Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 15:49:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084817.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_SRR3084817 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084817.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 15:49:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084817.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,150,558
Mapped reads	1,986,686 / 92.38%
Unmapped reads	163,872 / 7.62%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,653 / 0.73%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	79,818 / 3.71%
Duplication rate	3.48%
Clipped reads	796,609 / 37.04%

2.2. ACGT Content

Number/percentage of A's	37,358,267 / 27.81%
Number/percentage of C's	24,785,610 / 18.45%
Number/percentage of T's	42,608,590 / 31.71%
Number/percentage of G's	29,578,628 / 22.02%
Number/percentage of N's	19,324 / 0.01%
GC Percentage	40.46%

2.3. Coverage

Mean	0.0434

Standard Deviation	0.2953

2.4. Mapping Quality

Mean Mapping Quality	46.3

2.5. Mismatches and indels

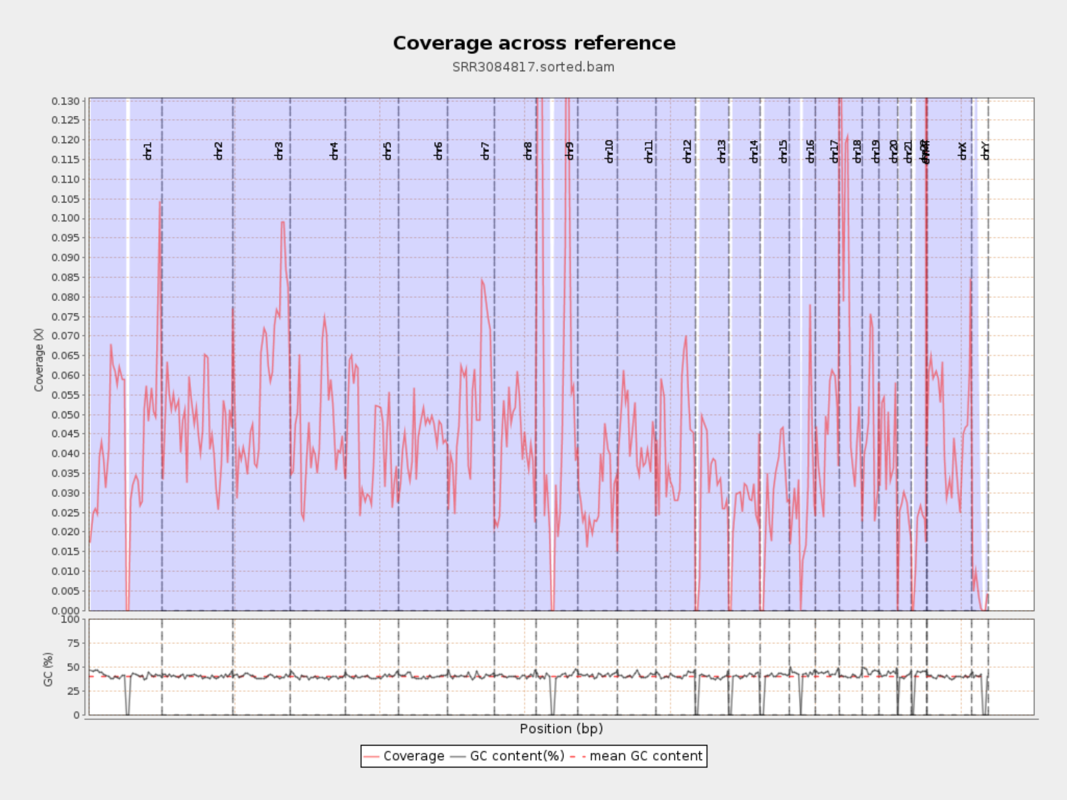
General error rate	0.78%
Mismatches	1,024,537
Insertions	10,573
Mapped reads with at least one insertion	0.53%
Deletions	31,334
Mapped reads with at least one deletion	1.56%
Homopolymer indels	49.01%

2.6. Chromosome stats

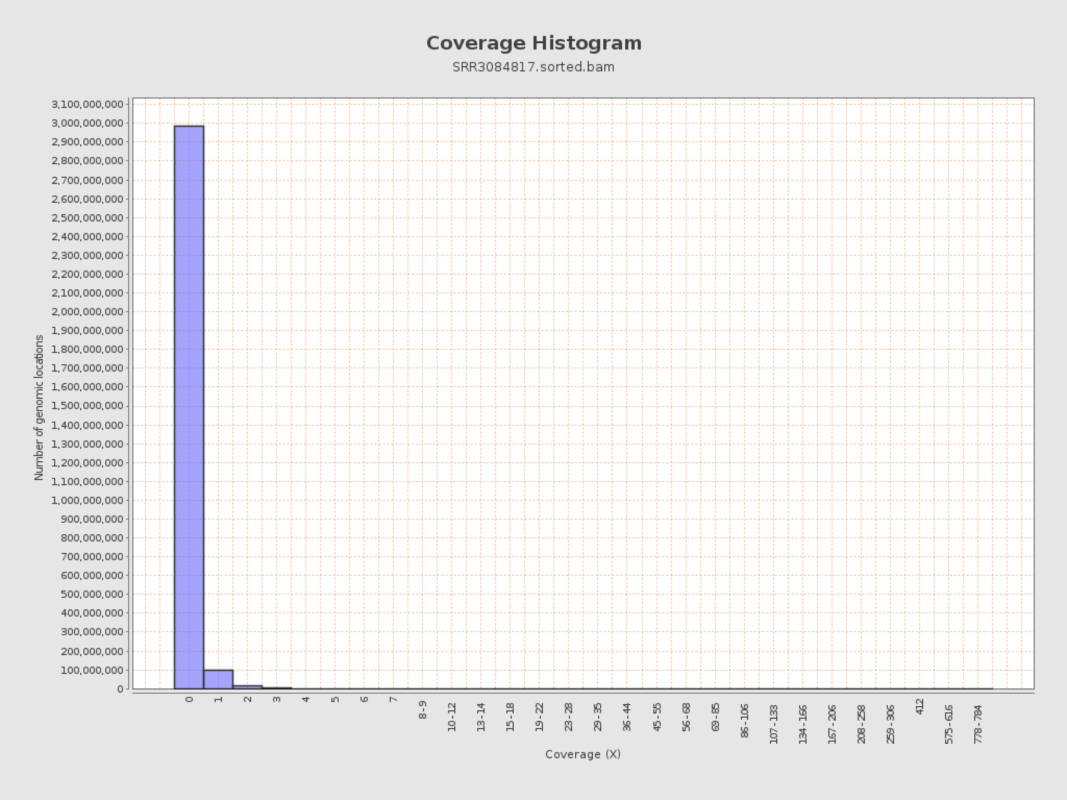
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10847931	0.0435	0.3616
chr2	243199373	11554171	0.0475	0.4476
chr3	198022430	11733096	0.0593	0.2828
chr4	191154276	8742085	0.0457	0.2496
chr5	180915260	7740941	0.0428	0.2416
chr6	171115067	7466252	0.0436	0.2603
chr7	159138663	8550328	0.0537	0.3593

chr8	146364022	6120274	0.0418	0.3147
chr9	141213431	9888944	0.07	0.3569
chr10	135534747	3928839	0.029	0.2068
chr11	135006516	5903761	0.0437	0.2769
chr12	133851895	5827411	0.0435	0.2428
chr13	115169878	3471241	0.0301	0.2005
chr14	107349540	2632561	0.0245	0.1826
chr15	102531392	2831379	0.0276	0.1981
chr16	90354753	2590428	0.0287	0.2022
chr17	81195210	3717825	0.0458	0.2517
chr18	78077248	5774737	0.074	0.4642
chr19	59128983	2756803	0.0466	0.3035
chr20	63025520	2729645	0.0433	0.246
chr21	48129895	1116698	0.0232	0.1811
chr22	51304566	867421	0.0169	0.1472
chrMT	16571	39622	2.391	2.1434
chrX	155270560	7329049	0.0472	0.2621
chrY	59373566	240418	0.004	0.0892

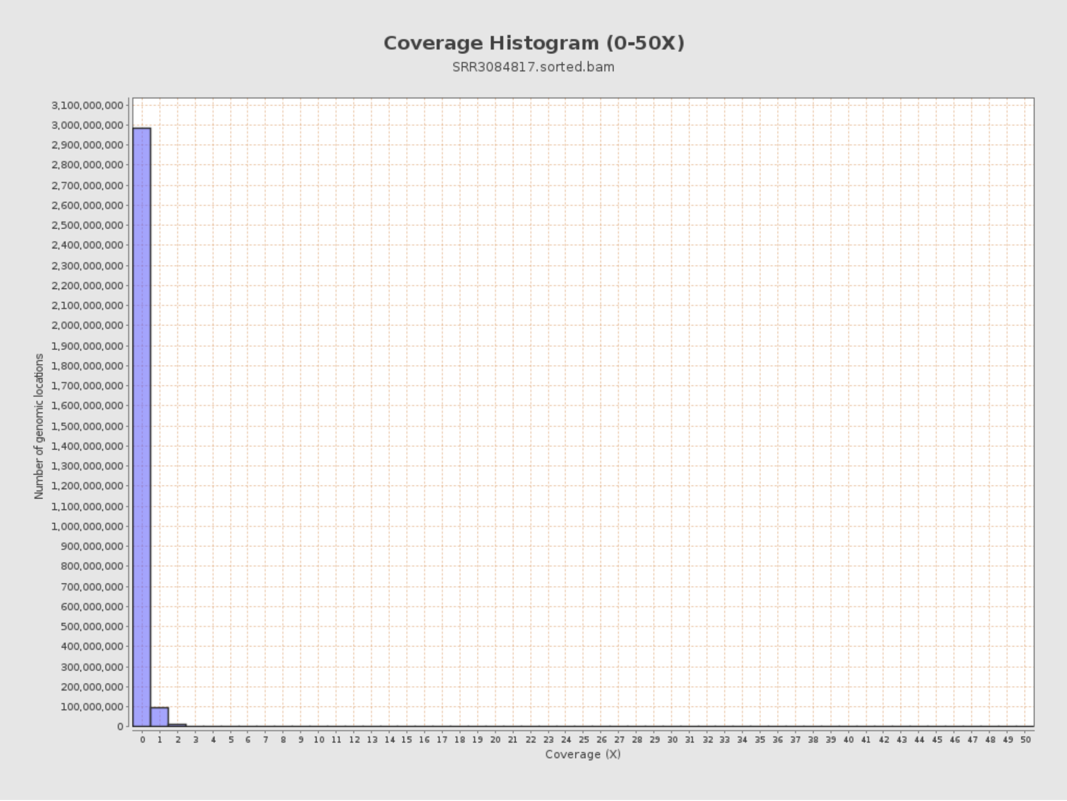
3. Results : Coverage across reference



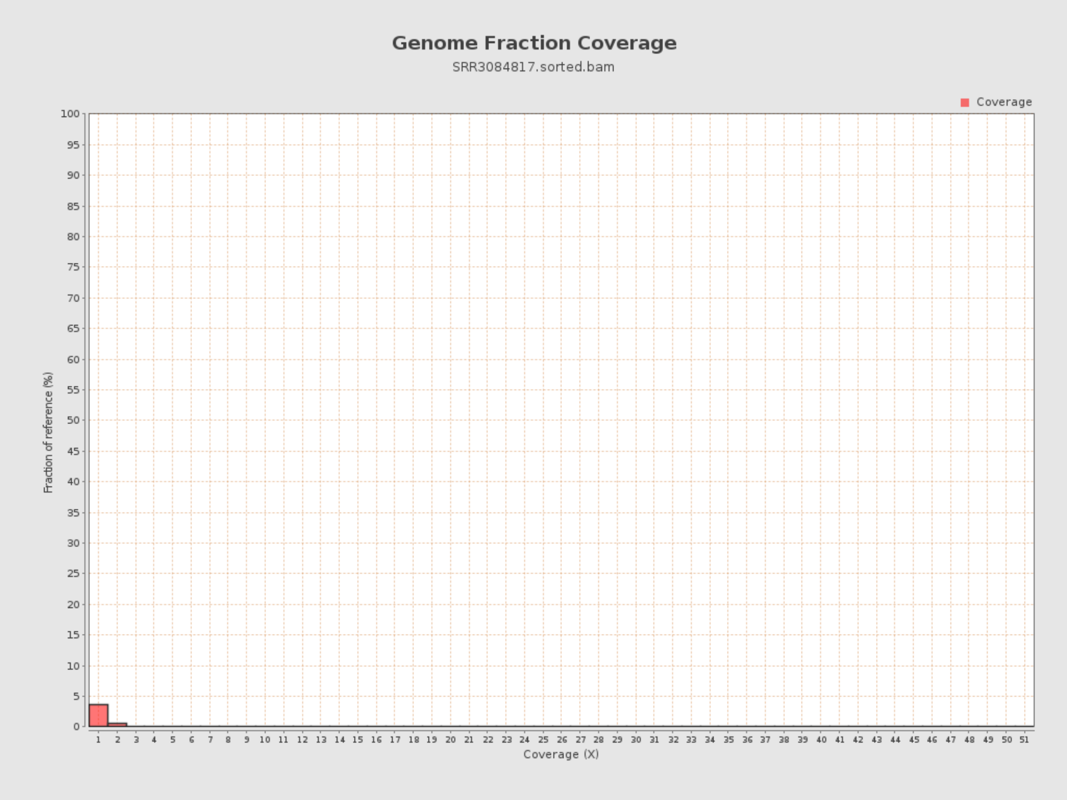
4. Results : Coverage Histogram



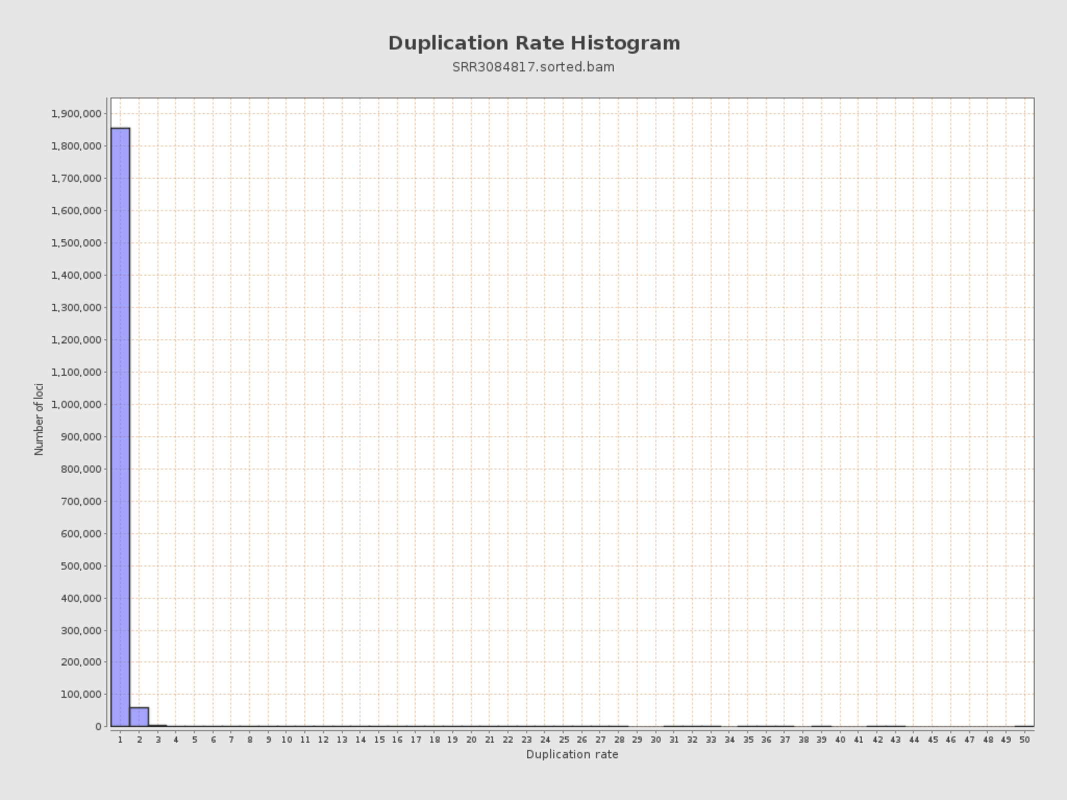
5. Results : Coverage Histogram (0-50X)



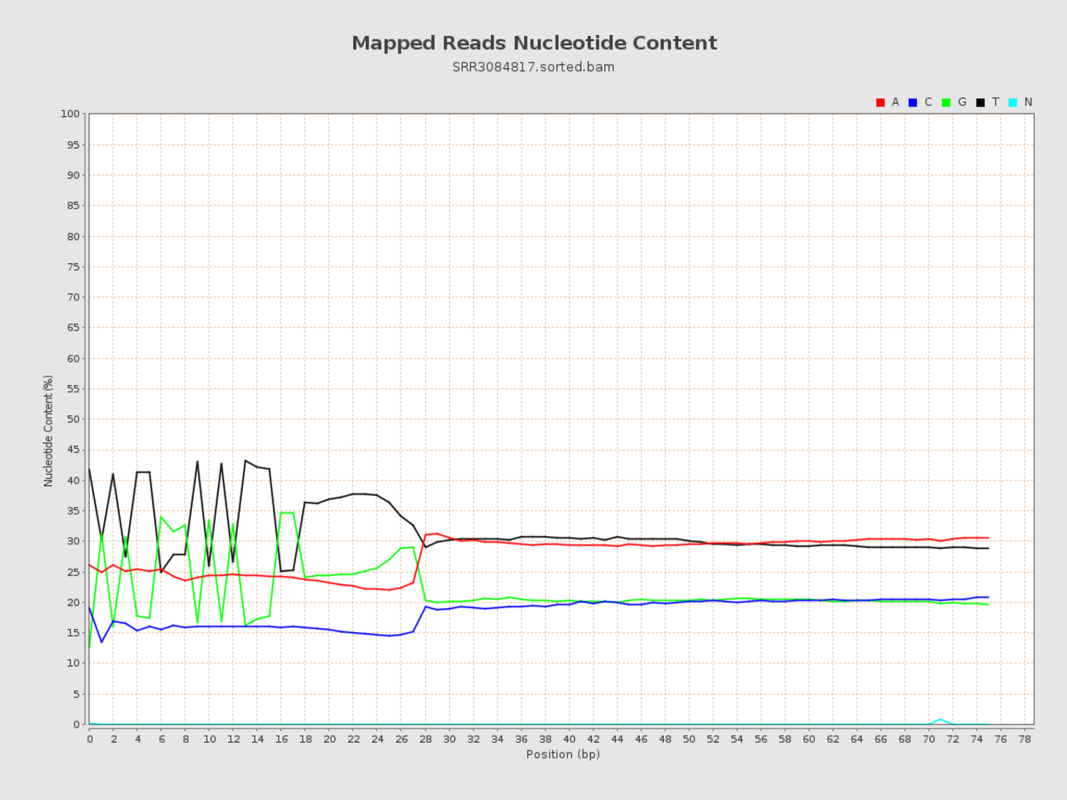
6. Results : Genome Fraction Coverage



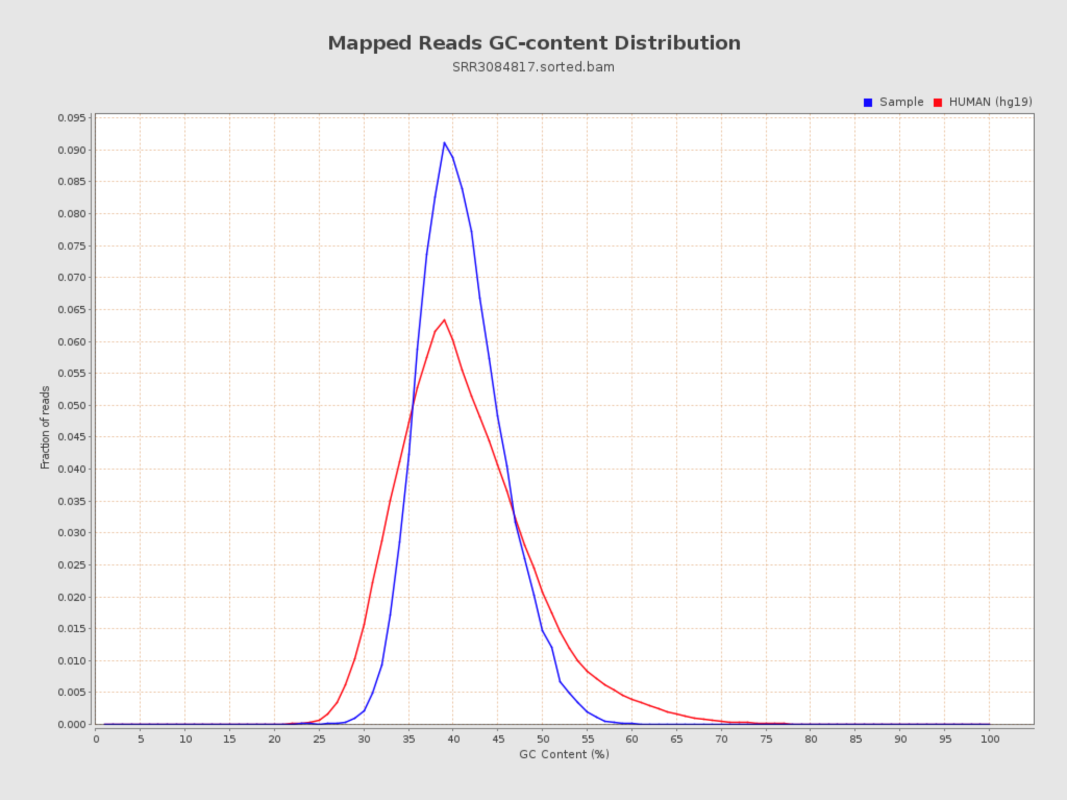
7. Results : Duplication Rate Histogram



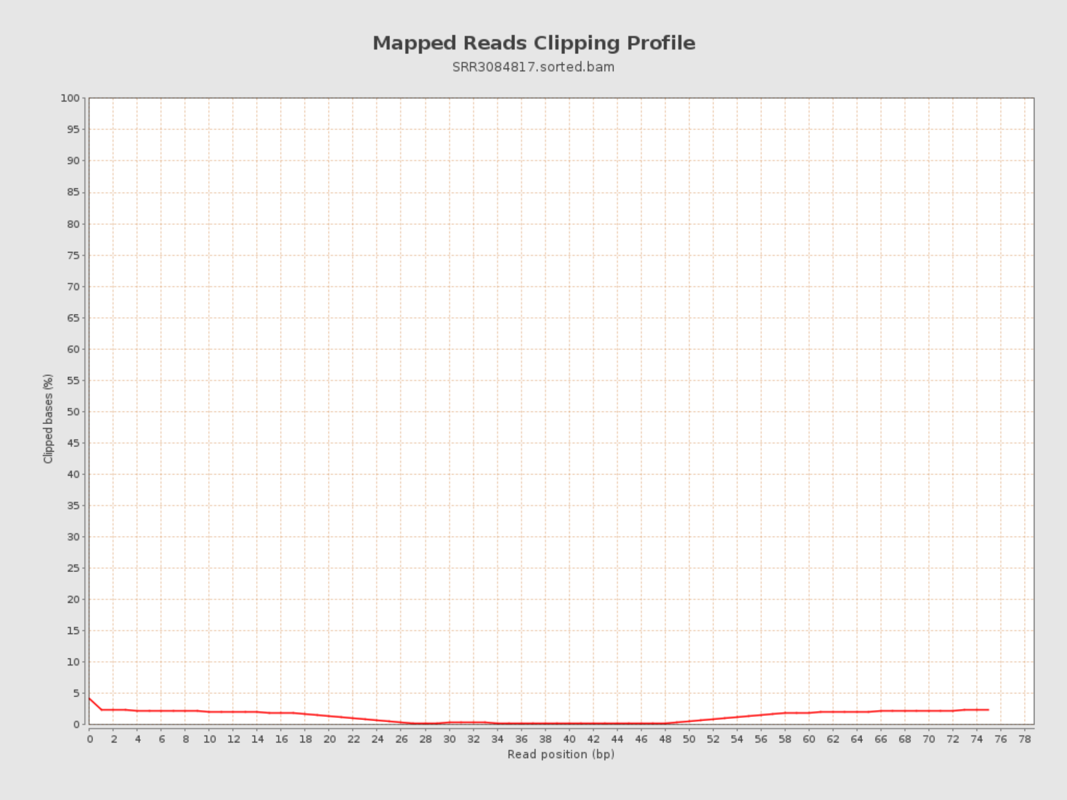
8. Results : Mapped Reads Nucleotide Content



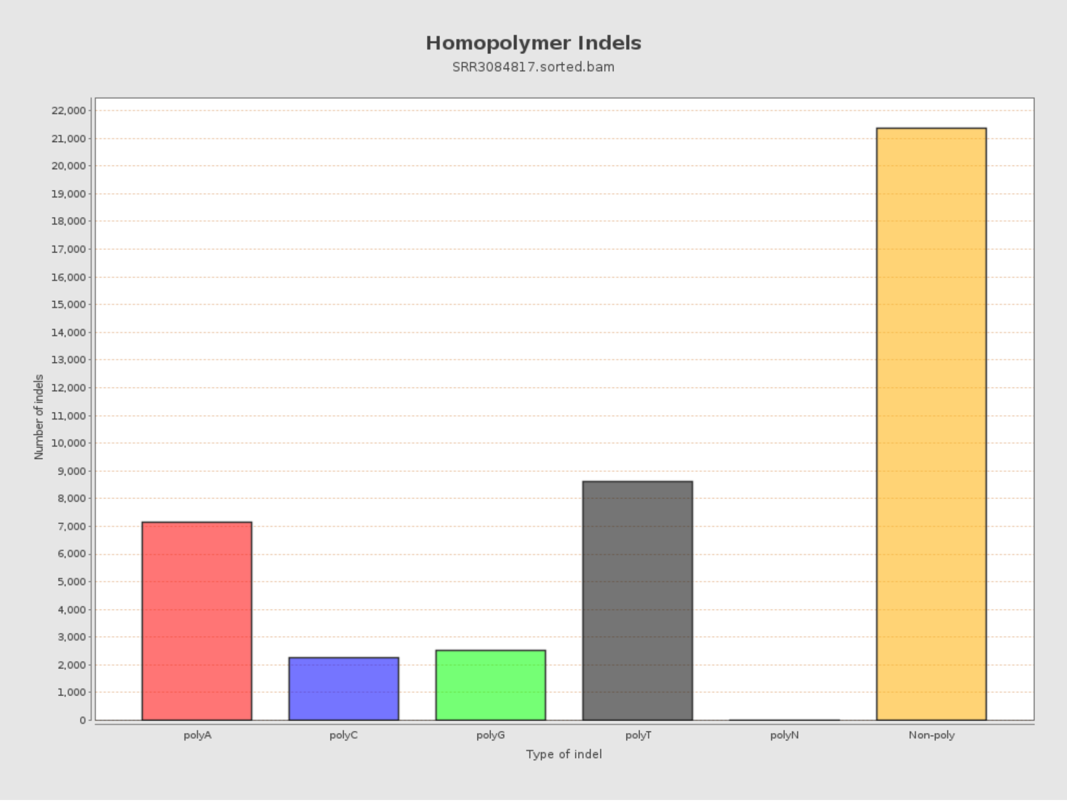
9. Results : Mapped Reads GC-content Distribution



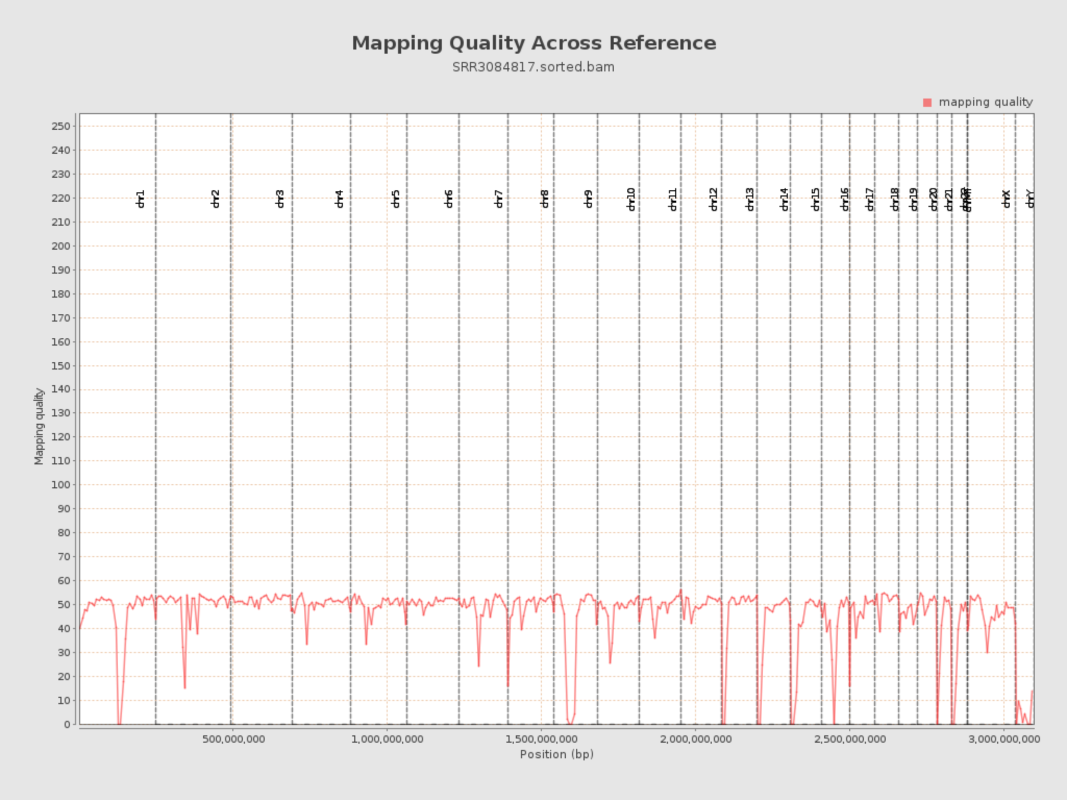
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram