Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 10:17:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084347.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_SRR3084347 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084347.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 10:17:15 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084347.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,974,509
Mapped reads	1,801,027 / 91.21%
Unmapped reads	173,482 / 8.79%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,644 / 0.54%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	58,371 / 2.96%
Duplication rate	2.78%
Clipped reads	745,921 / 37.78%

2.2. ACGT Content

Number/percentage of A's	34,446,401 / 28.32%
Number/percentage of C's	22,984,706 / 18.9%
Number/percentage of T's	37,778,426 / 31.06%
Number/percentage of G's	26,282,756 / 21.61%
Number/percentage of N's	149,754 / 0.12%
GC Percentage	40.5%

2.3. Coverage

Mean	0.0393

Standard Deviation	0.2802

2.4. Mapping Quality

Mean Mapping Quality	46.67

2.5. Mismatches and indels

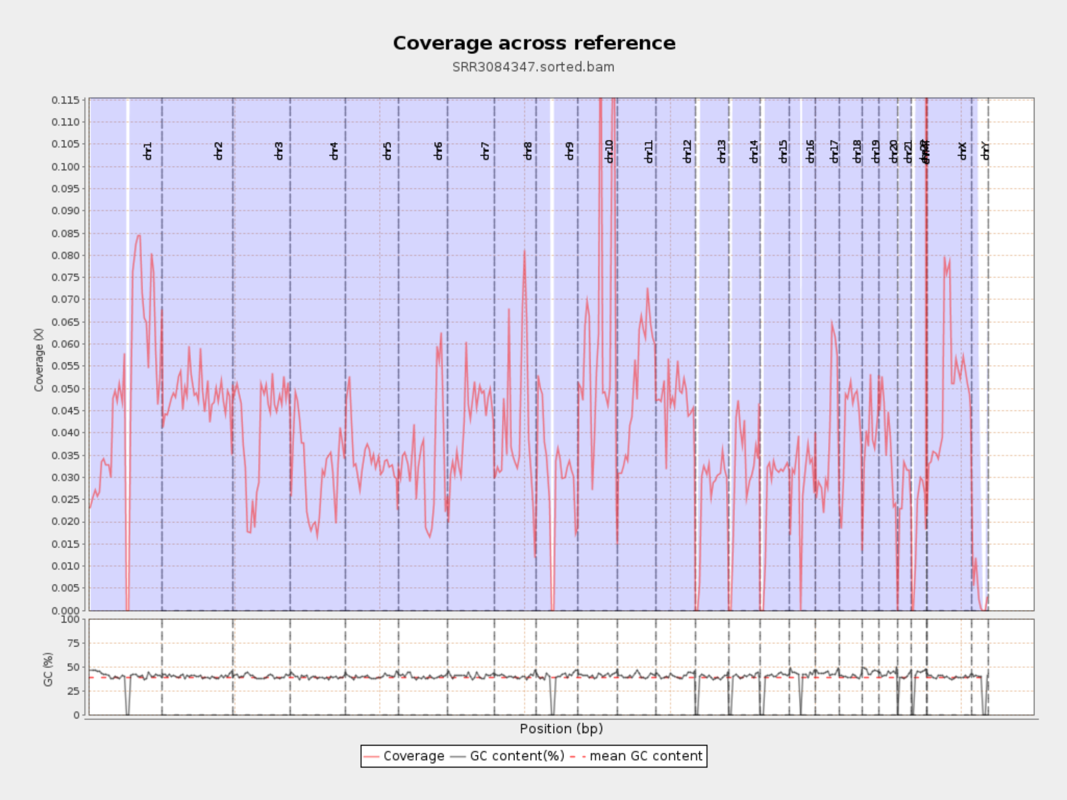
General error rate	0.97%
Mismatches	1,160,404
Insertions	8,360
Mapped reads with at least one insertion	0.46%
Deletions	24,805
Mapped reads with at least one deletion	1.36%
Homopolymer indels	48.09%

2.6. Chromosome stats

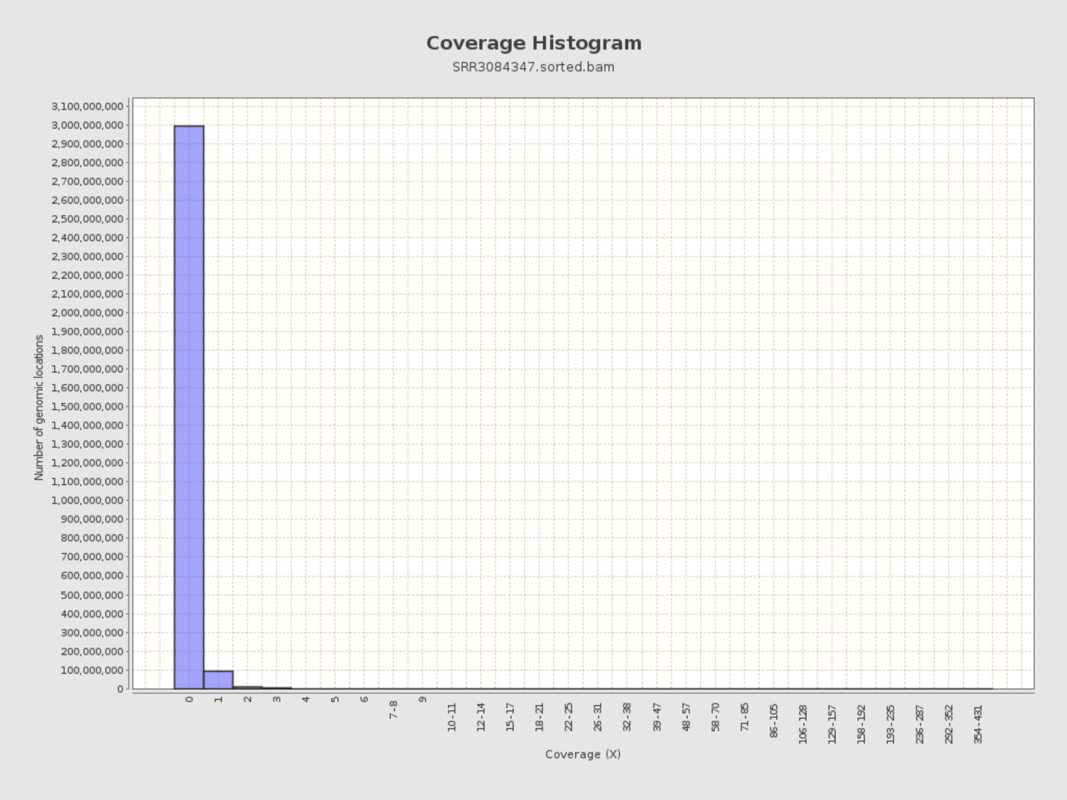
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11998658	0.0481	0.4477
chr2	243199373	11775754	0.0484	0.3085
chr3	198022430	8200396	0.0414	0.2311
chr4	191154276	5978464	0.0313	0.2053
chr5	180915260	6246461	0.0345	0.2094
chr6	171115067	5765413	0.0337	0.2201
chr7	159138663	6767205	0.0425	0.3633

chr8	146364022	5954864	0.0407	0.2778
chr9	141213431	4371891	0.031	0.2397
chr10	135534747	8712739	0.0643	0.3892
chr11	135006516	6766477	0.0501	0.2886
chr12	133851895	6366213	0.0476	0.2468
chr13	115169878	2944224	0.0256	0.1789
chr14	107349540	3262166	0.0304	0.2
chr15	102531392	2654269	0.0259	0.1837
chr16	90354753	2633791	0.0291	0.2018
chr17	81195210	3136801	0.0386	0.2308
chr18	78077248	3257701	0.0417	0.3487
chr19	59128983	2342510	0.0396	0.3364
chr20	63025520	2347596	0.0372	0.2193
chr21	48129895	1215963	0.0253	0.1836
chr22	51304566	966365	0.0188	0.1533
chrMT	16571	117005	7.0608	4.7689
chrX	155270560	7654034	0.0493	0.2682
chrY	59373566	248683	0.0042	0.0917

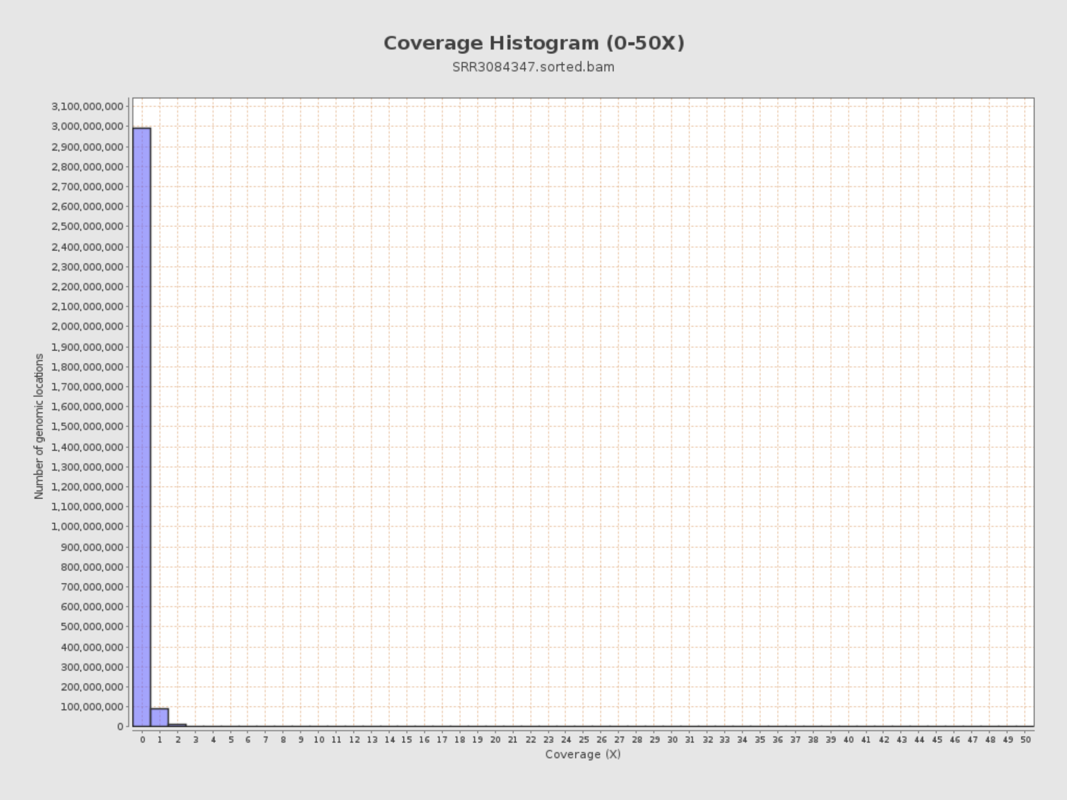
3. Results : Coverage across reference



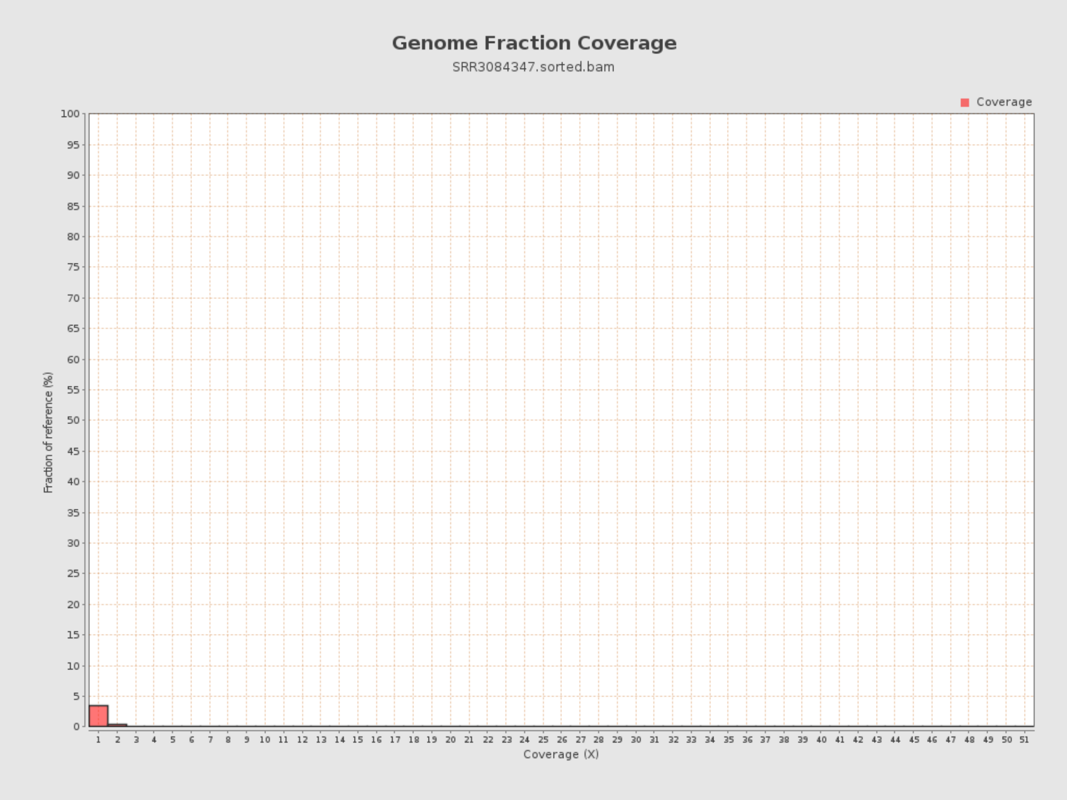
4. Results : Coverage Histogram



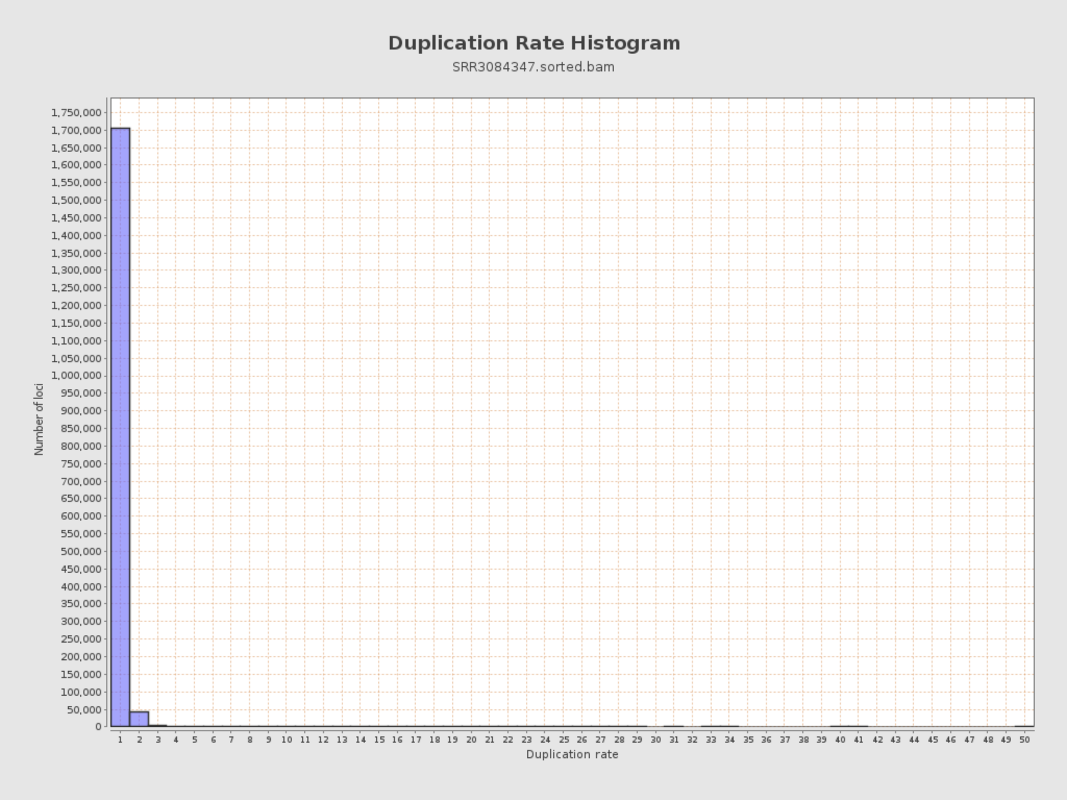
5. Results : Coverage Histogram (0-50X)



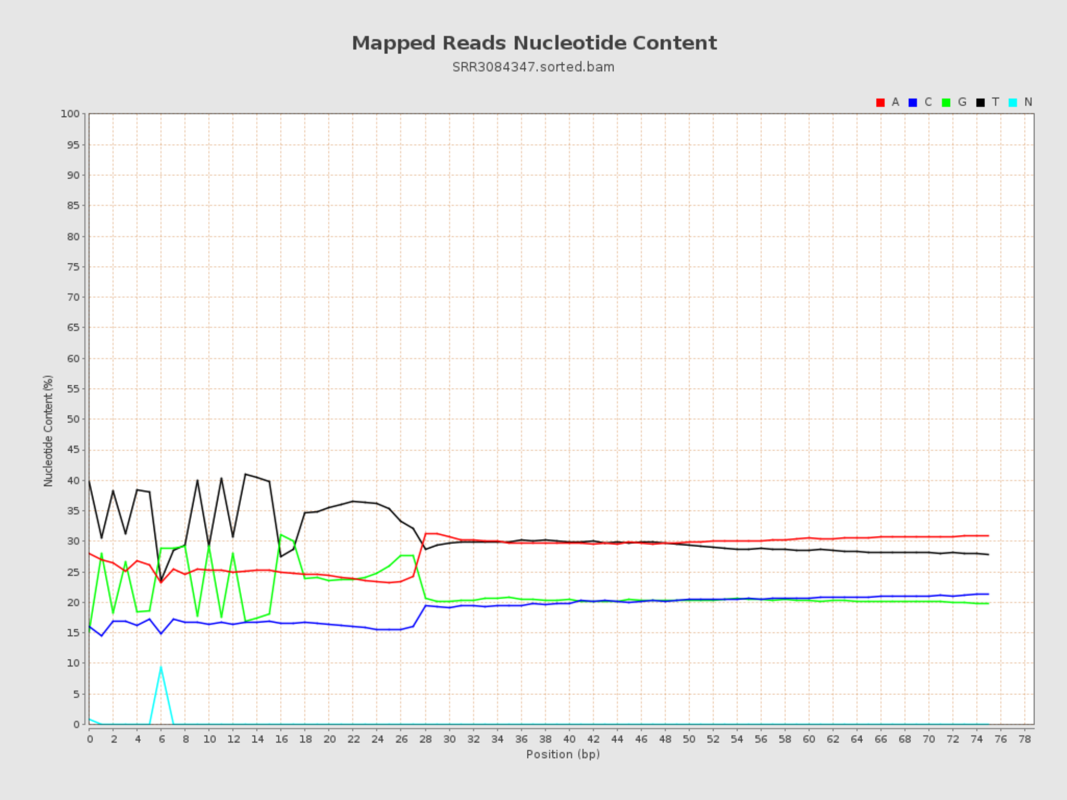
6. Results : Genome Fraction Coverage



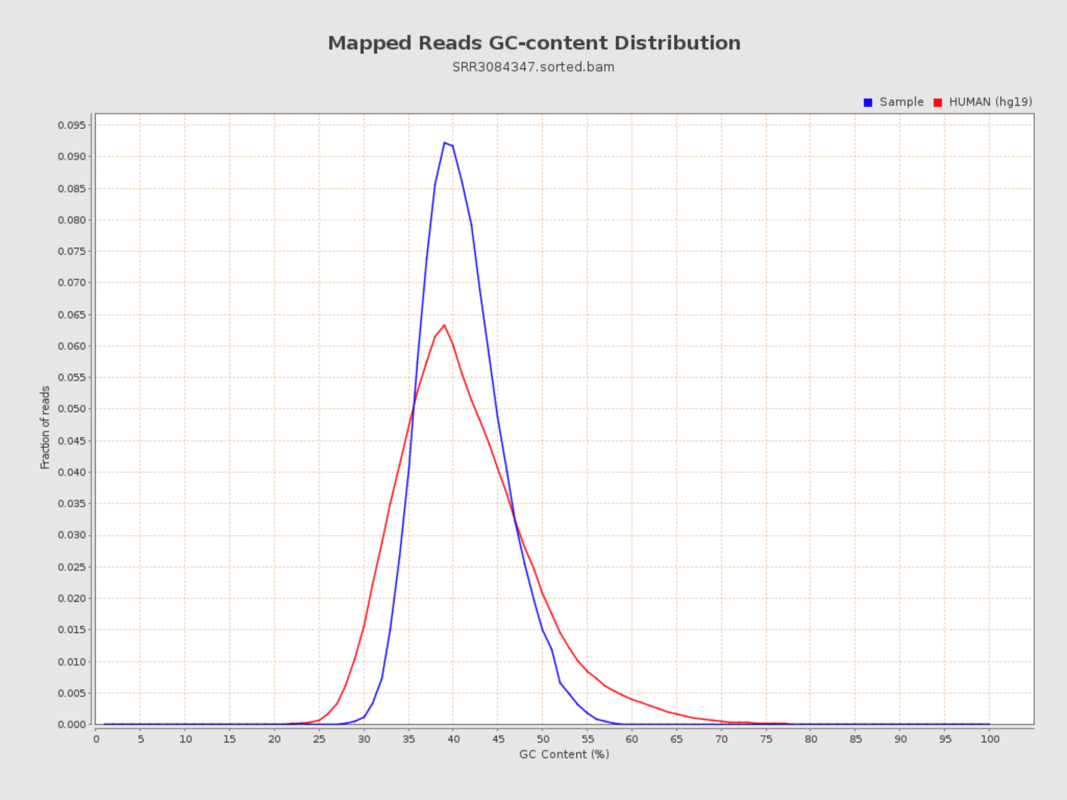
7. Results : Duplication Rate Histogram



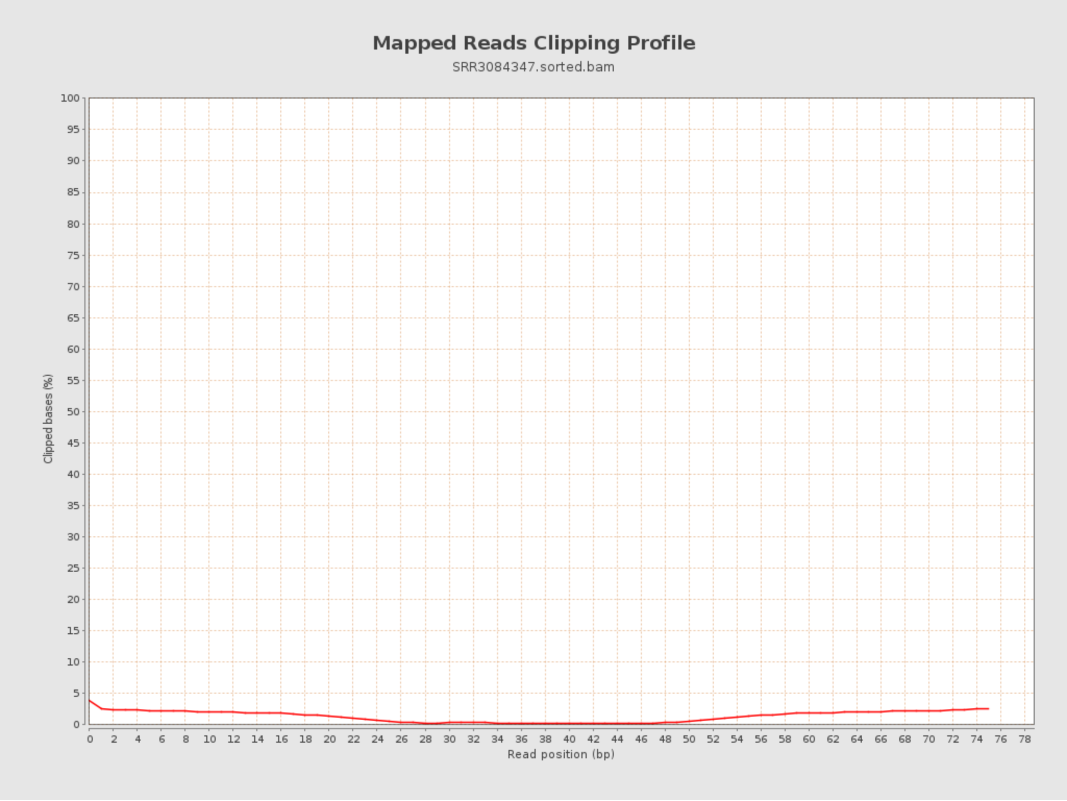
8. Results : Mapped Reads Nucleotide Content



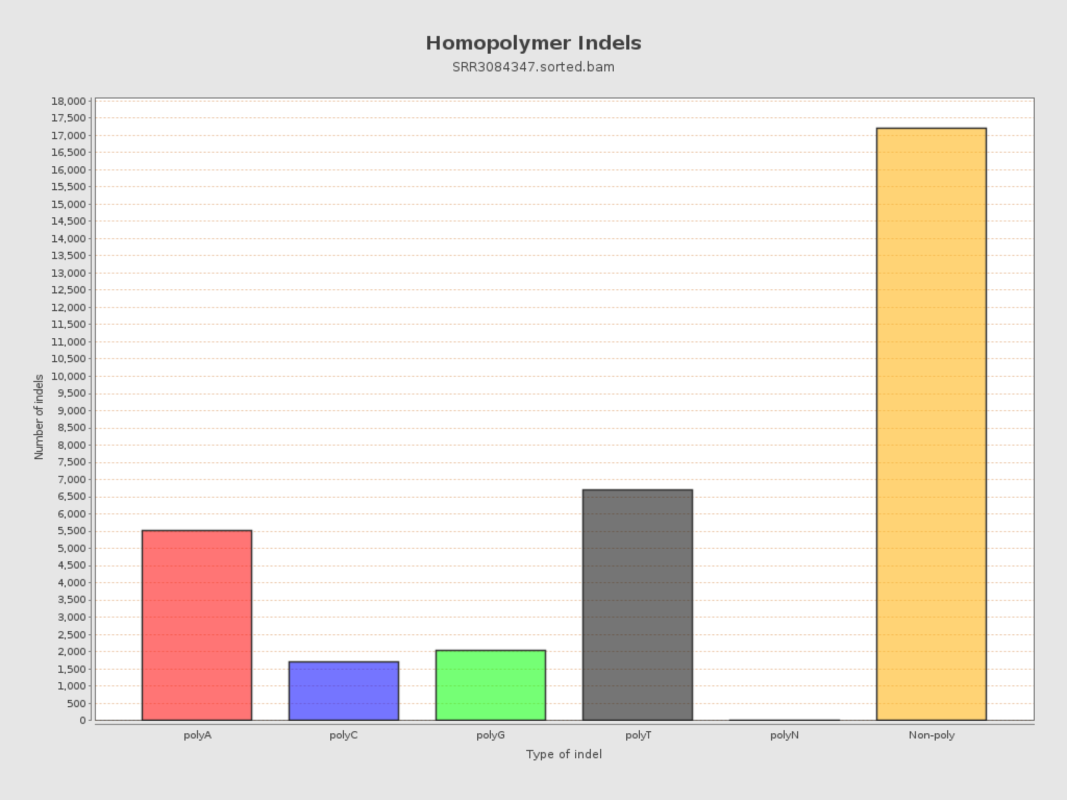
9. Results : Mapped Reads GC-content Distribution



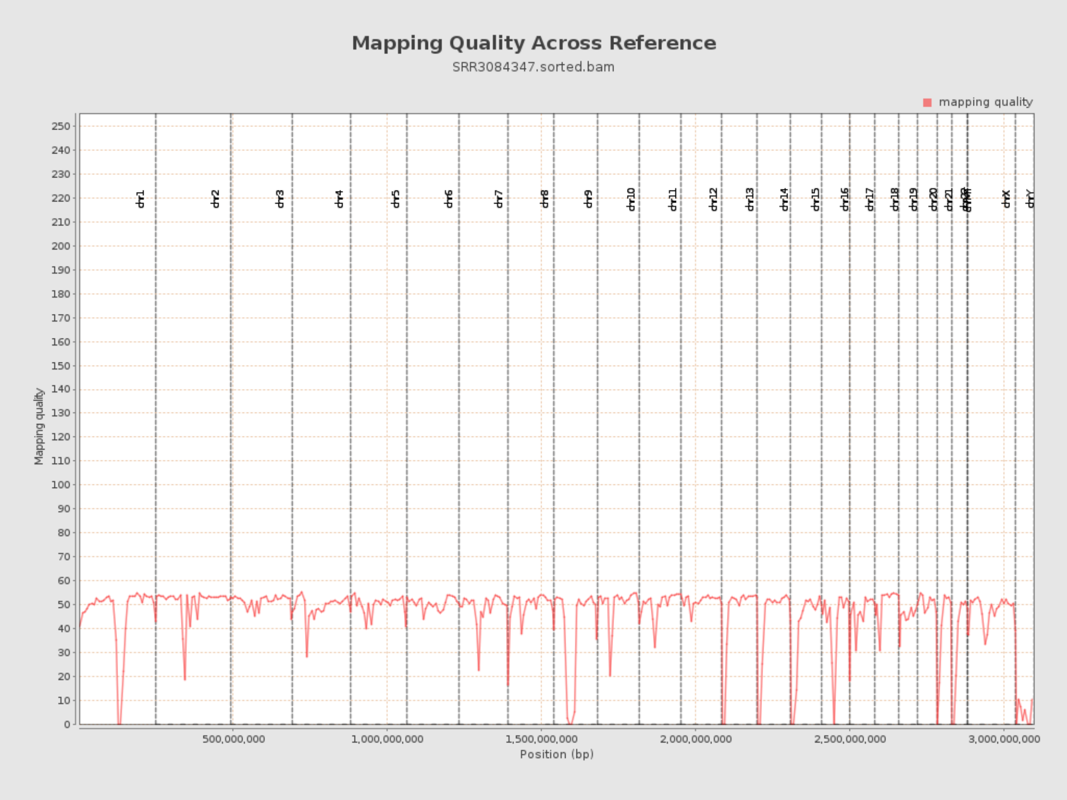
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram