Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 11:49:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084392.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_SRR3084392 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084392.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 11:49:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084392.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,336
Mapped reads	1,183 / 35.46%
Unmapped reads	2,153 / 64.54%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4 / 0.12%
Read min/max/mean length	31 / 76 / 76.04
Duplicated reads (estimated)	0 / 0%
Duplication rate	0%
Clipped reads	554 / 16.61%

2.2. ACGT Content

Number/percentage of A's	22,323 / 28.55%
Number/percentage of C's	14,695 / 18.8%
Number/percentage of T's	23,724 / 30.35%
Number/percentage of G's	17,303 / 22.13%
Number/percentage of N's	134 / 0.17%
GC Percentage	40.93%

2.3. Coverage

Mean	0

Standard Deviation	0.005

2.4. Mapping Quality

Mean Mapping Quality	39.42

2.5. Mismatches and indels

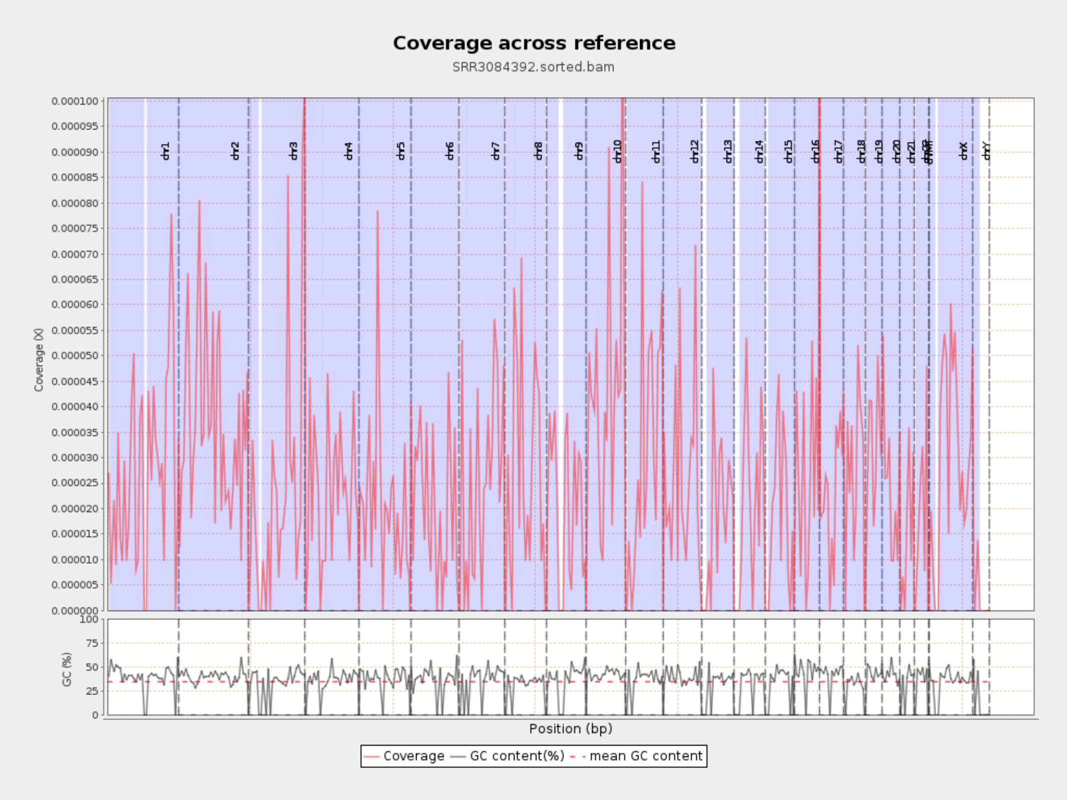
General error rate	1.24%
Mismatches	944
Insertions	10
Mapped reads with at least one insertion	0.85%
Deletions	15
Mapped reads with at least one deletion	1.27%
Homopolymer indels	40%

2.6. Chromosome stats

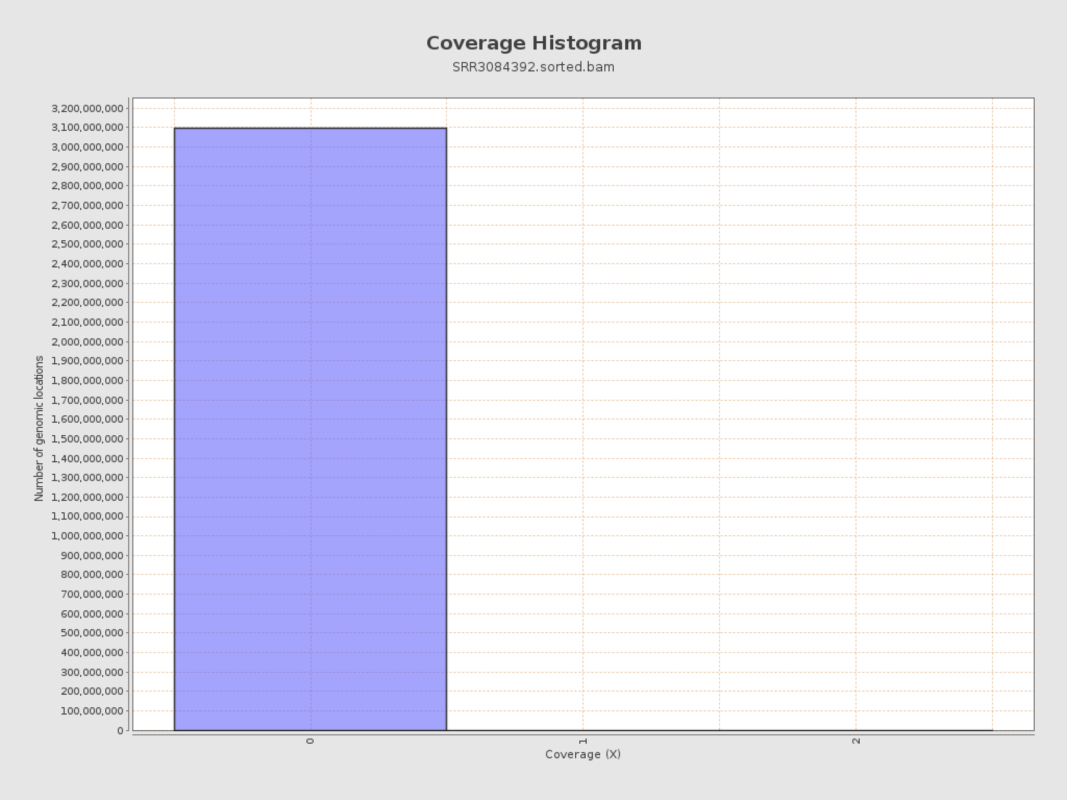
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6685	0	0.0052
chr2	243199373	8944	0	0.0061
chr3	198022430	4412	0	0.0047
chr4	191154276	4469	0	0.0048
chr5	180915260	3810	0	0.0046
chr6	171115067	3556	0	0.0046
chr7	159138663	4028	0	0.005

chr8	146364022	3837	0	0.0051
chr9	141213431	2804	0	0.0045
chr10	135534747	5953	0	0.0066
chr11	135006516	4020	0	0.0055
chr12	133851895	3588	0	0.0052
chr13	115169878	2087	0	0.0043
chr14	107349540	2178	0	0.0045
chr15	102531392	1860	0	0.0043
chr16	90354753	2340	0	0.0051
chr17	81195210	1789	0	0.0047
chr18	78077248	2106	0	0.0053
chr19	59128983	1849	0	0.0056
chr20	63025520	1462	0	0.0048
chr21	48129895	710	0	0.0038
chr22	51304566	957	0	0.0043
chrMT	16571	0	0	0
chrX	155270560	4617	0	0.0055
chrY	59373566	150	0	0.0016

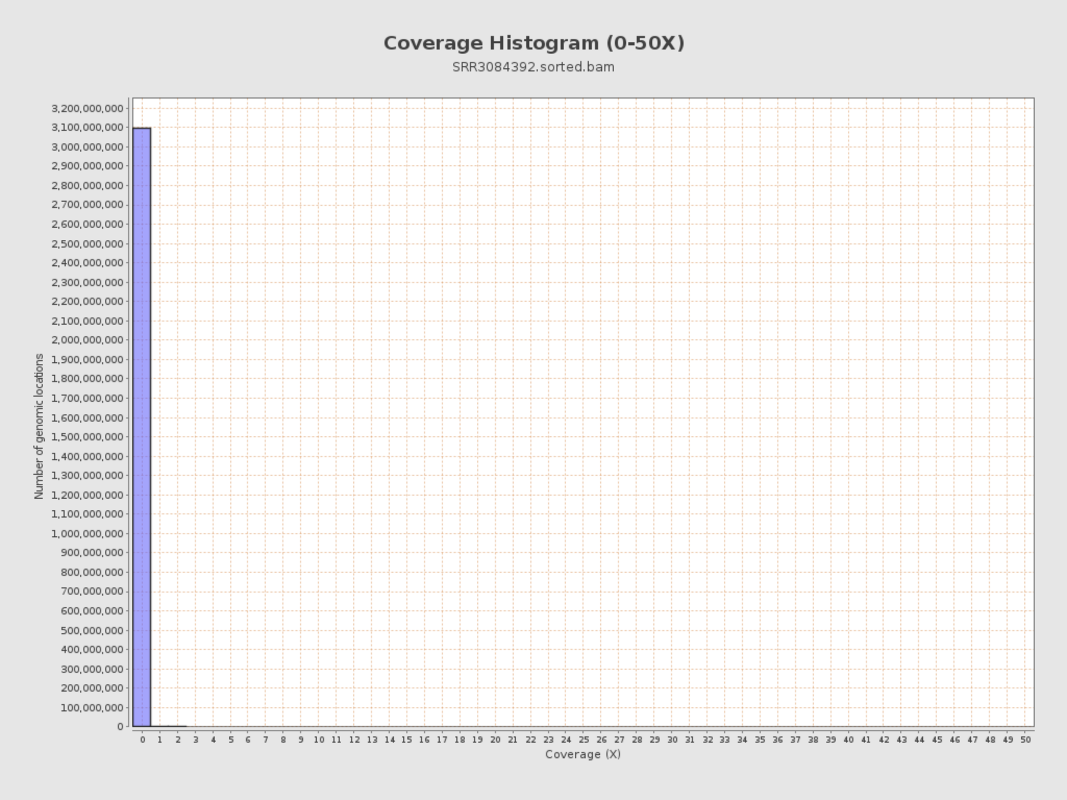
3. Results : Coverage across reference



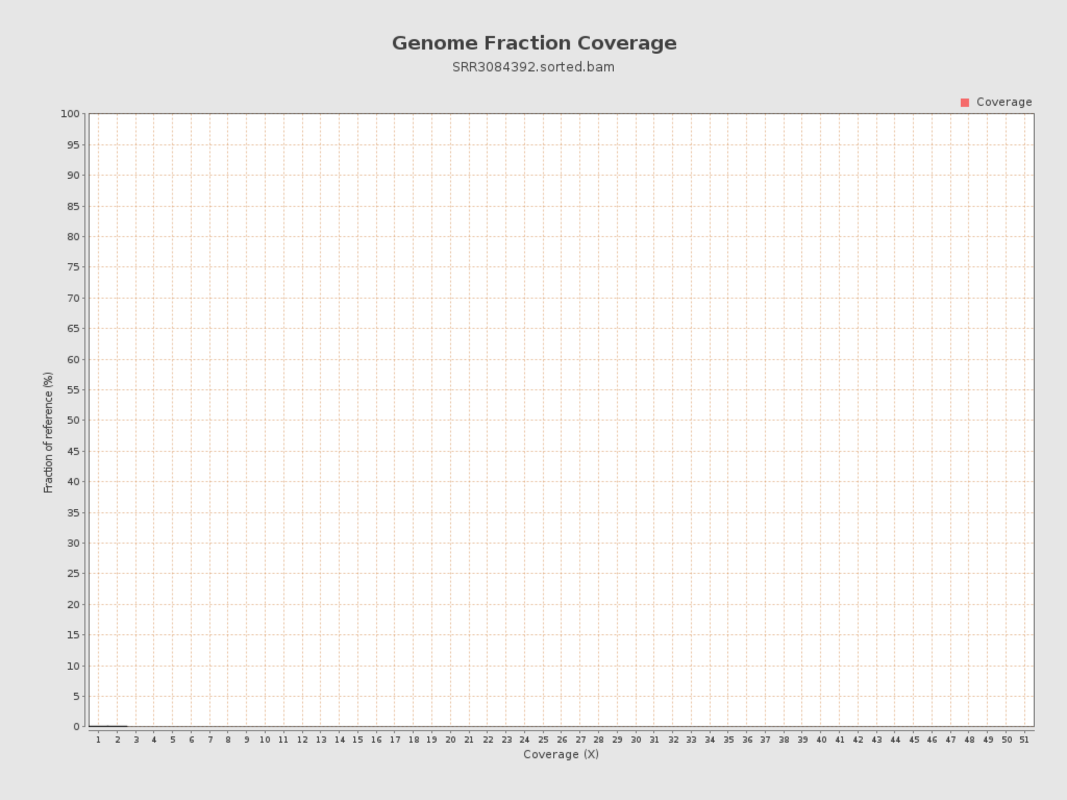
4. Results : Coverage Histogram



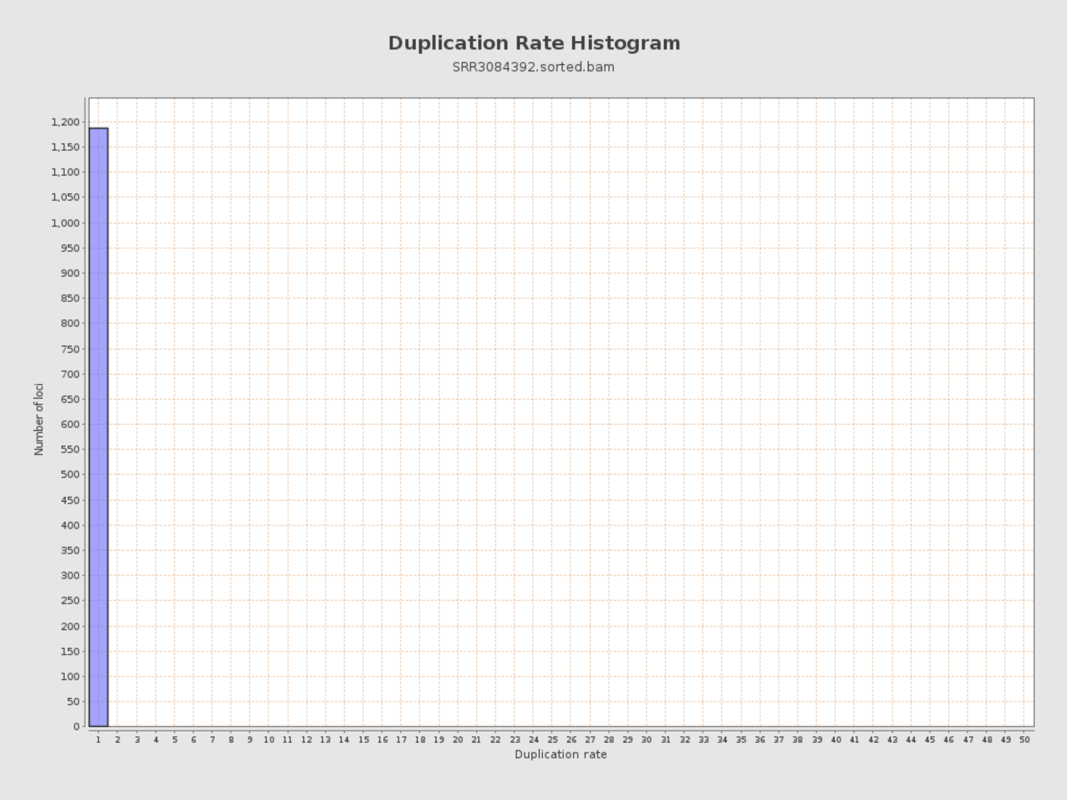
5. Results : Coverage Histogram (0-50X)



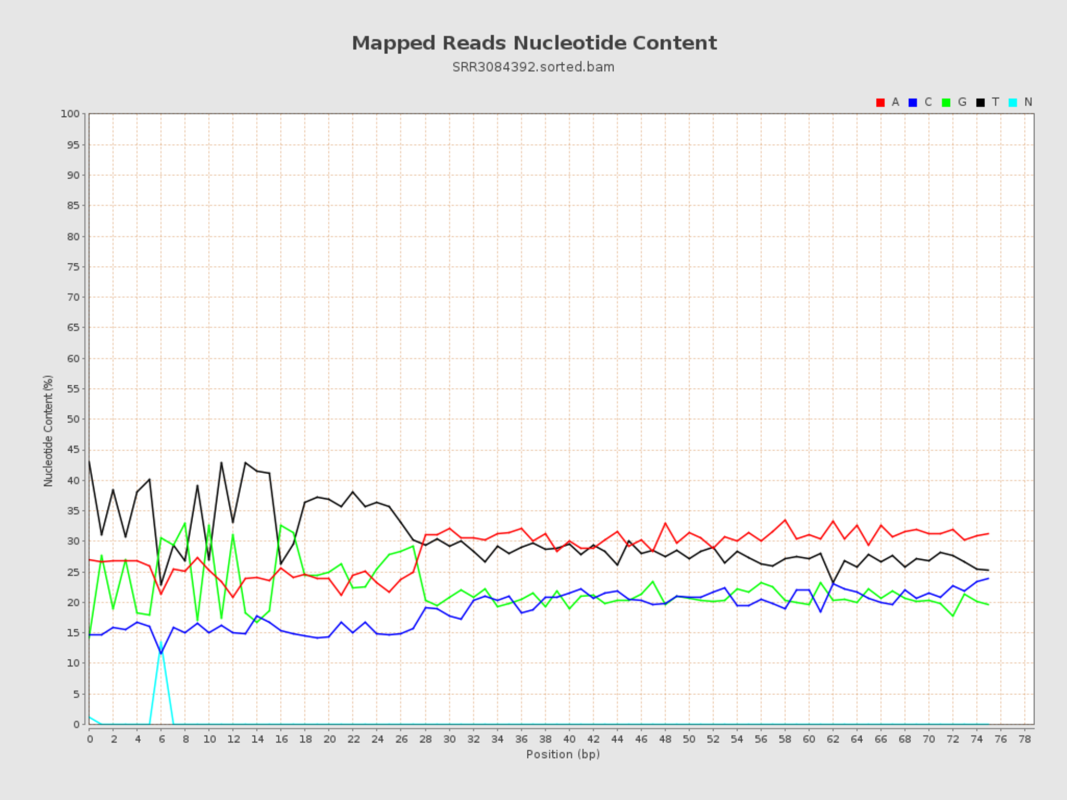
6. Results : Genome Fraction Coverage



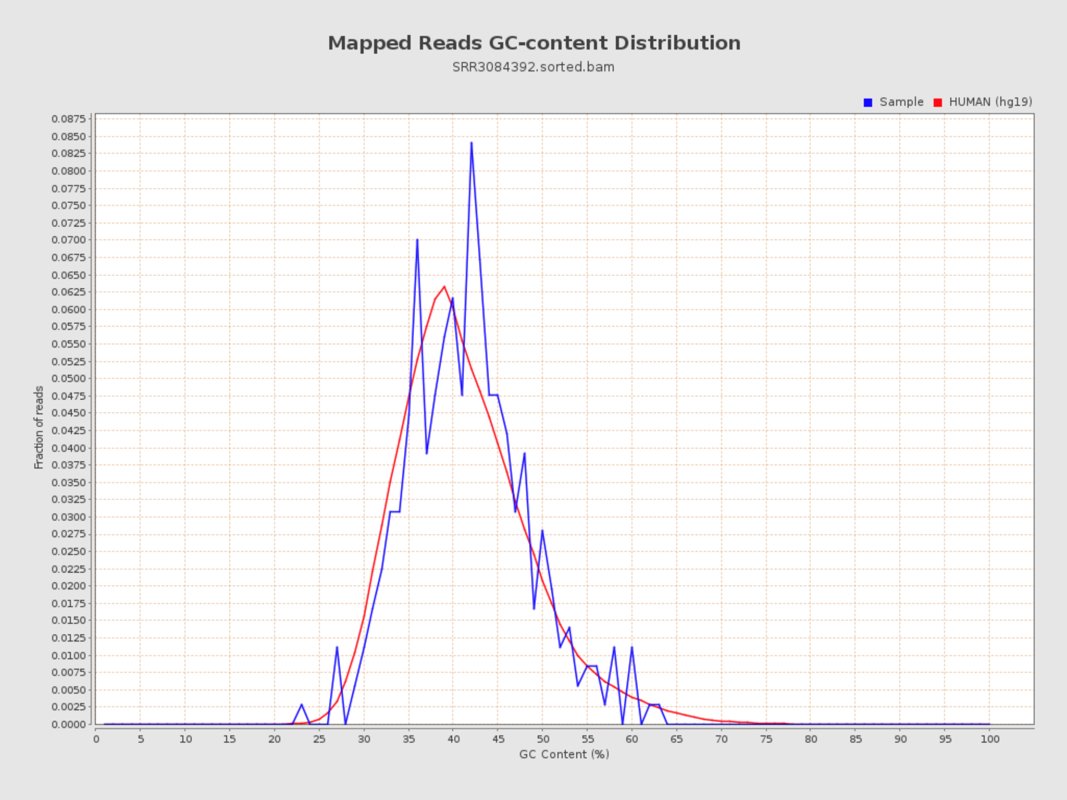
7. Results : Duplication Rate Histogram



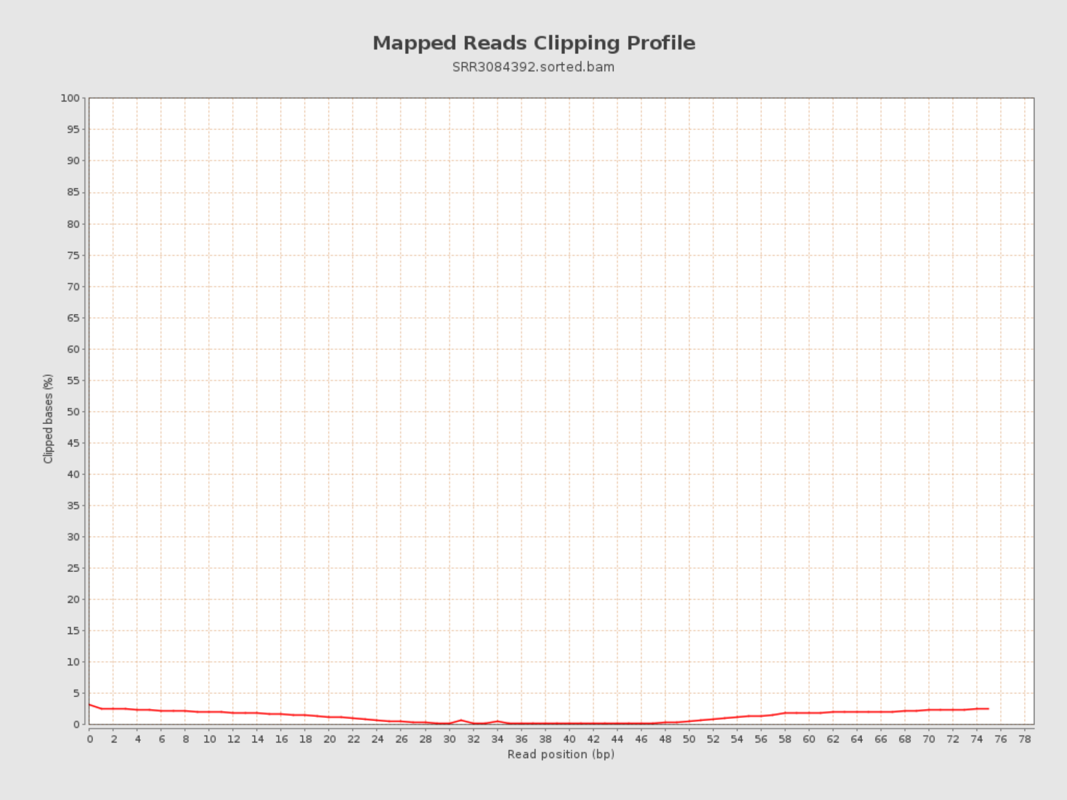
8. Results : Mapped Reads Nucleotide Content



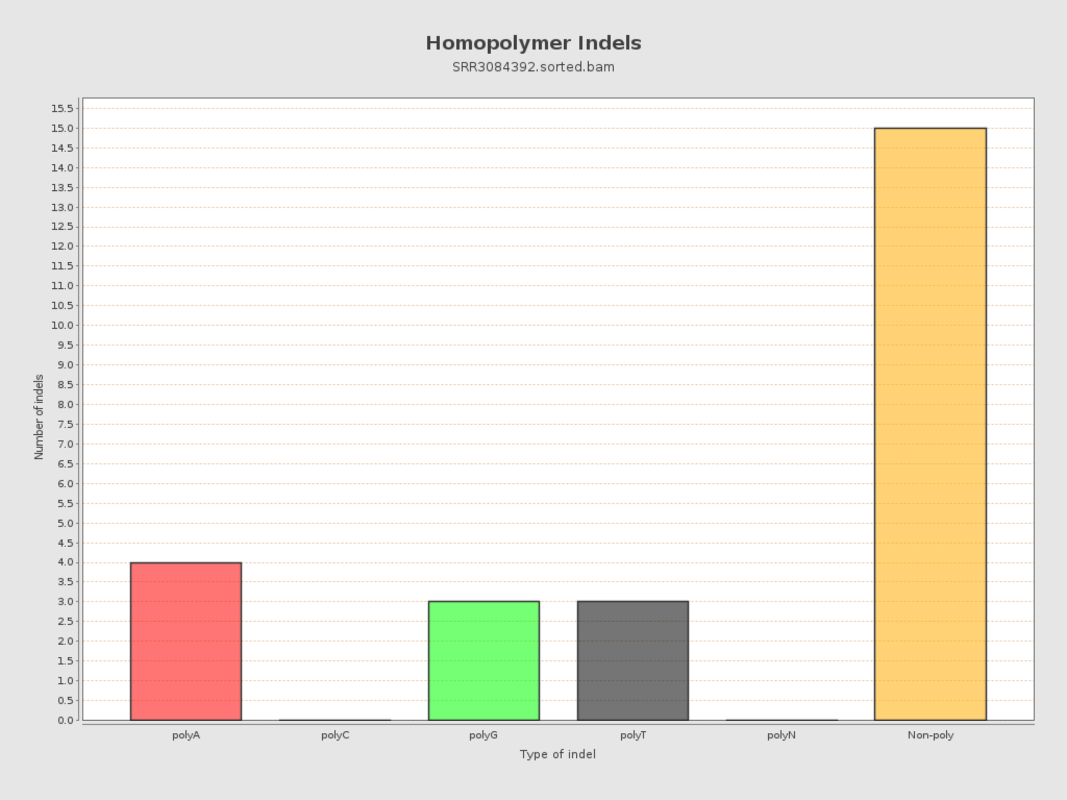
9. Results : Mapped Reads GC-content Distribution



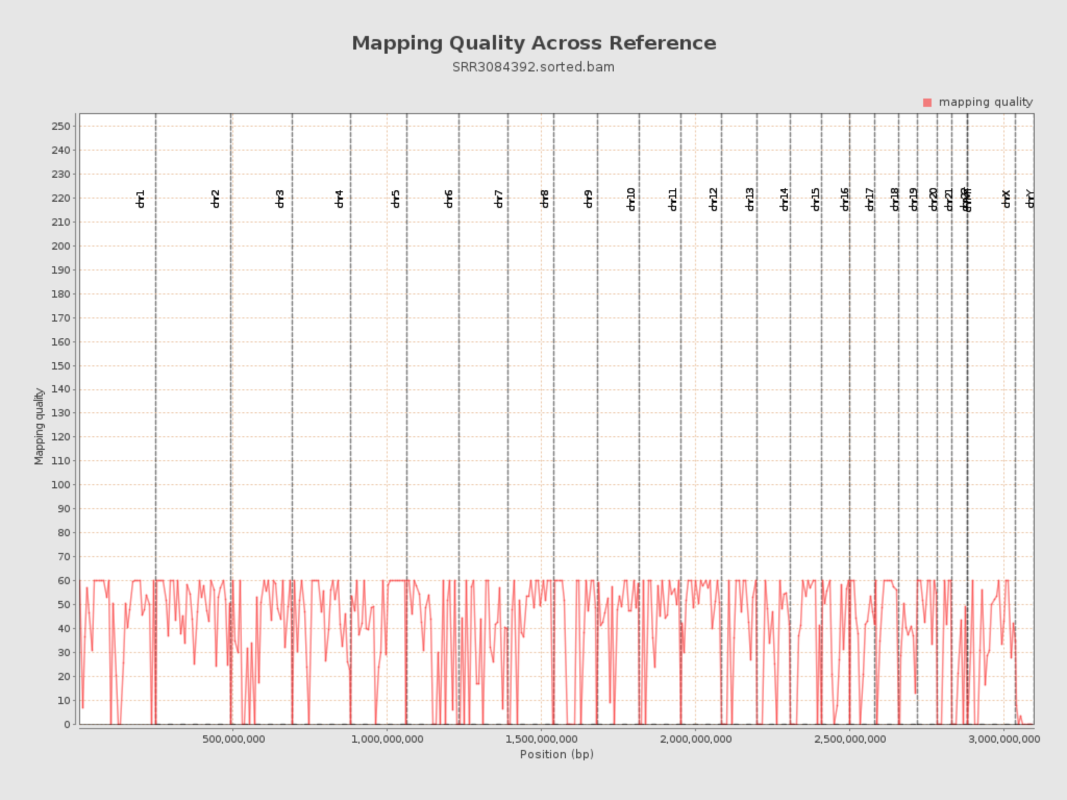
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram