Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 17:18:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084847.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_SRR3084847 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084847.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 17:18:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084847.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,521,349
Mapped reads	2,186,574 / 86.72%
Unmapped reads	334,775 / 13.28%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,570 / 0.74%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	106,941 / 4.24%
Duplication rate	4.2%
Clipped reads	768,677 / 30.49%

2.2. ACGT Content

Number/percentage of A's	43,833,478 / 29.06%
Number/percentage of C's	27,711,727 / 18.37%
Number/percentage of T's	48,316,124 / 32.03%
Number/percentage of G's	30,977,234 / 20.53%
Number/percentage of N's	24,098 / 0.02%
GC Percentage	38.9%

2.3. Coverage

Mean	0.0488

Standard Deviation	0.3815

2.4. Mapping Quality

Mean Mapping Quality	48.04

2.5. Mismatches and indels

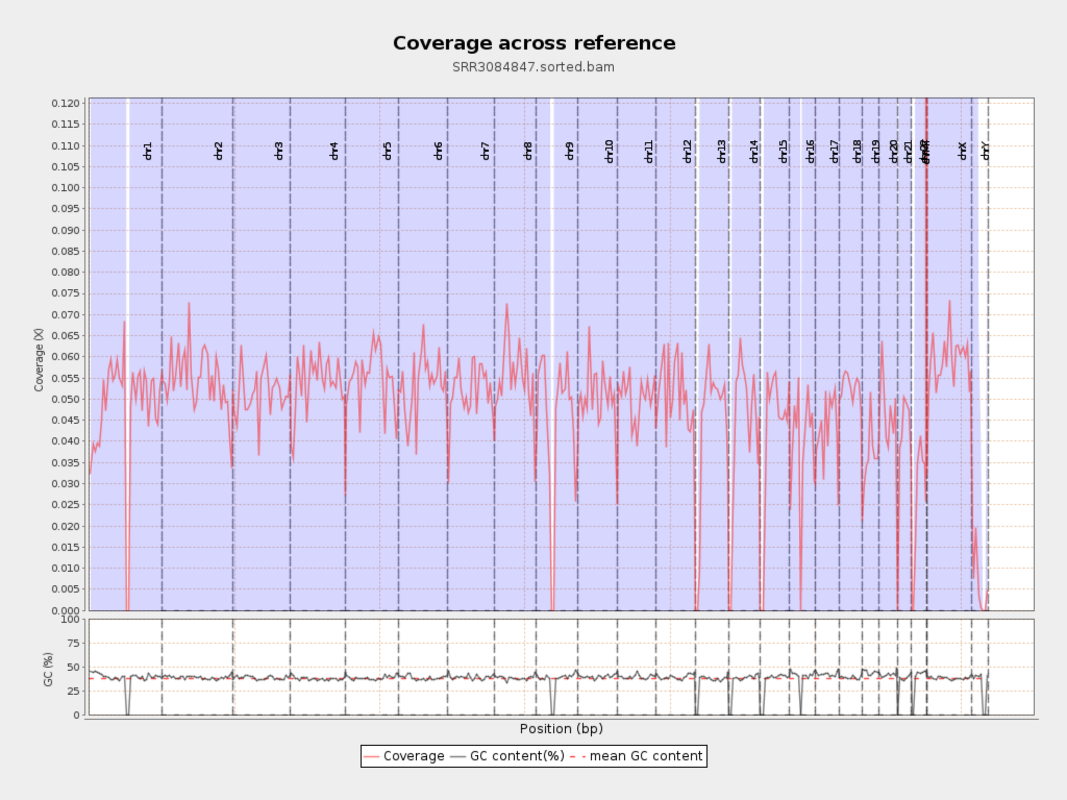
General error rate	0.83%
Mismatches	1,227,377
Insertions	12,005
Mapped reads with at least one insertion	0.54%
Deletions	32,217
Mapped reads with at least one deletion	1.46%
Homopolymer indels	48.3%

2.6. Chromosome stats

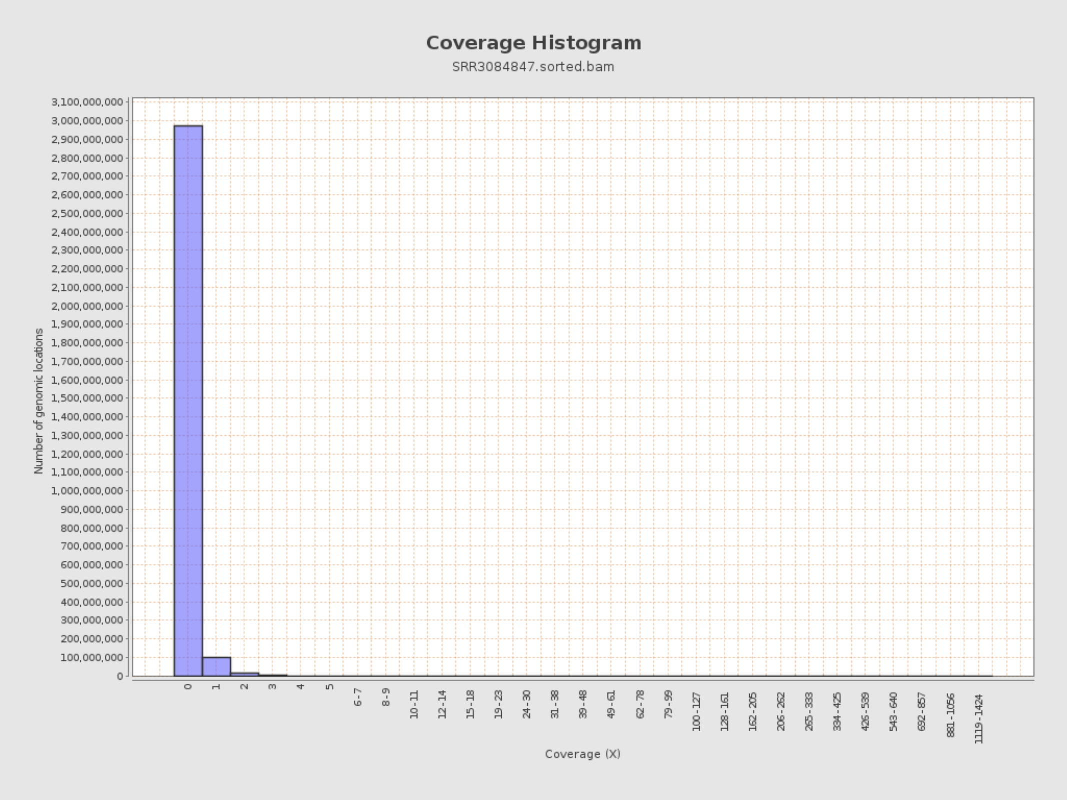
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11828387	0.0475	0.5374
chr2	243199373	13281350	0.0546	0.3581
chr3	198022430	10214383	0.0516	0.2688
chr4	191154276	10316422	0.054	0.2854
chr5	180915260	9926428	0.0549	0.2775
chr6	171115067	9152339	0.0535	0.2841
chr7	159138663	8312702	0.0522	0.3039

chr8	146364022	8037417	0.0549	0.9385
chr9	141213431	6324791	0.0448	0.3216
chr10	135534747	6909607	0.051	0.3451
chr11	135006516	6760115	0.0501	0.2949
chr12	133851895	6837515	0.0511	0.2681
chr13	115169878	4969024	0.0431	0.2468
chr14	107349540	4601473	0.0429	0.2556
chr15	102531392	4233353	0.0413	0.2405
chr16	90354753	3528901	0.0391	0.2475
chr17	81195210	3471634	0.0428	0.2654
chr18	78077248	4141396	0.053	0.5705
chr19	59128983	2179226	0.0369	0.3543
chr20	63025520	2958869	0.0469	0.2628
chr21	48129895	1916915	0.0398	0.2508
chr22	51304566	1297819	0.0253	0.1846
chrMT	16571	278652	16.8156	8.4318
chrX	155270560	9072138	0.0584	0.2953
chrY	59373566	369716	0.0062	0.1487

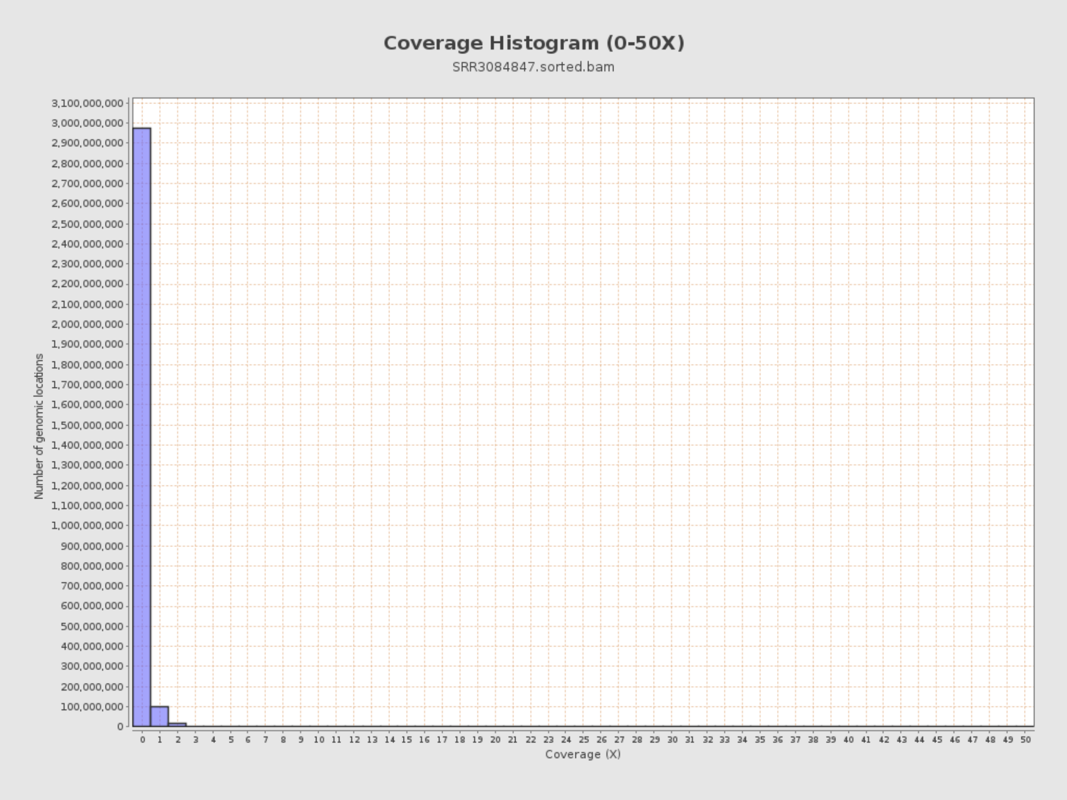
3. Results : Coverage across reference



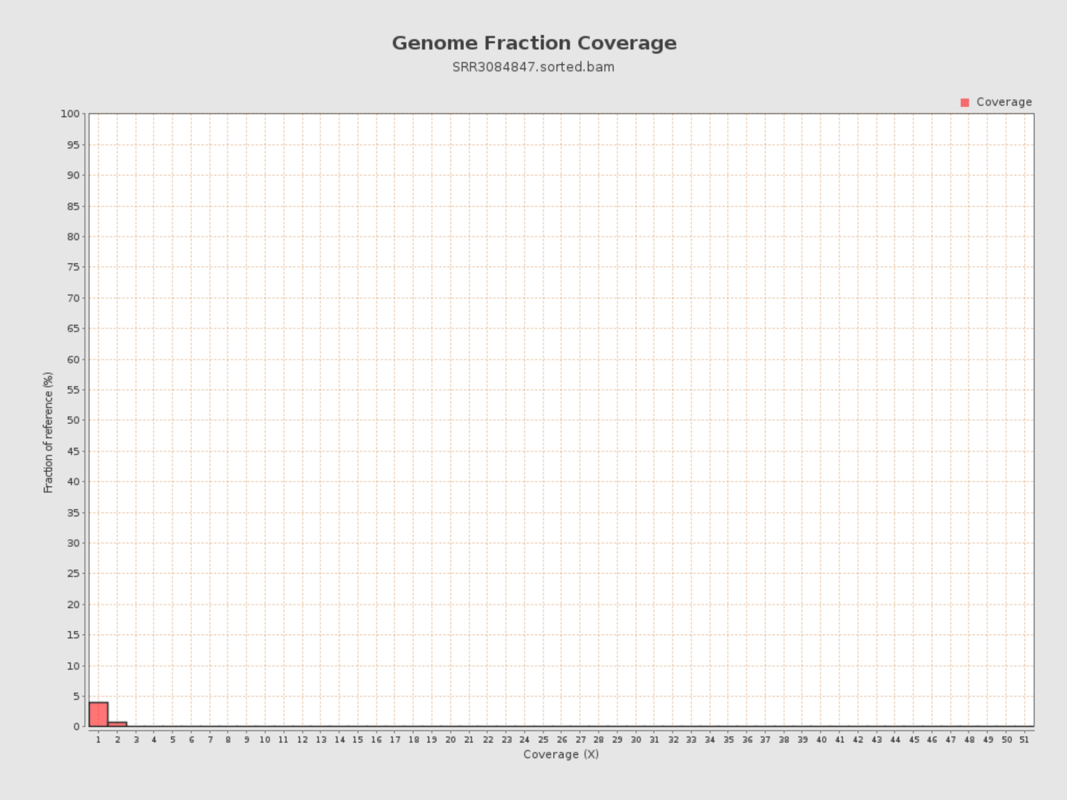
4. Results : Coverage Histogram



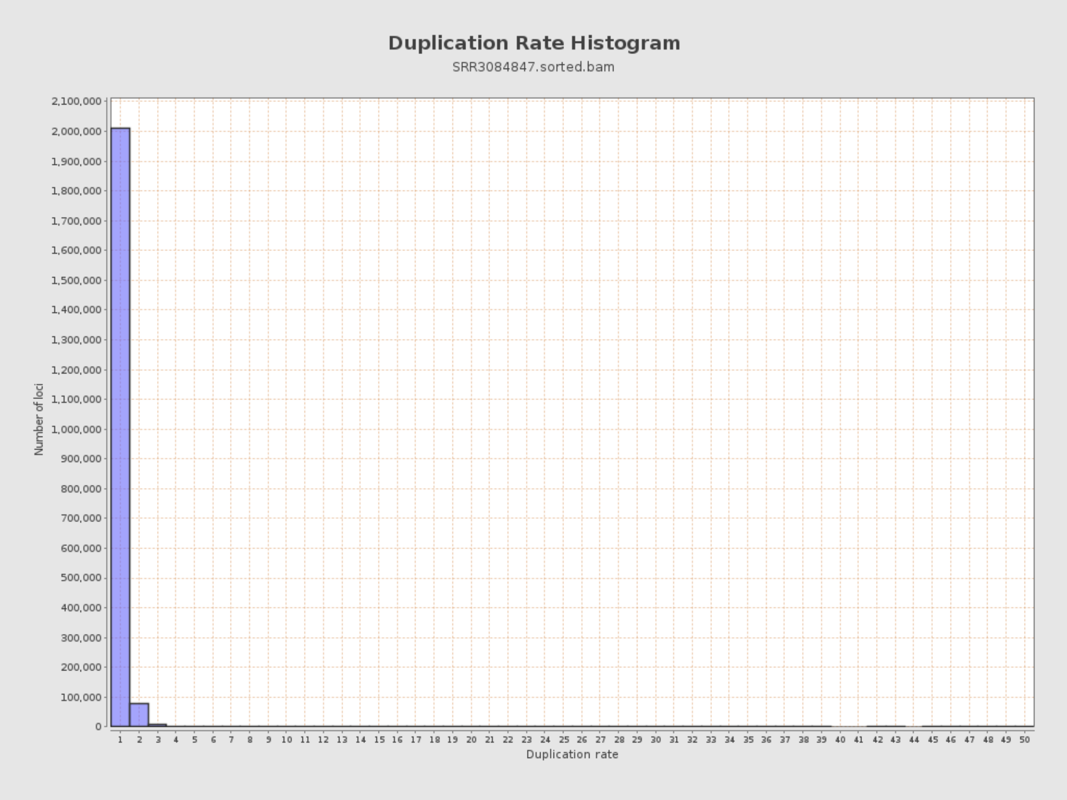
5. Results : Coverage Histogram (0-50X)



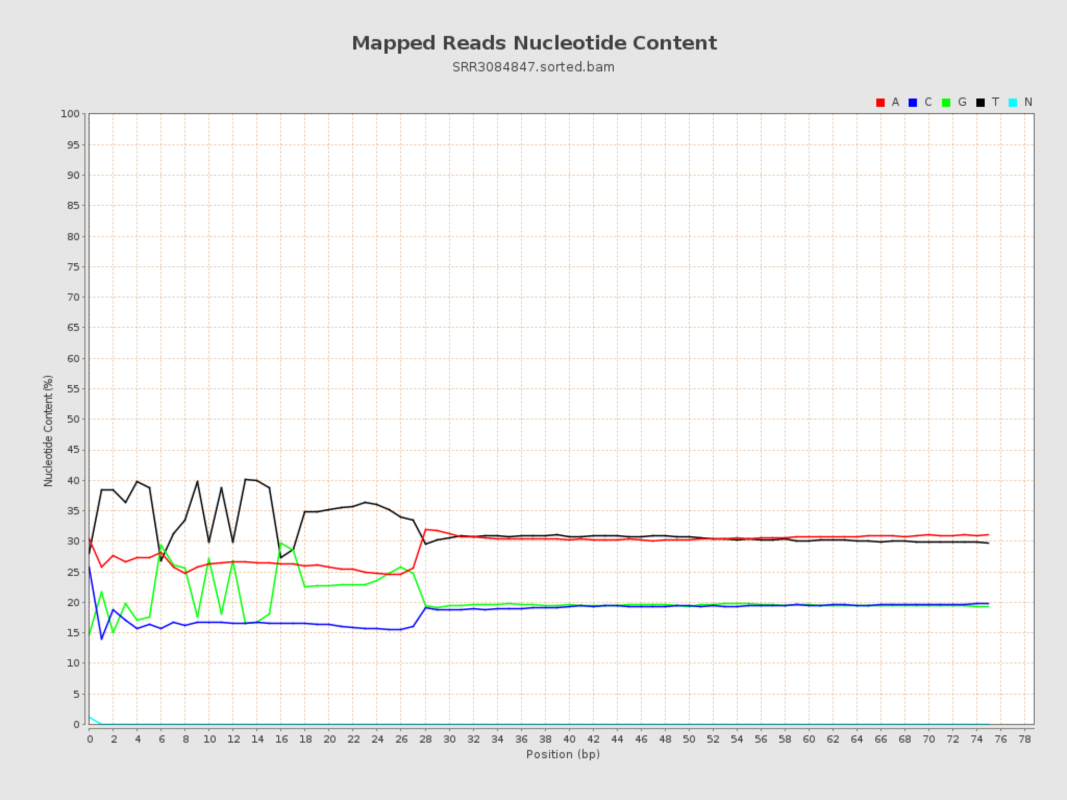
6. Results : Genome Fraction Coverage



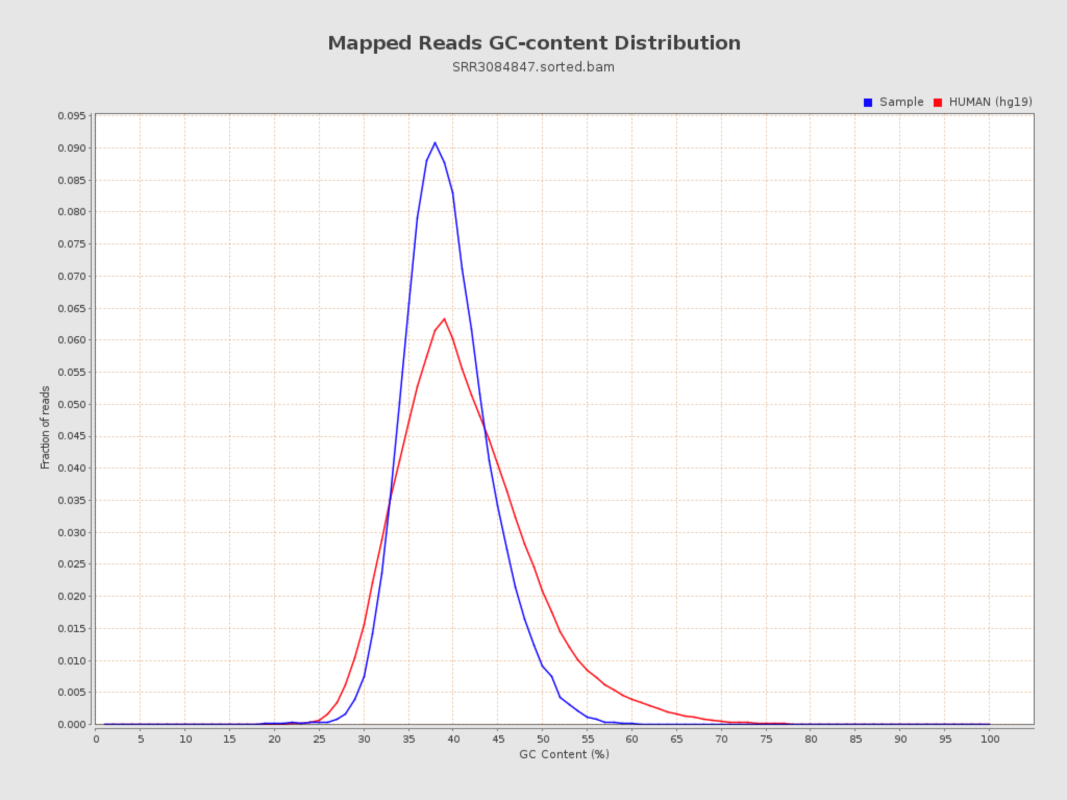
7. Results : Duplication Rate Histogram



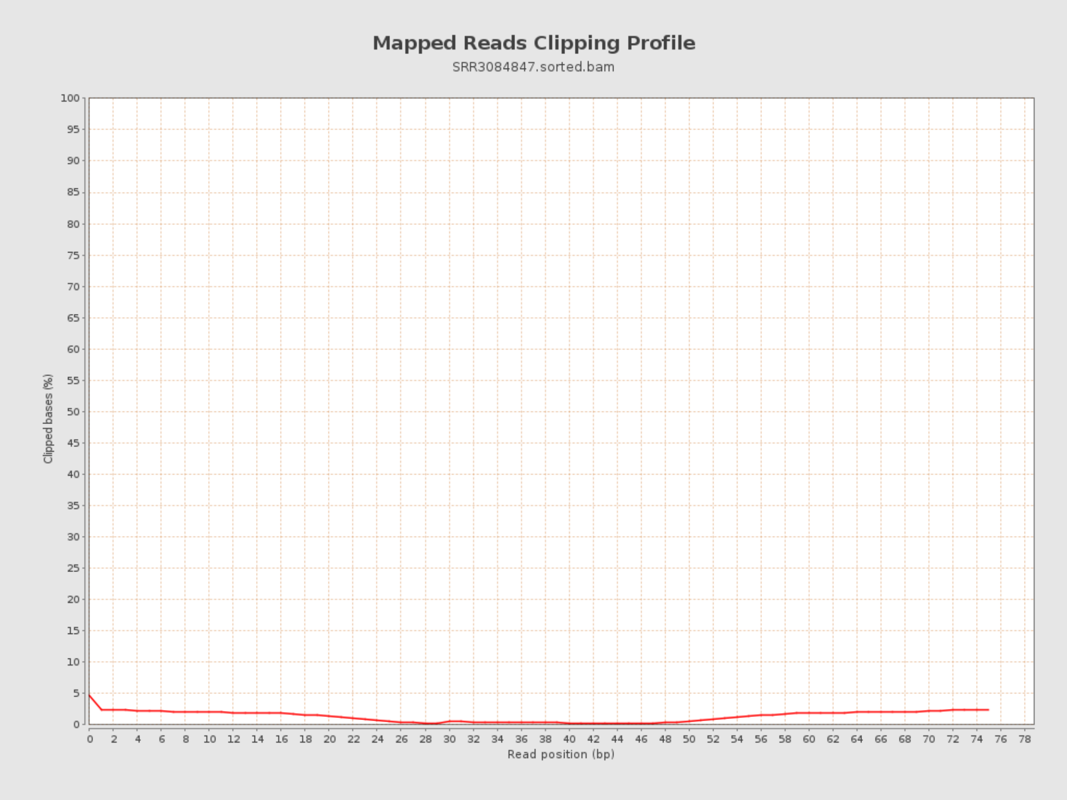
8. Results : Mapped Reads Nucleotide Content



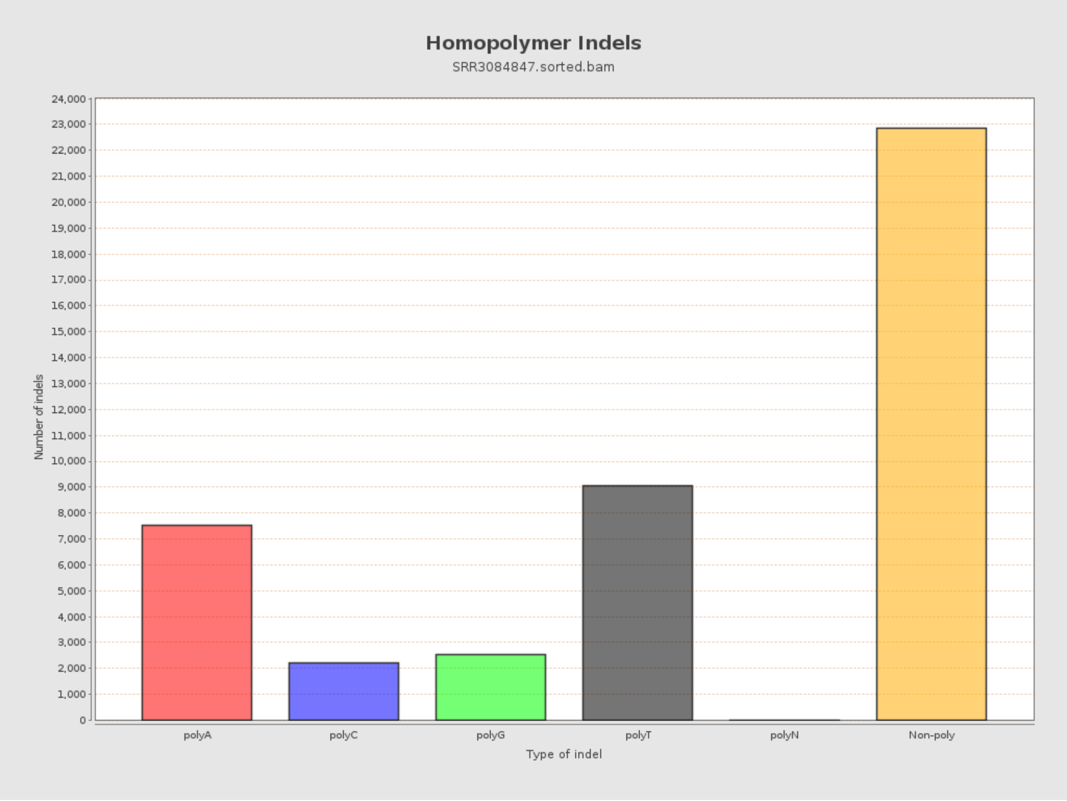
9. Results : Mapped Reads GC-content Distribution



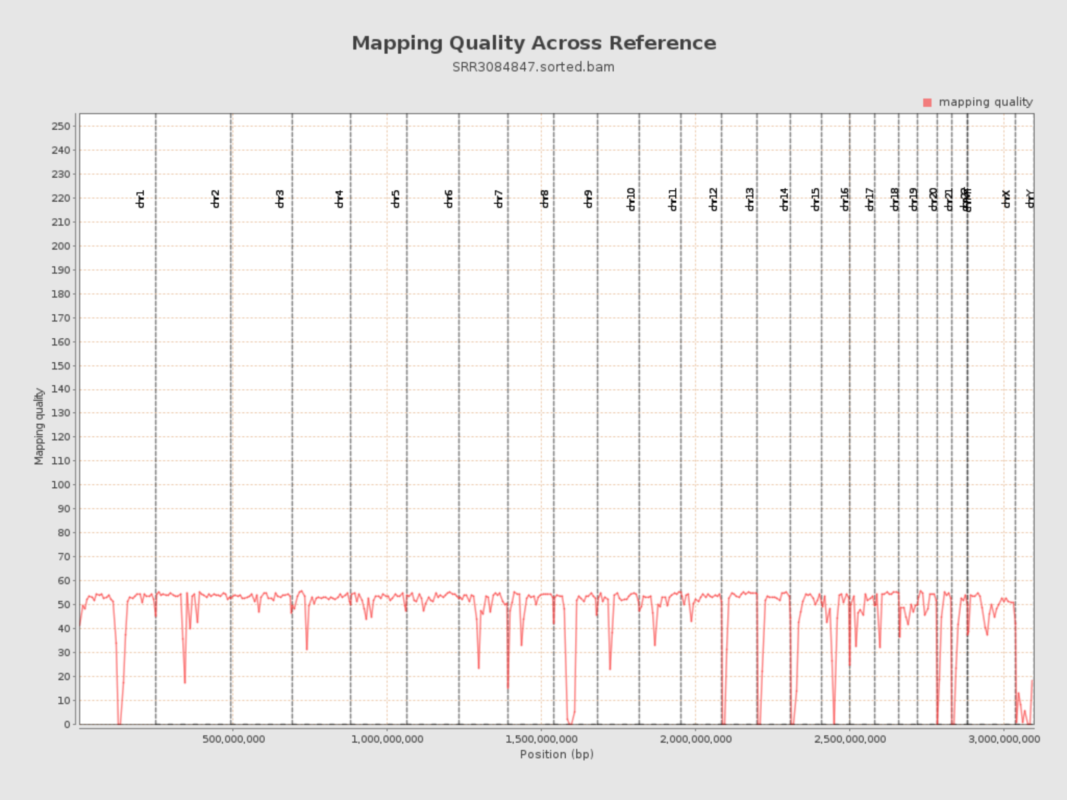
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram