Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 08:16:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084259.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_SRR3084259 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084259.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 08:16:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084259.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,082,603
Mapped reads	1,783,769 / 85.65%
Unmapped reads	298,834 / 14.35%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,036 / 0.58%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	61,045 / 2.93%
Duplication rate	2.92%
Clipped reads	1,053,157 / 50.57%

2.2. ACGT Content

Number/percentage of A's	32,127,744 / 28.69%
Number/percentage of C's	21,444,144 / 19.15%
Number/percentage of T's	34,023,462 / 30.38%
Number/percentage of G's	24,393,882 / 21.78%
Number/percentage of N's	1,206 / 0%
GC Percentage	40.93%

2.3. Coverage

Mean	0.0362

Standard Deviation	0.2561

2.4. Mapping Quality

Mean Mapping Quality	46.08

2.5. Mismatches and indels

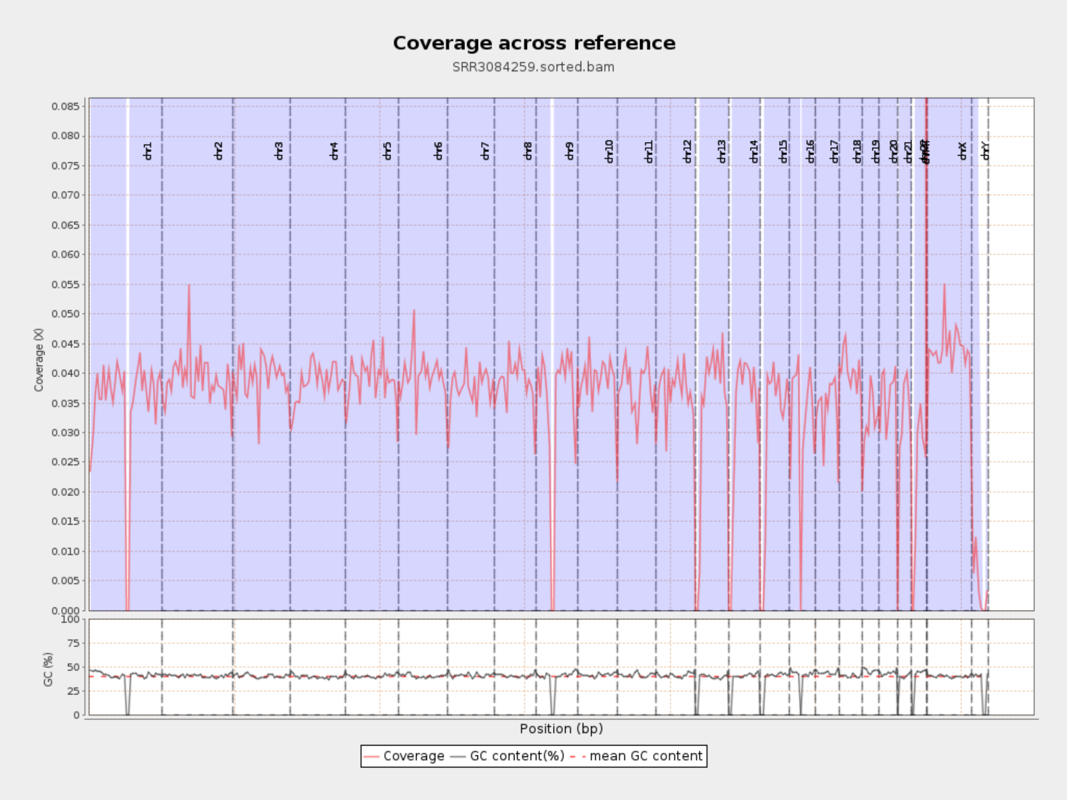
General error rate	0.84%
Mismatches	923,511
Insertions	7,967
Mapped reads with at least one insertion	0.44%
Deletions	22,425
Mapped reads with at least one deletion	1.25%
Homopolymer indels	46.43%

2.6. Chromosome stats

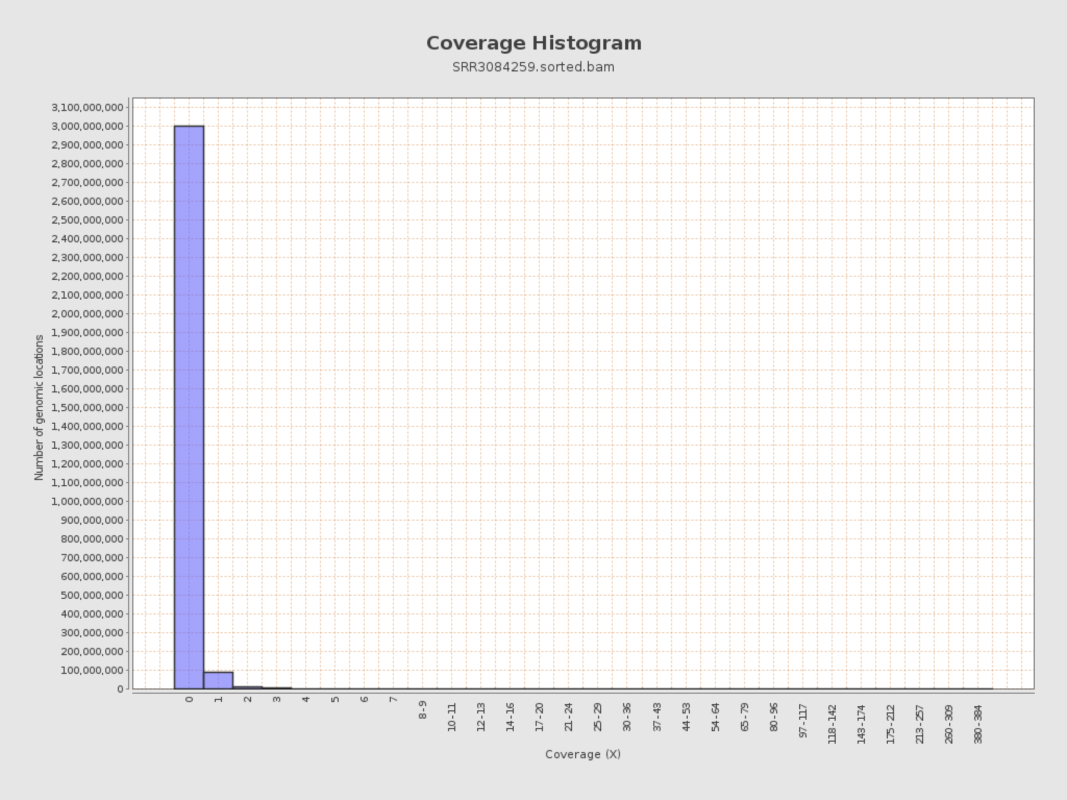
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8710560	0.0349	0.3053
chr2	243199373	9510722	0.0391	0.3211
chr3	198022430	7836602	0.0396	0.2211
chr4	191154276	7344165	0.0384	0.2229
chr5	180915260	7099693	0.0392	0.2206
chr6	171115067	6772359	0.0396	0.252
chr7	159138663	6040512	0.038	0.2774

chr8	146364022	5648439	0.0386	0.278
chr9	141213431	4845189	0.0343	0.2523
chr10	135534747	5277202	0.0389	0.2601
chr11	135006516	5061989	0.0375	0.2479
chr12	133851895	4936606	0.0369	0.215
chr13	115169878	3801422	0.033	0.2029
chr14	107349540	3428688	0.0319	0.21
chr15	102531392	3091767	0.0302	0.2
chr16	90354753	2929221	0.0324	0.2139
chr17	81195210	2754324	0.0339	0.2211
chr18	78077248	3179826	0.0407	0.4771
chr19	59128983	1912455	0.0323	0.2594
chr20	63025520	2250863	0.0357	0.2162
chr21	48129895	1450557	0.0301	0.2004
chr22	51304566	1078429	0.021	0.1601
chrMT	16571	25282	1.5257	1.4338
chrX	155270560	6775703	0.0436	0.2472
chrY	59373566	263158	0.0044	0.0917

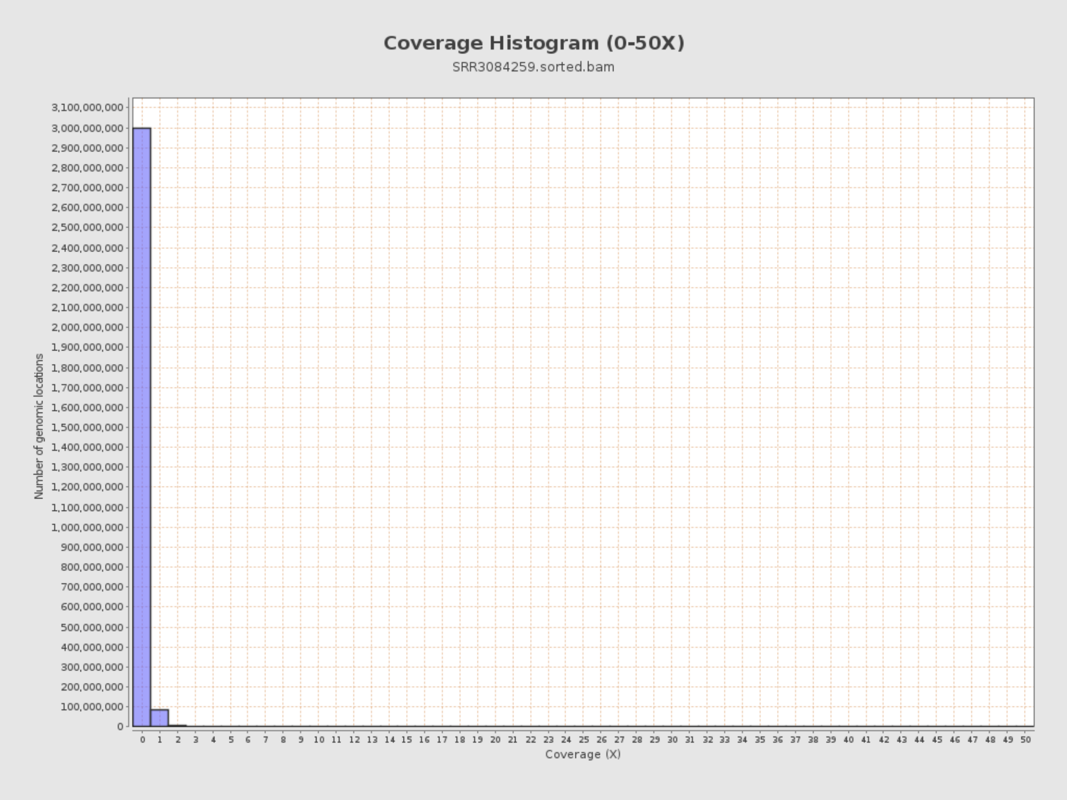
3. Results : Coverage across reference



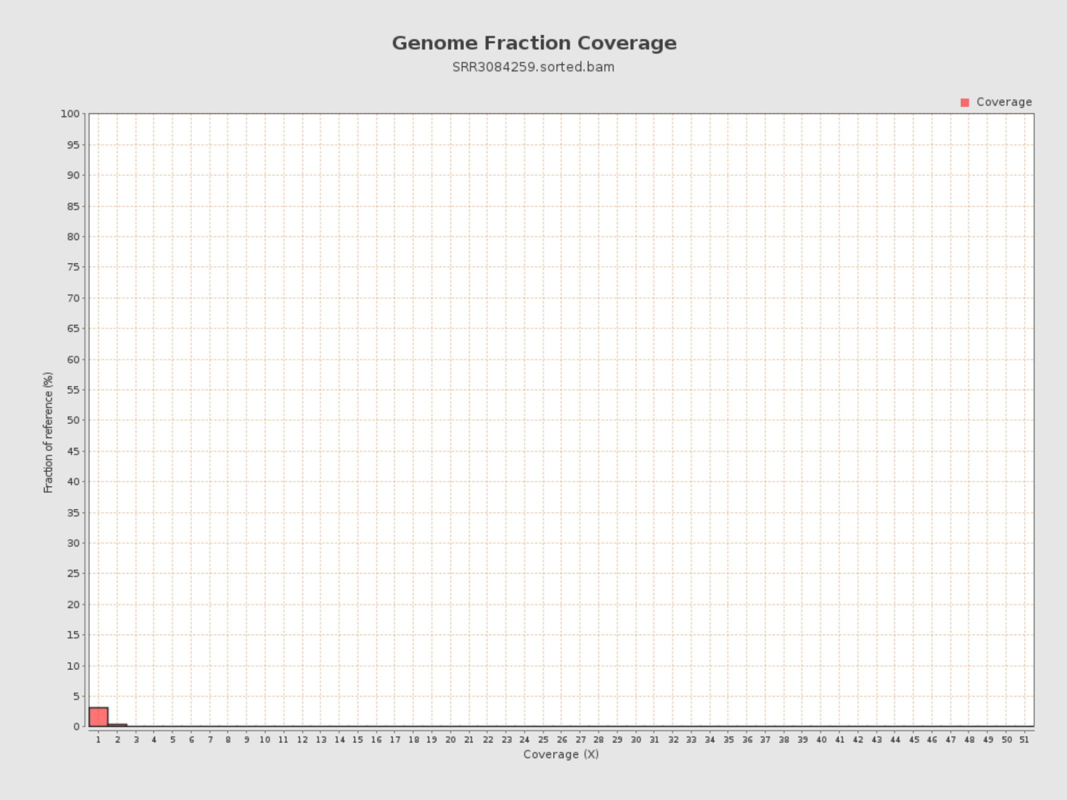
4. Results : Coverage Histogram



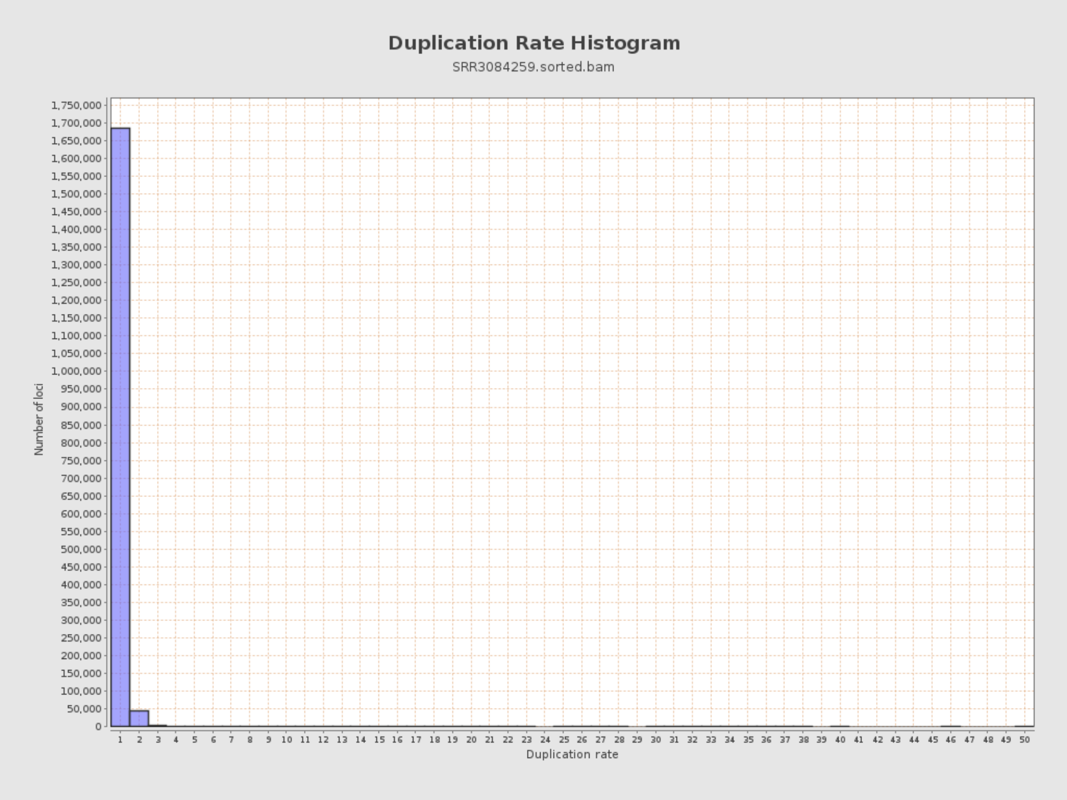
5. Results : Coverage Histogram (0-50X)



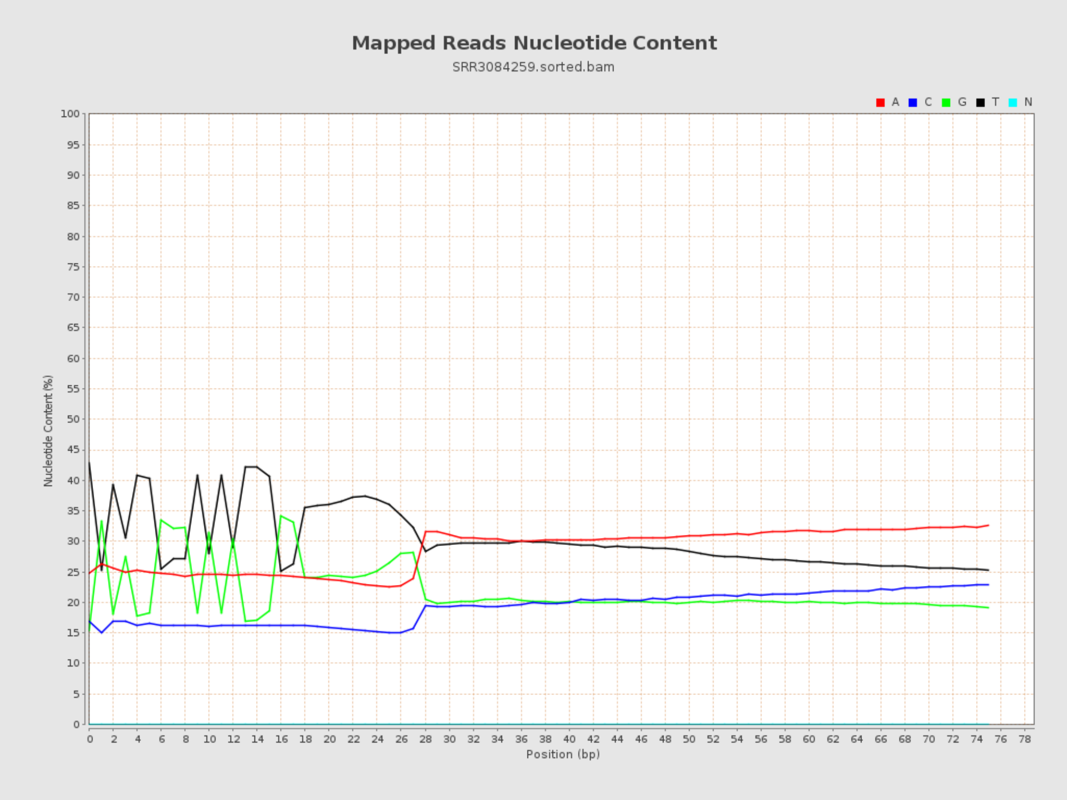
6. Results : Genome Fraction Coverage



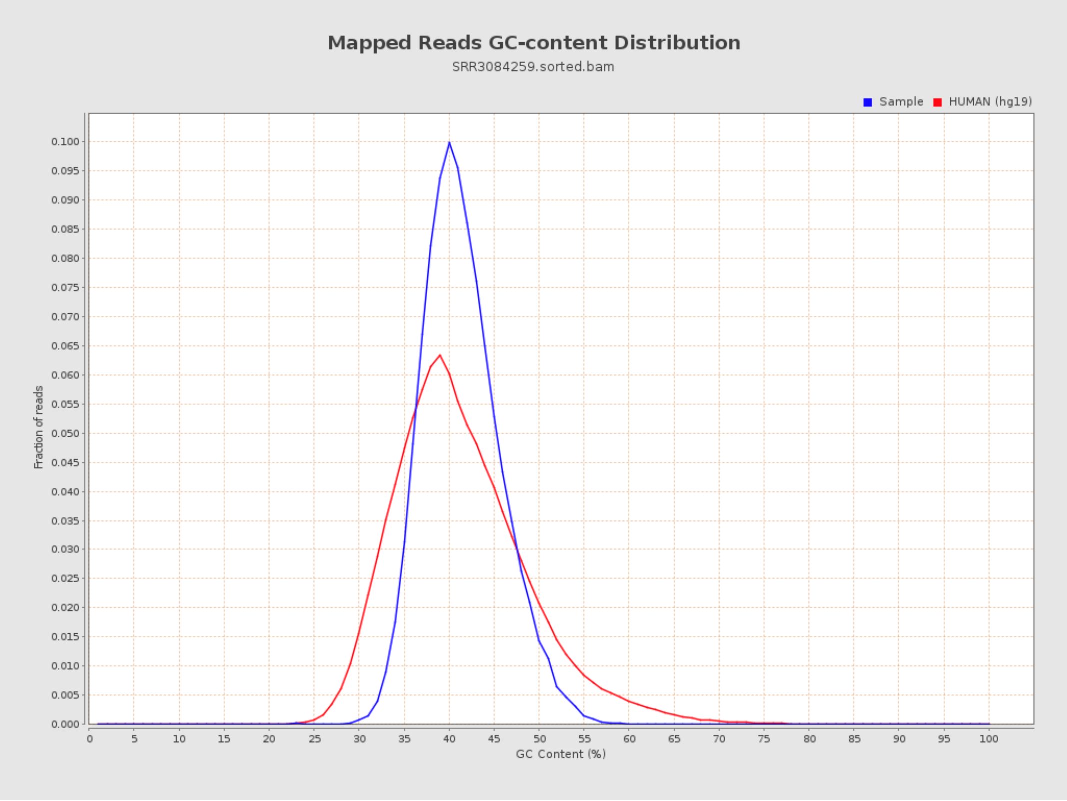
7. Results : Duplication Rate Histogram



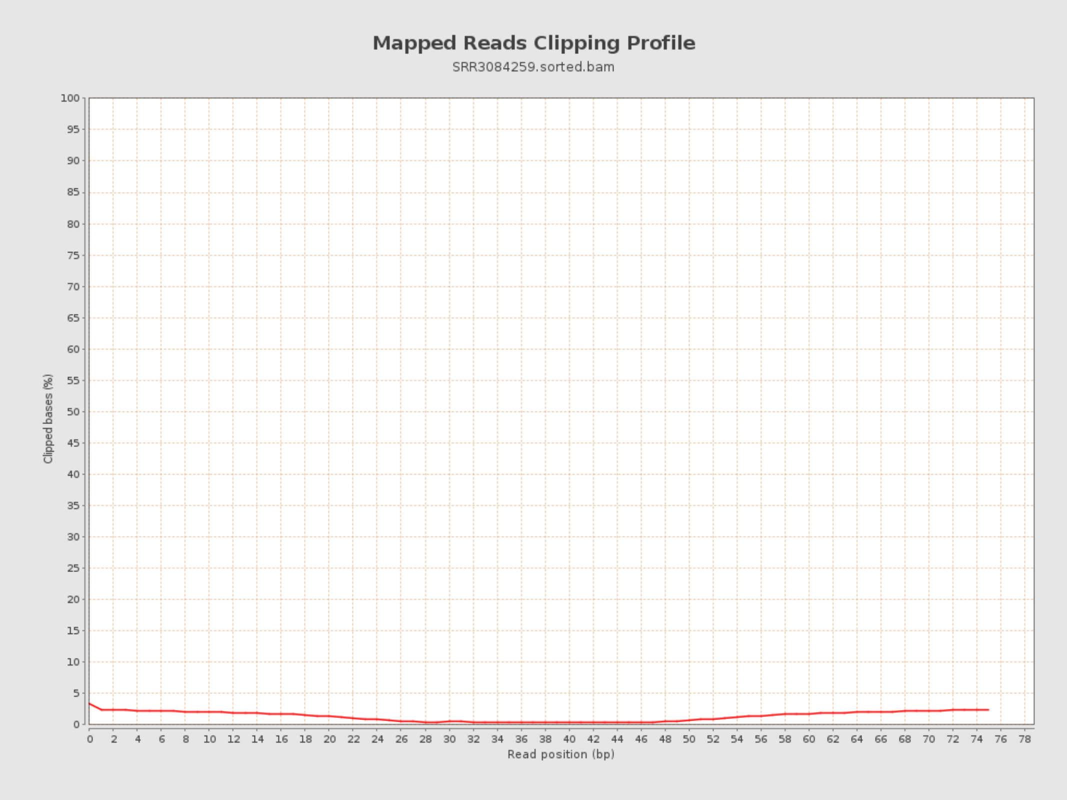
8. Results : Mapped Reads Nucleotide Content



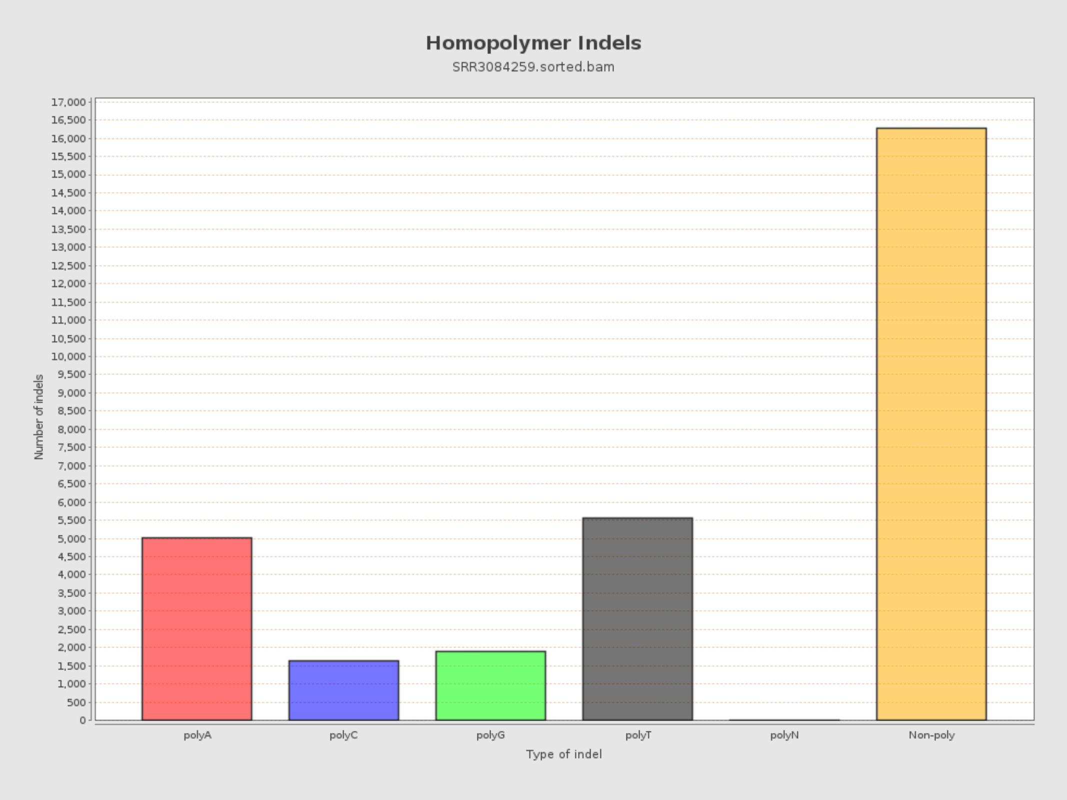
9. Results : Mapped Reads GC-content Distribution



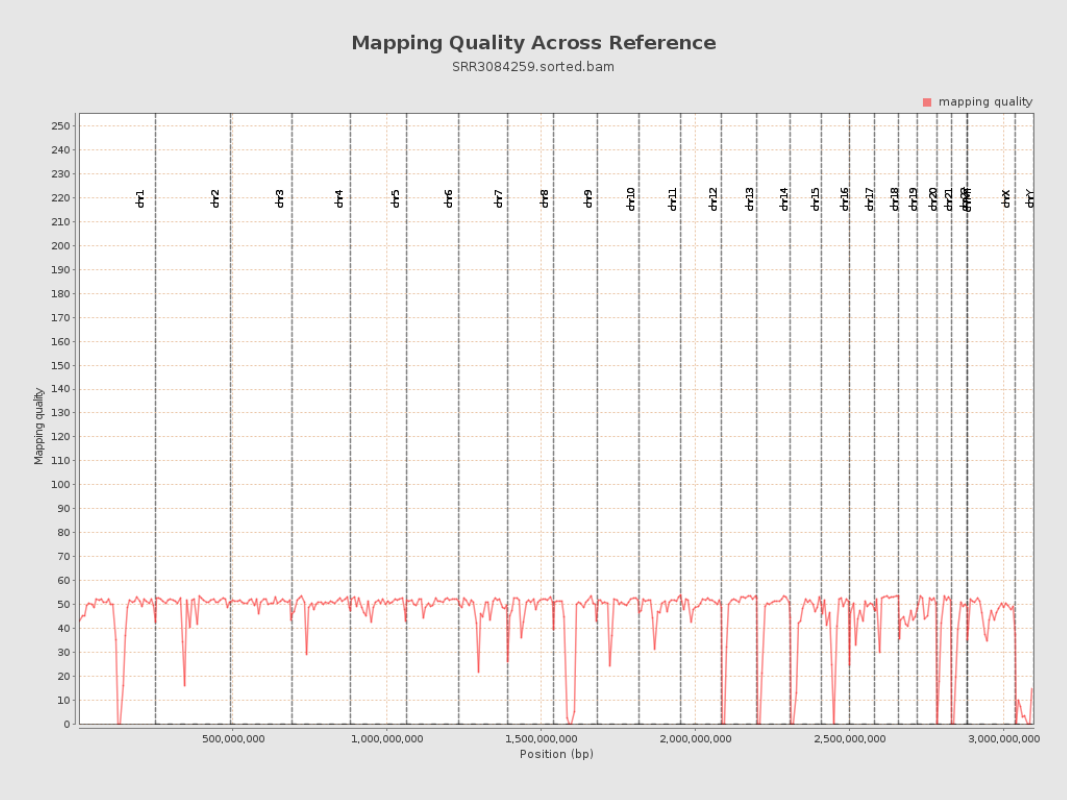
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram