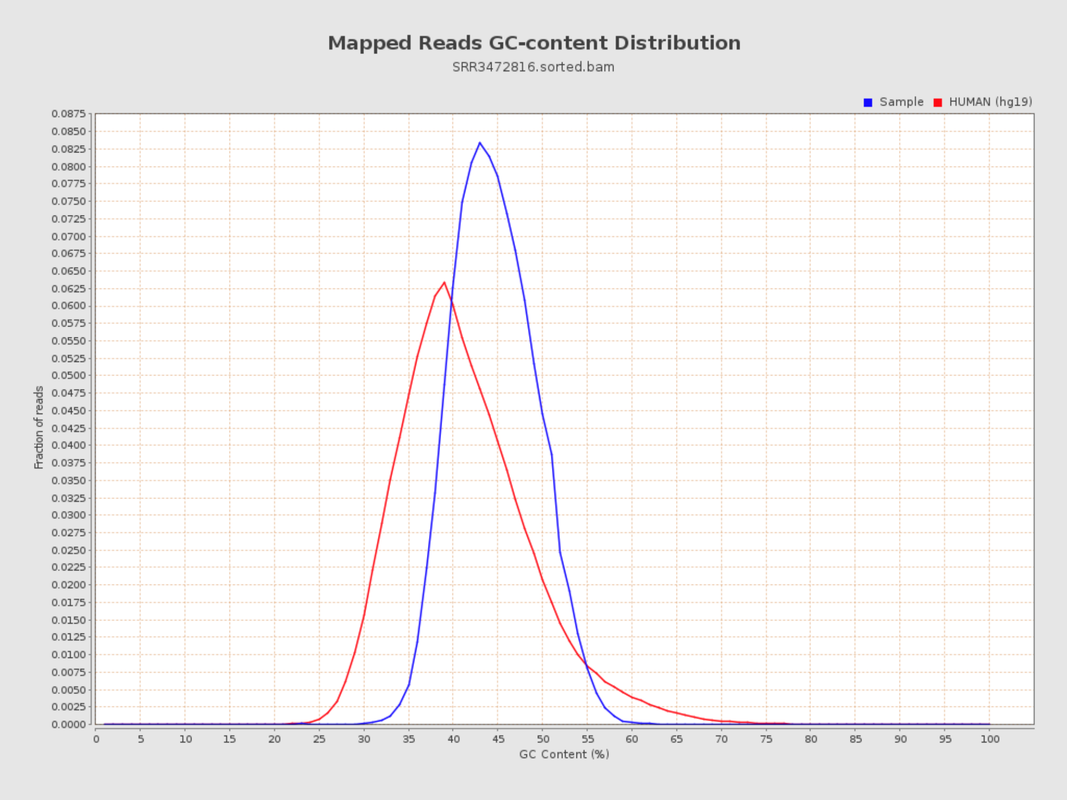
7. Results : Duplication Rate Histogram



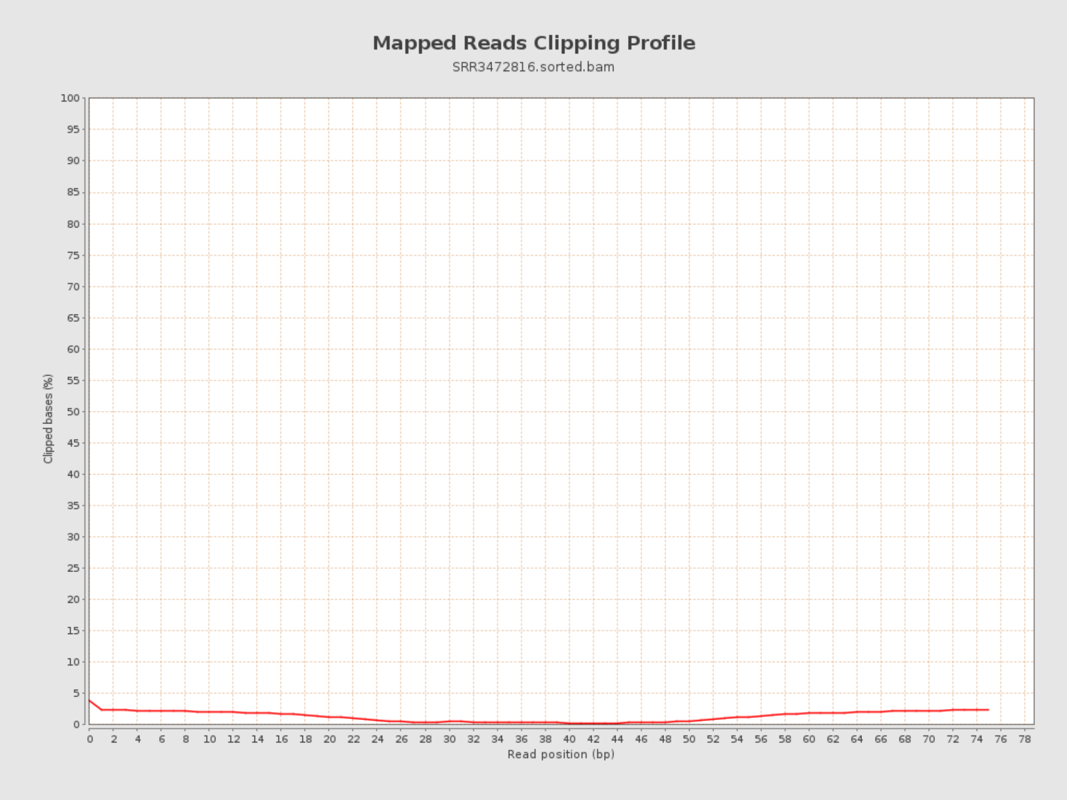
8. Results : Mapped Reads Nucleotide Content



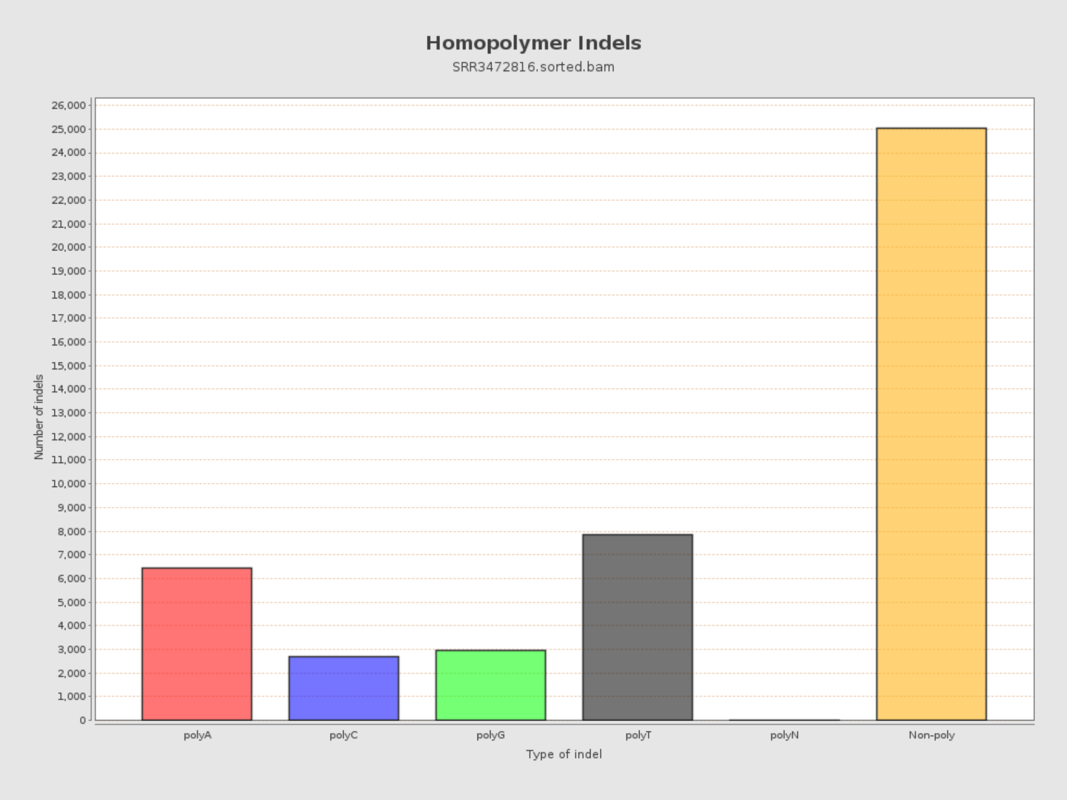
9. Results : Mapped Reads GC-content Distribution



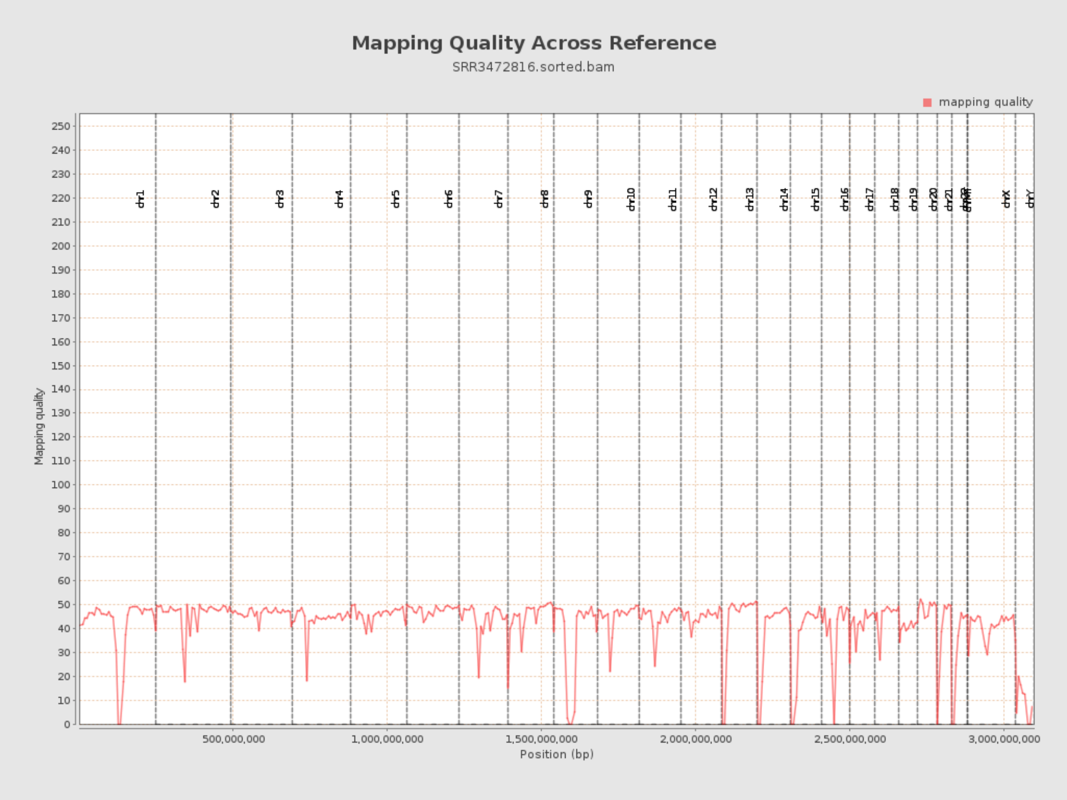
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram