Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 18:52:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084875.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_SRR3084875 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084875.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 18:52:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084875.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,575,290
Mapped reads	2,333,063 / 90.59%
Unmapped reads	242,227 / 9.41%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,019 / 0.66%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	99,724 / 3.87%
Duplication rate	3.44%
Clipped reads	713,865 / 27.72%

2.2. ACGT Content

Number/percentage of A's	48,134,854 / 29.45%
Number/percentage of C's	30,045,879 / 18.38%
Number/percentage of T's	52,307,039 / 32%
Number/percentage of G's	32,940,080 / 20.15%
Number/percentage of N's	27,135 / 0.02%
GC Percentage	38.53%

2.3. Coverage

Mean	0.0528

Standard Deviation	0.4698

2.4. Mapping Quality

Mean Mapping Quality	48.01

2.5. Mismatches and indels

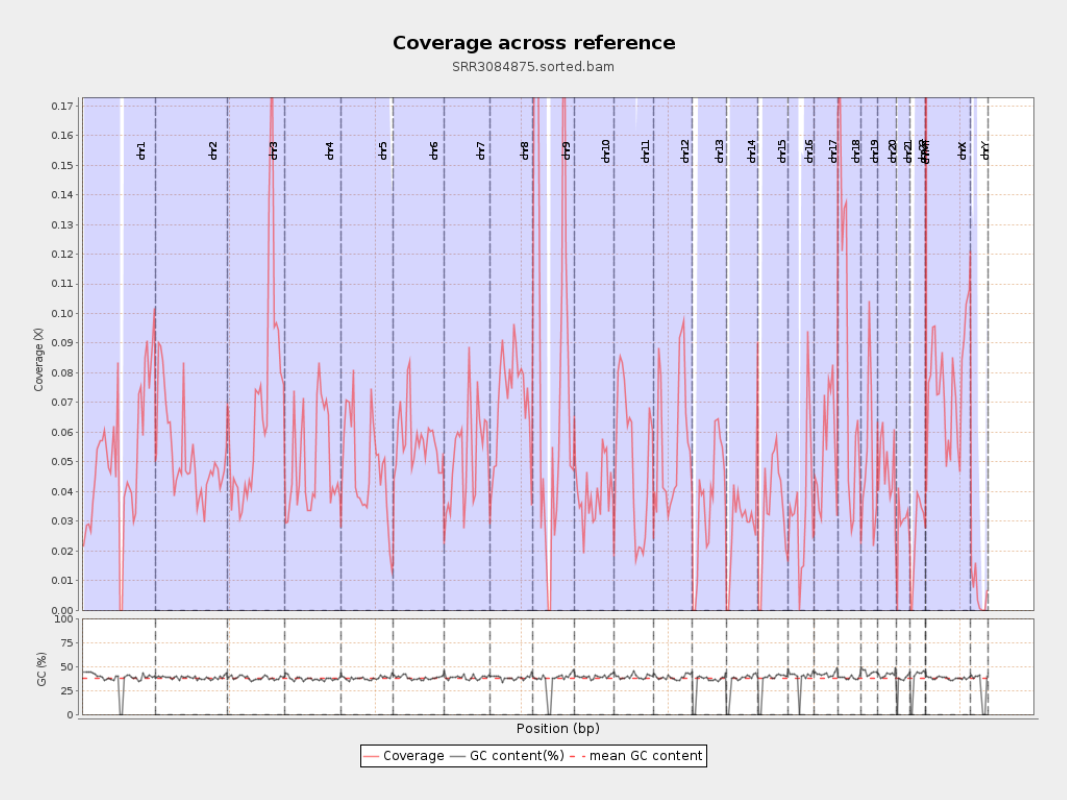
General error rate	0.83%
Mismatches	1,336,904
Insertions	13,000
Mapped reads with at least one insertion	0.55%
Deletions	35,933
Mapped reads with at least one deletion	1.52%
Homopolymer indels	48.12%

2.6. Chromosome stats

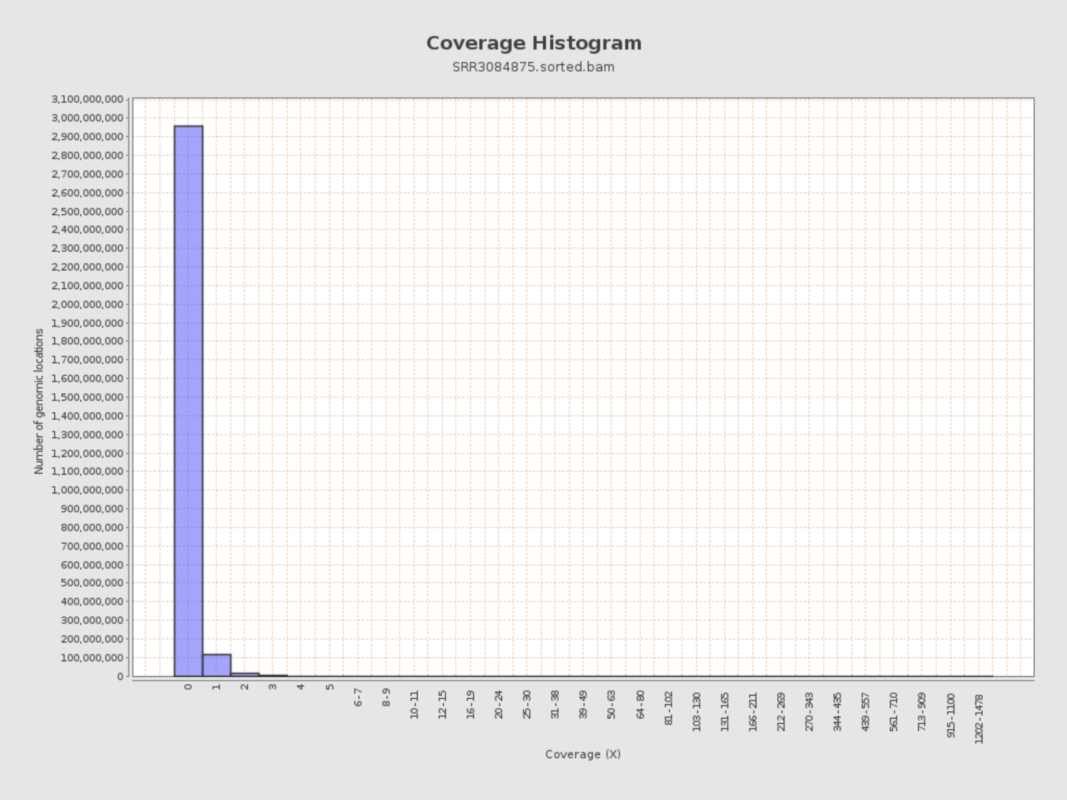
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12683594	0.0509	0.9441
chr2	243199373	12711051	0.0523	0.4348
chr3	198022430	13354914	0.0674	0.2968
chr4	191154276	9491497	0.0497	0.255
chr5	180915260	8599422	0.0475	0.2596
chr6	171115067	9885892	0.0578	0.2845
chr7	159138663	8216789	0.0516	0.3442

chr8	146364022	10431470	0.0713	1.003
chr9	141213431	12014138	0.0851	0.4704
chr10	135534747	5375684	0.0397	0.2904
chr11	135006516	6848776	0.0507	0.3397
chr12	133851895	7592723	0.0567	0.2763
chr13	115169878	4282180	0.0372	0.2179
chr14	107349540	3063010	0.0285	0.2157
chr15	102531392	3486673	0.034	0.2087
chr16	90354753	3020217	0.0334	0.2494
chr17	81195210	4517620	0.0556	0.2775
chr18	78077248	6971650	0.0893	0.8117
chr19	59128983	3061211	0.0518	0.5467
chr20	63025520	3072725	0.0488	0.2652
chr21	48129895	1386819	0.0288	0.2087
chr22	51304566	1294314	0.0252	0.1769
chrMT	16571	38077	2.2978	1.8174
chrX	155270560	11778824	0.0759	0.3461
chrY	59373566	338838	0.0057	0.1392

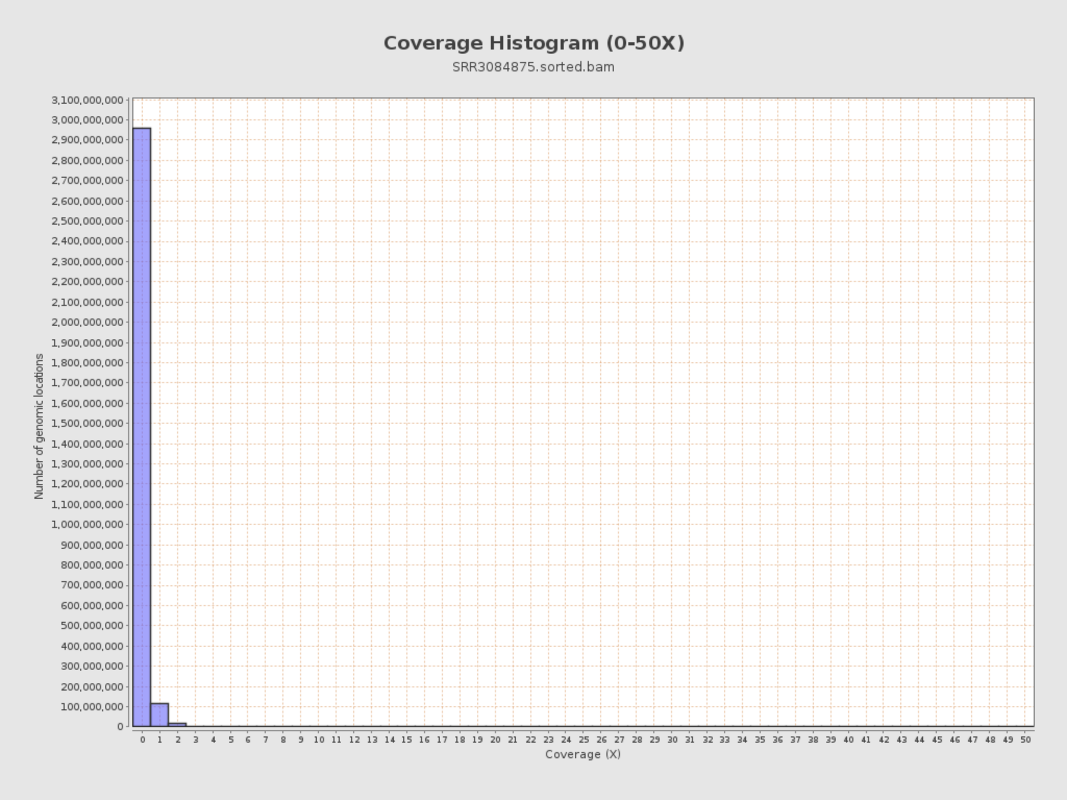
3. Results : Coverage across reference



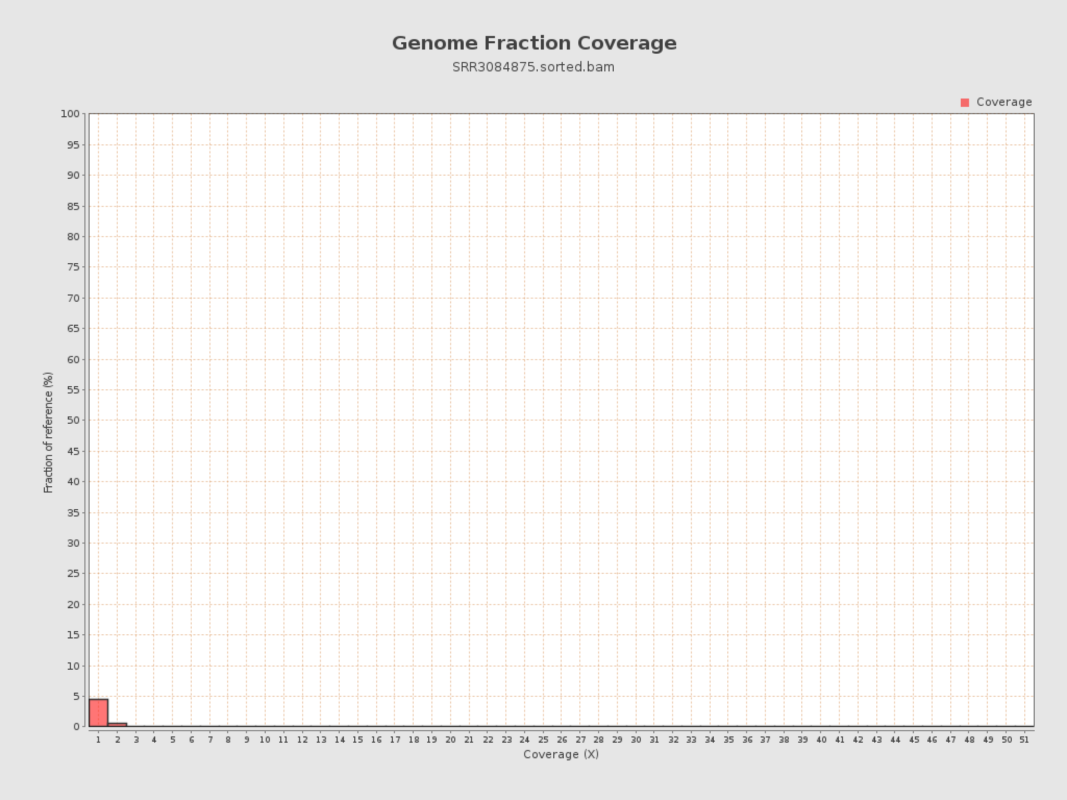
4. Results : Coverage Histogram



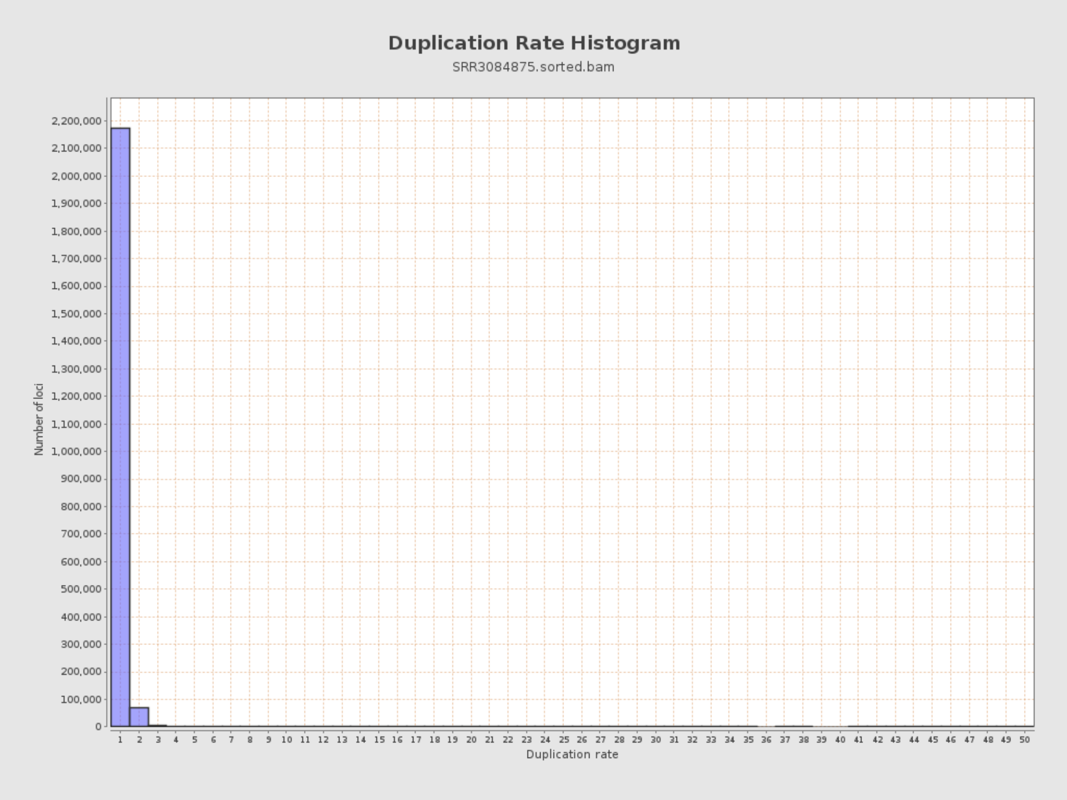
5. Results : Coverage Histogram (0-50X)



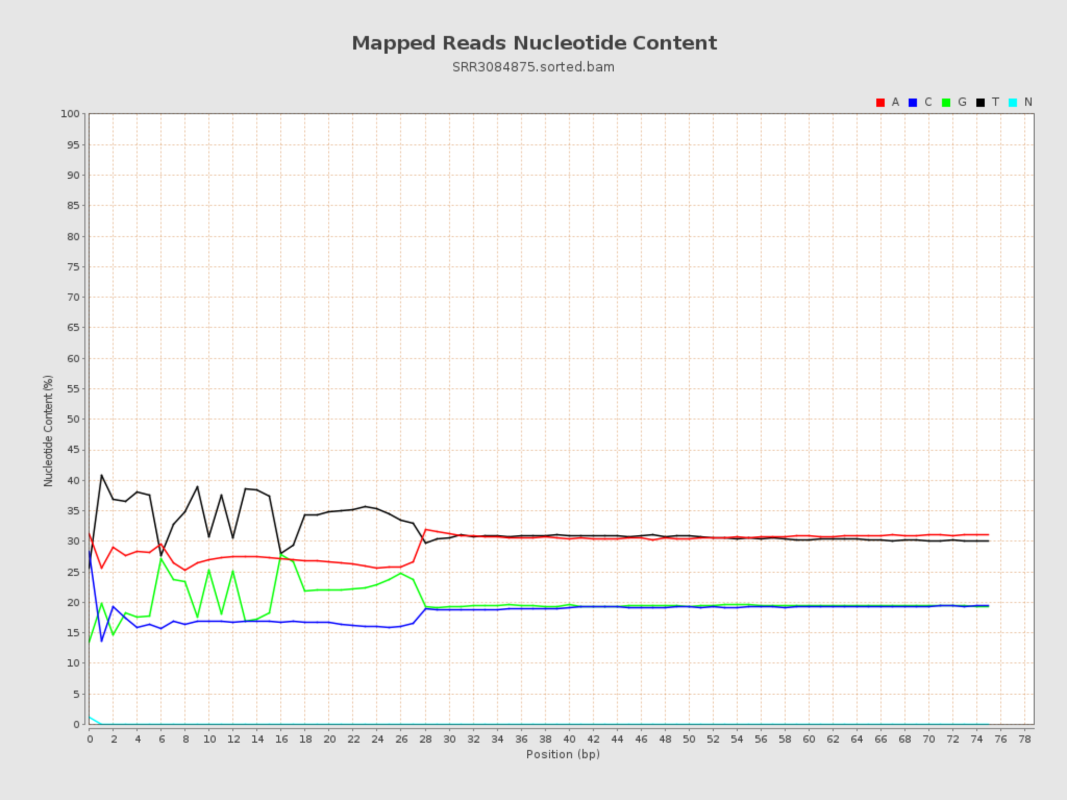
6. Results : Genome Fraction Coverage



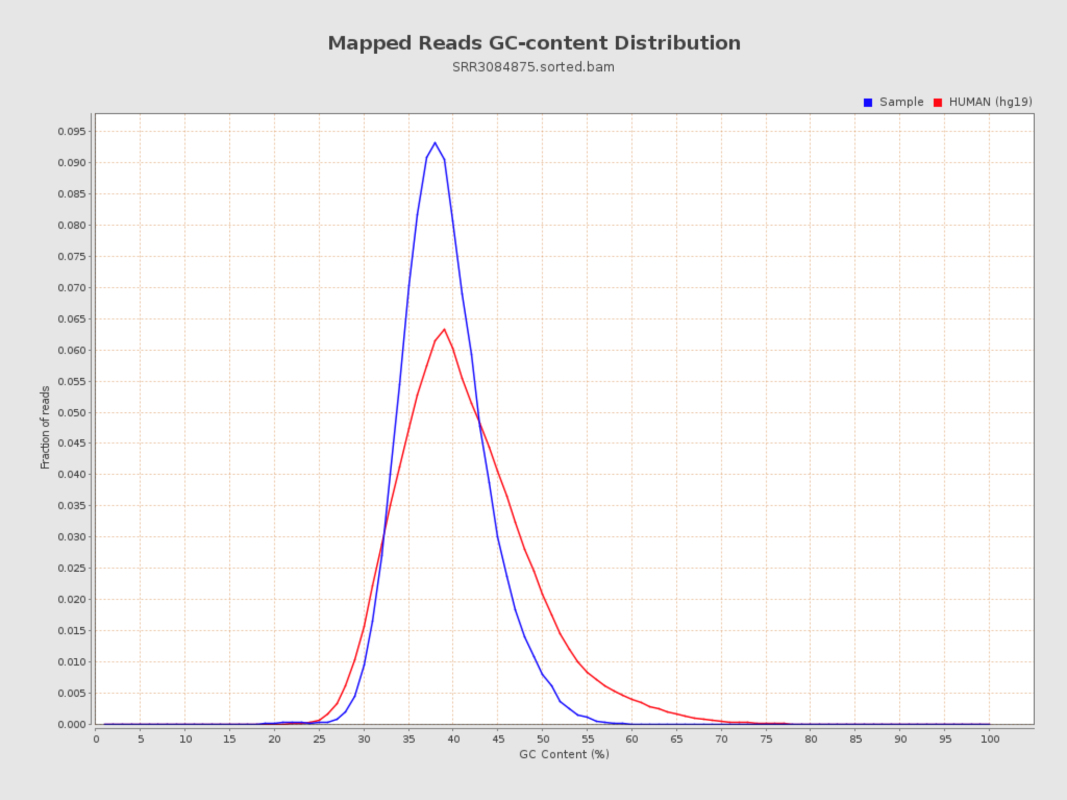
7. Results : Duplication Rate Histogram



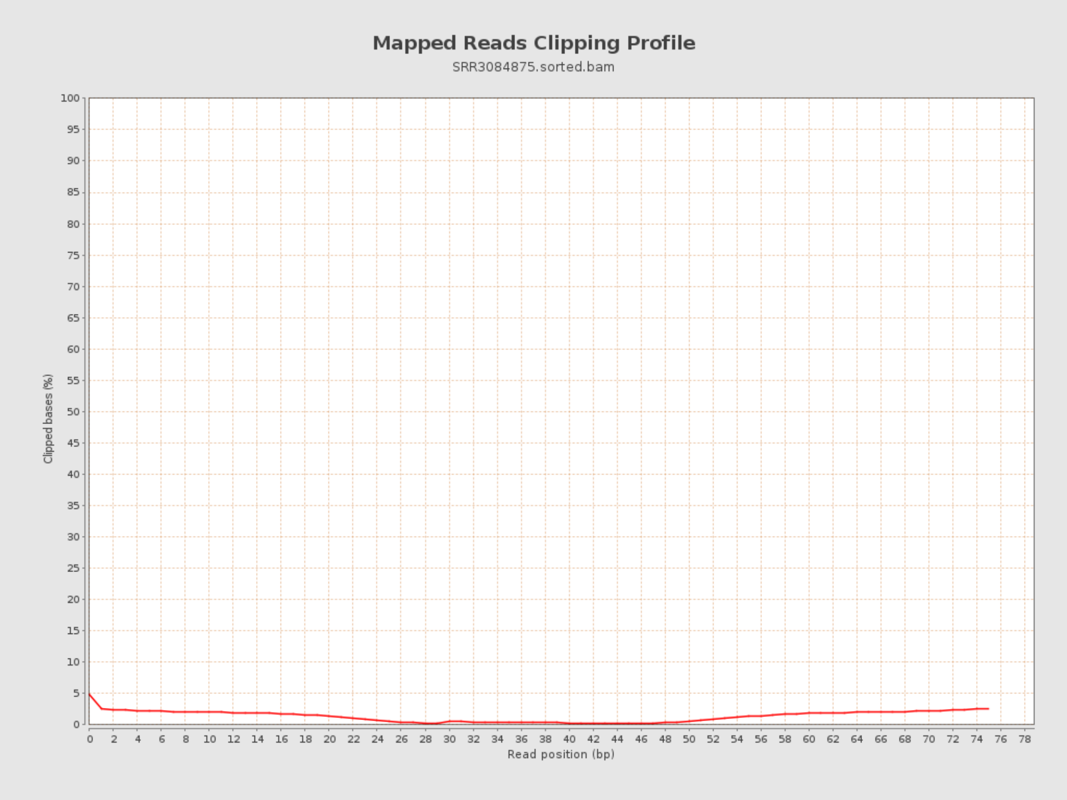
8. Results : Mapped Reads Nucleotide Content



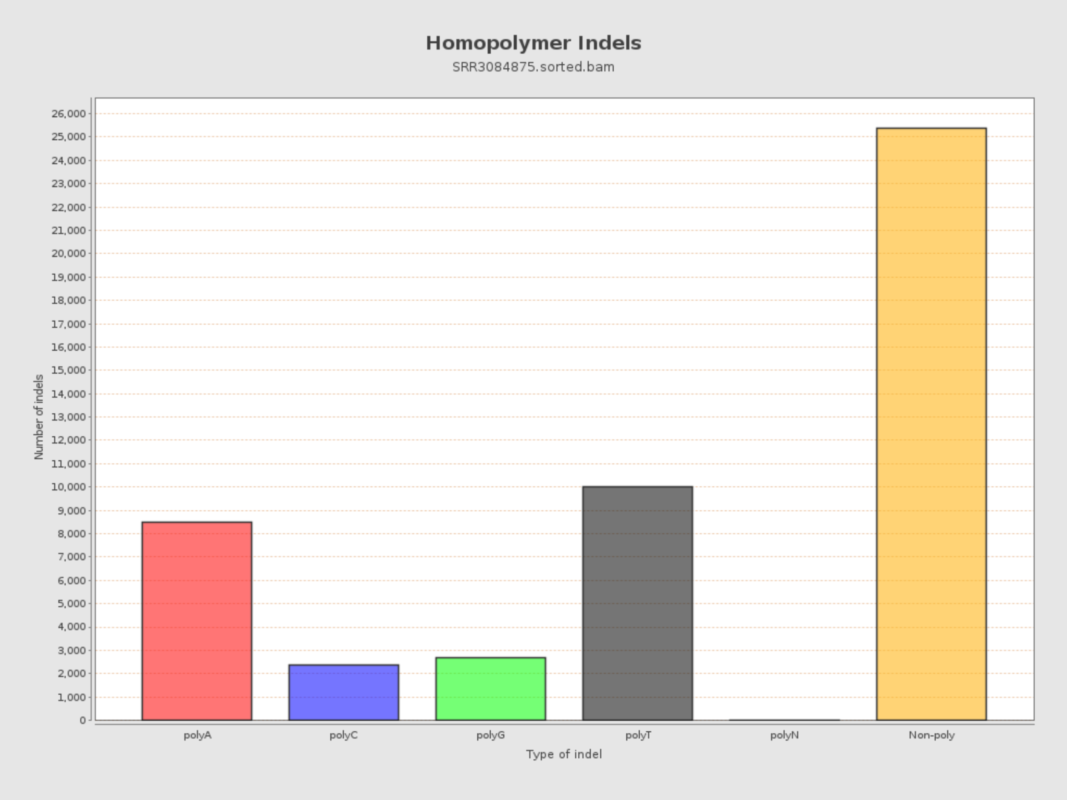
9. Results : Mapped Reads GC-content Distribution



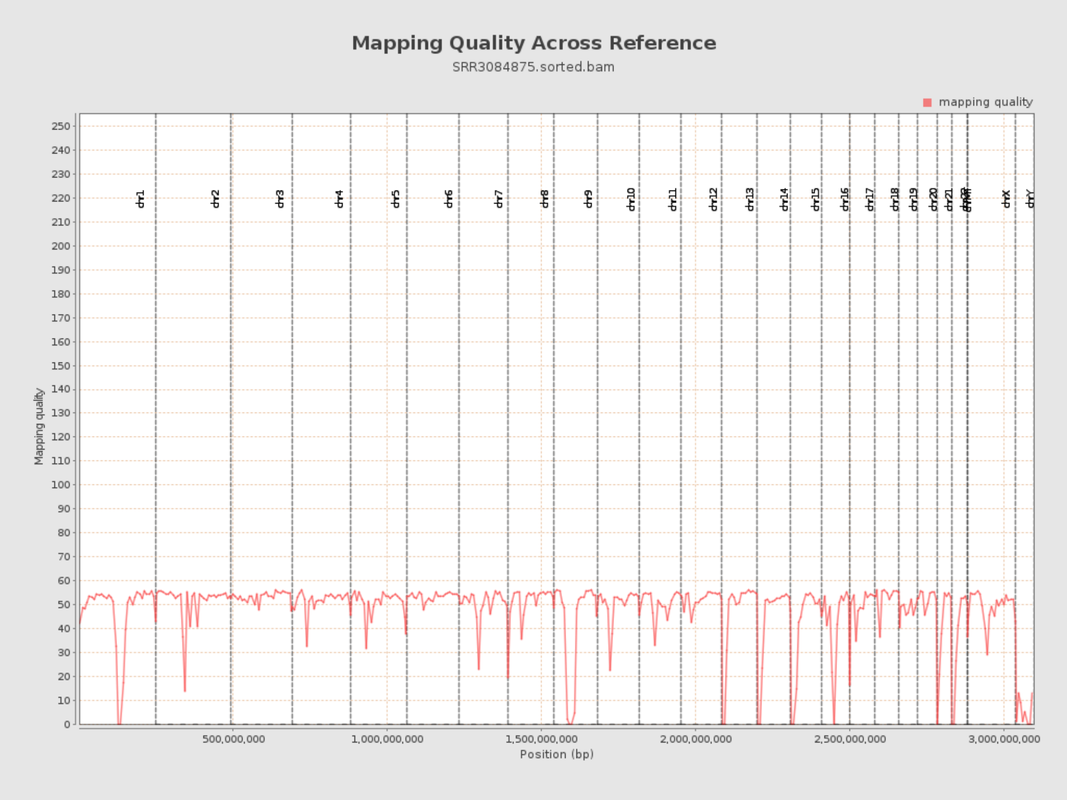
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram