Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 15:53:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084819.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_SRR3084819 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084819.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 15:53:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084819.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,979,796
Mapped reads	1,787,758 / 90.3%
Unmapped reads	192,038 / 9.7%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,611 / 0.94%
Read min/max/mean length	30 / 76 / 76.33
Duplicated reads (estimated)	81,691 / 4.13%
Duplication rate	3.98%
Clipped reads	800,406 / 40.43%

2.2. ACGT Content

Number/percentage of A's	32,393,686 / 27.16%
Number/percentage of C's	22,529,955 / 18.89%
Number/percentage of T's	37,284,127 / 31.26%
Number/percentage of G's	27,030,019 / 22.67%
Number/percentage of N's	16,677 / 0.01%
GC Percentage	41.56%

2.3. Coverage

Mean	0.0385

Standard Deviation	0.2714

2.4. Mapping Quality

Mean Mapping Quality	45.45

2.5. Mismatches and indels

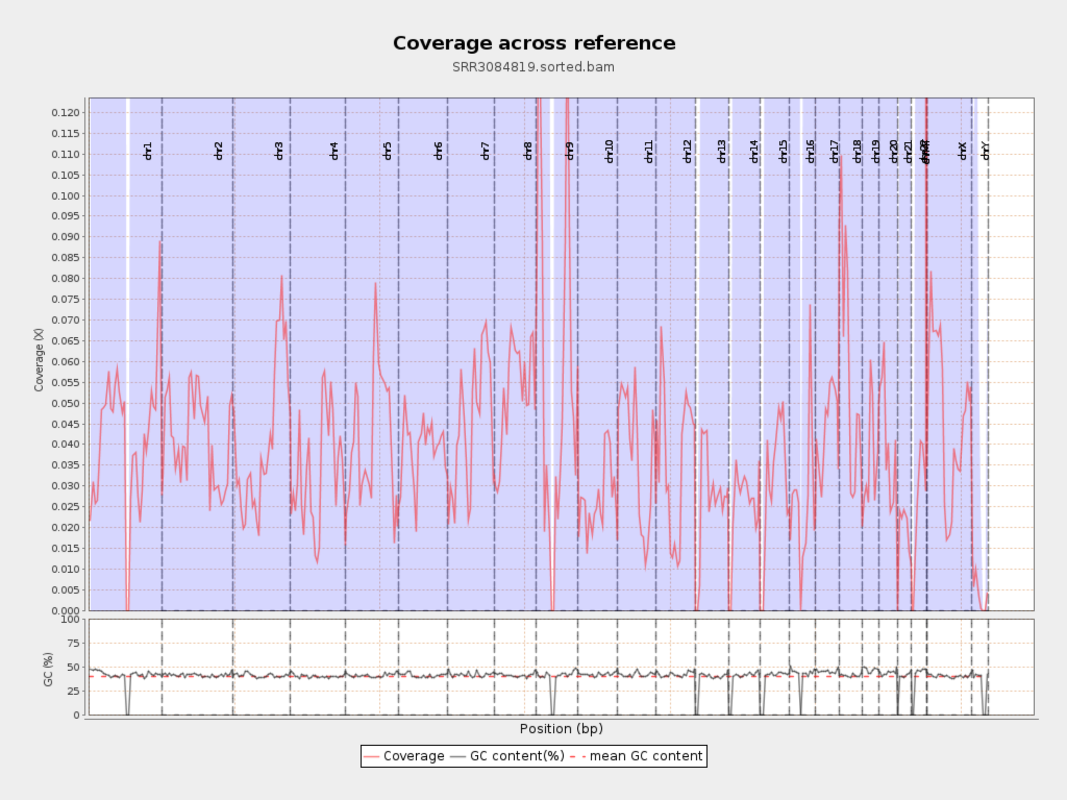
General error rate	0.77%
Mismatches	899,627
Insertions	9,478
Mapped reads with at least one insertion	0.53%
Deletions	28,484
Mapped reads with at least one deletion	1.58%
Homopolymer indels	47.87%

2.6. Chromosome stats

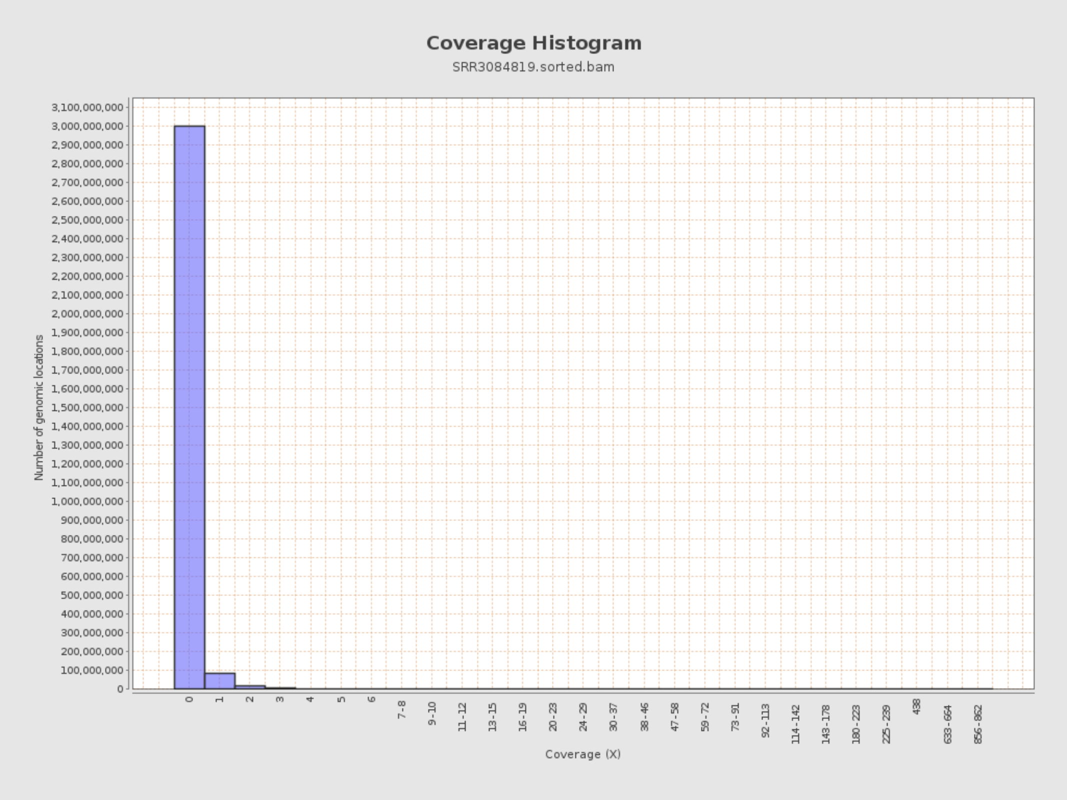
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10258431	0.0412	0.2754
chr2	243199373	10045601	0.0413	0.4448
chr3	198022430	8109773	0.041	0.2386
chr4	191154276	6421062	0.0336	0.2204
chr5	180915260	7536021	0.0417	0.2422
chr6	171115067	6648445	0.0389	0.2509
chr7	159138663	7195334	0.0452	0.2782

chr8	146364022	7685300	0.0525	0.2936
chr9	141213431	7992752	0.0566	0.3258
chr10	135534747	3676180	0.0271	0.2004
chr11	135006516	5024834	0.0372	0.2618
chr12	133851895	4830142	0.0361	0.2258
chr13	115169878	2987348	0.0259	0.1908
chr14	107349540	2607419	0.0243	0.187
chr15	102531392	3148818	0.0307	0.2136
chr16	90354753	2439487	0.027	0.2012
chr17	81195210	3626336	0.0447	0.2548
chr18	78077248	4593176	0.0588	0.4228
chr19	59128983	2182325	0.0369	0.2518
chr20	63025520	2588669	0.0411	0.2414
chr21	48129895	885177	0.0184	0.1657
chr22	51304566	1259703	0.0246	0.1839
chrMT	16571	31552	1.904	1.6355
chrX	155270560	7280048	0.0469	0.2626
chrY	59373566	247613	0.0042	0.0936

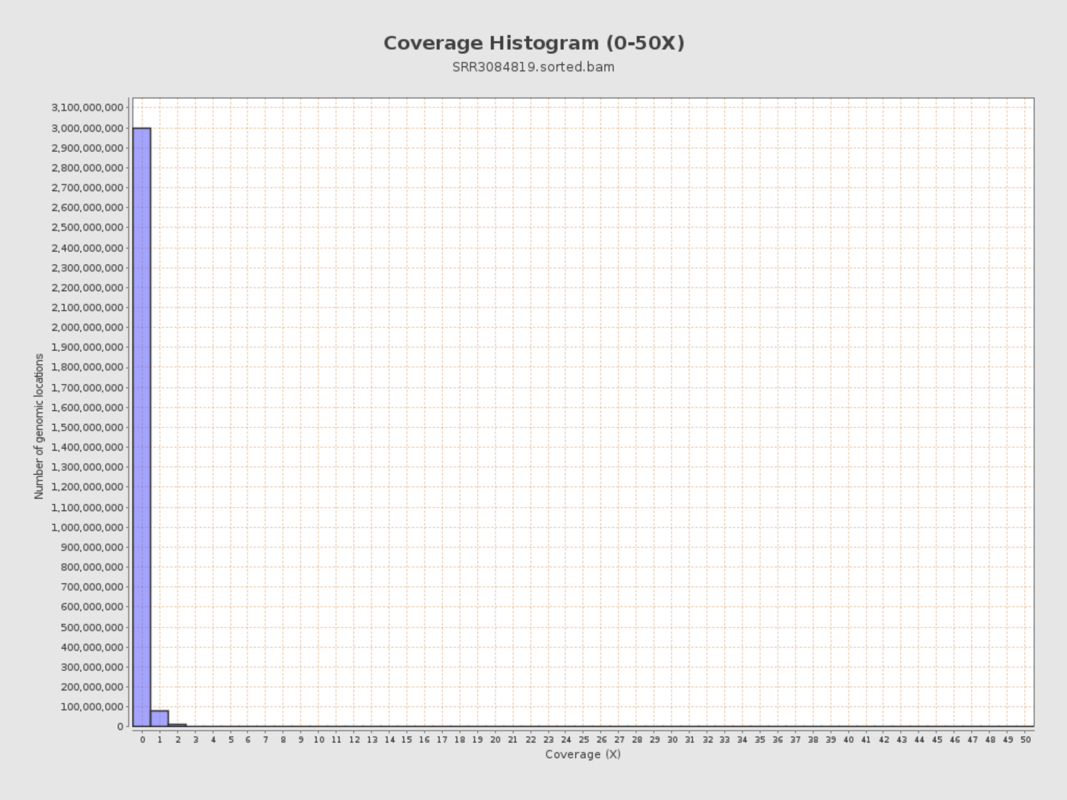
3. Results : Coverage across reference



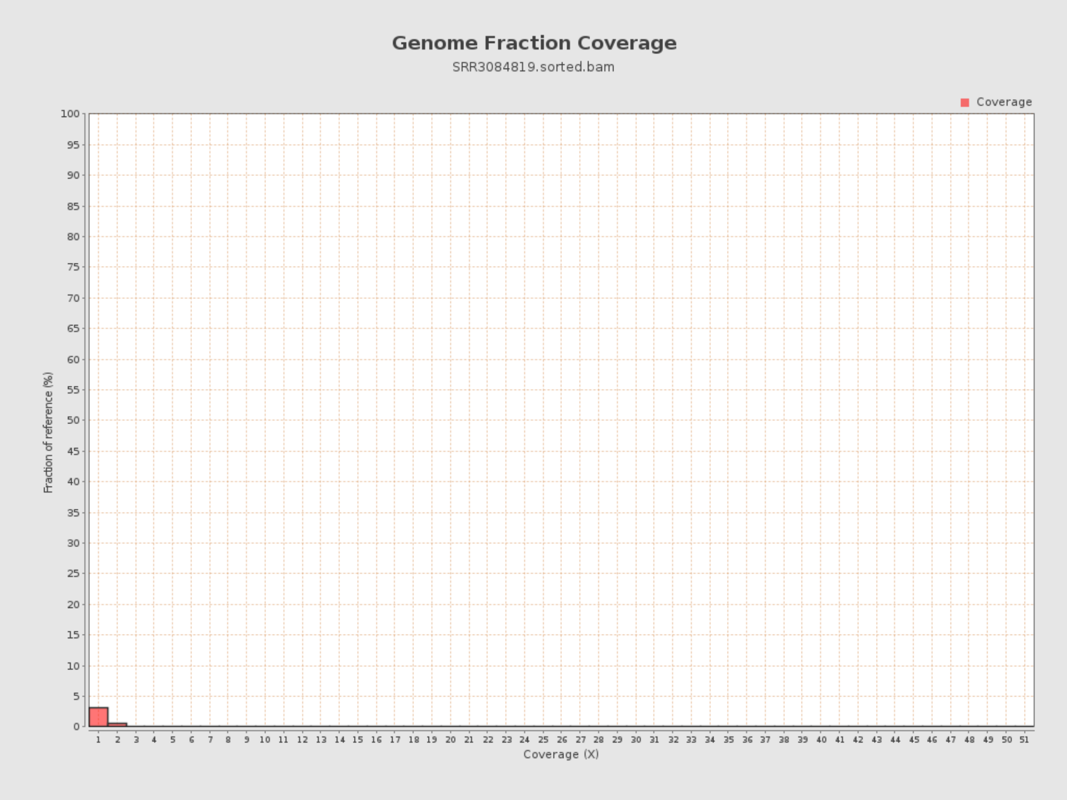
4. Results : Coverage Histogram



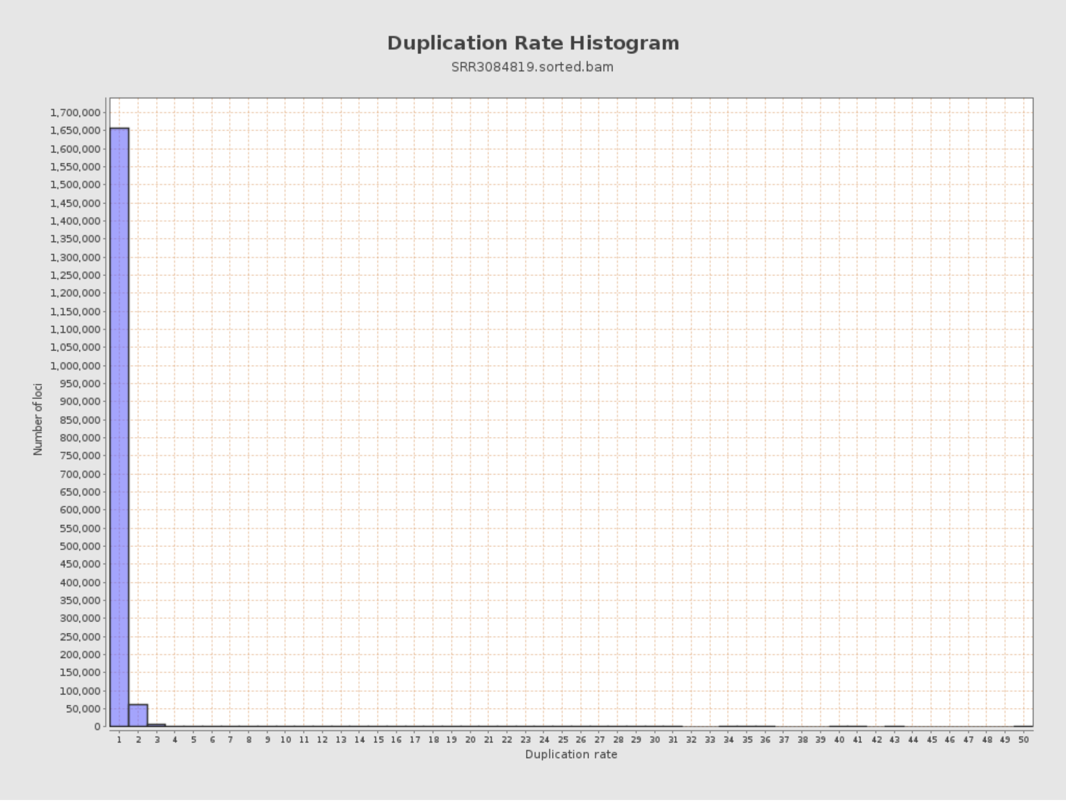
5. Results : Coverage Histogram (0-50X)



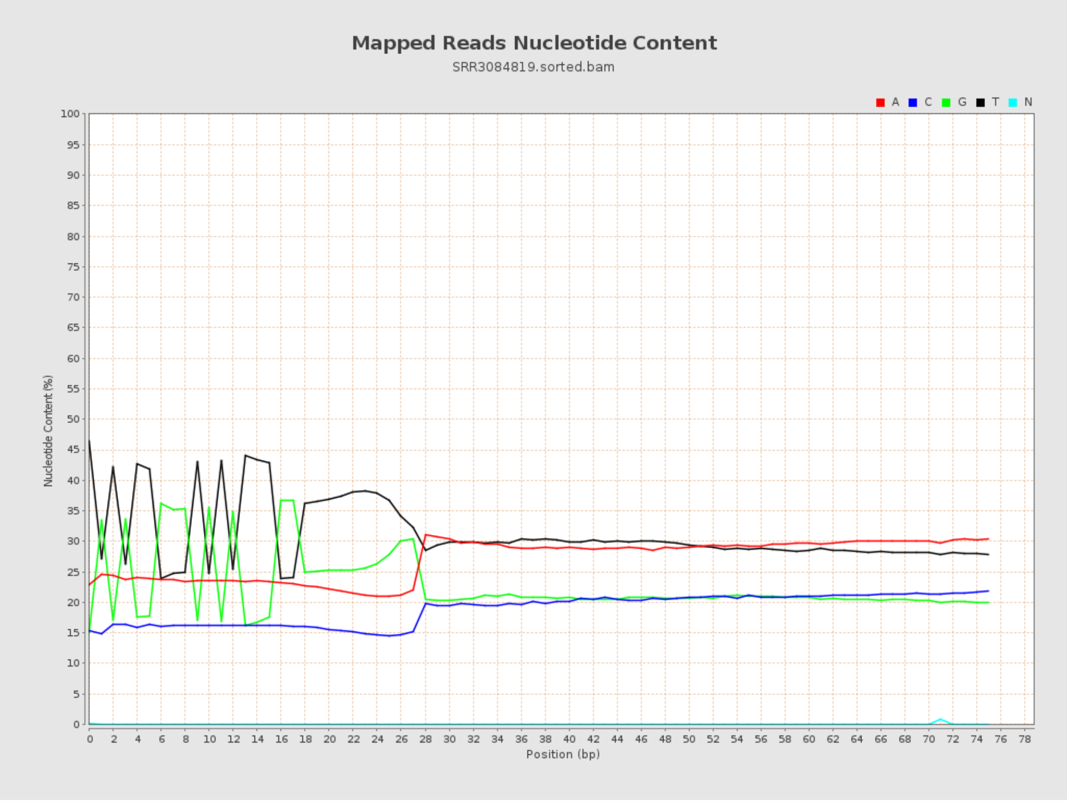
6. Results : Genome Fraction Coverage



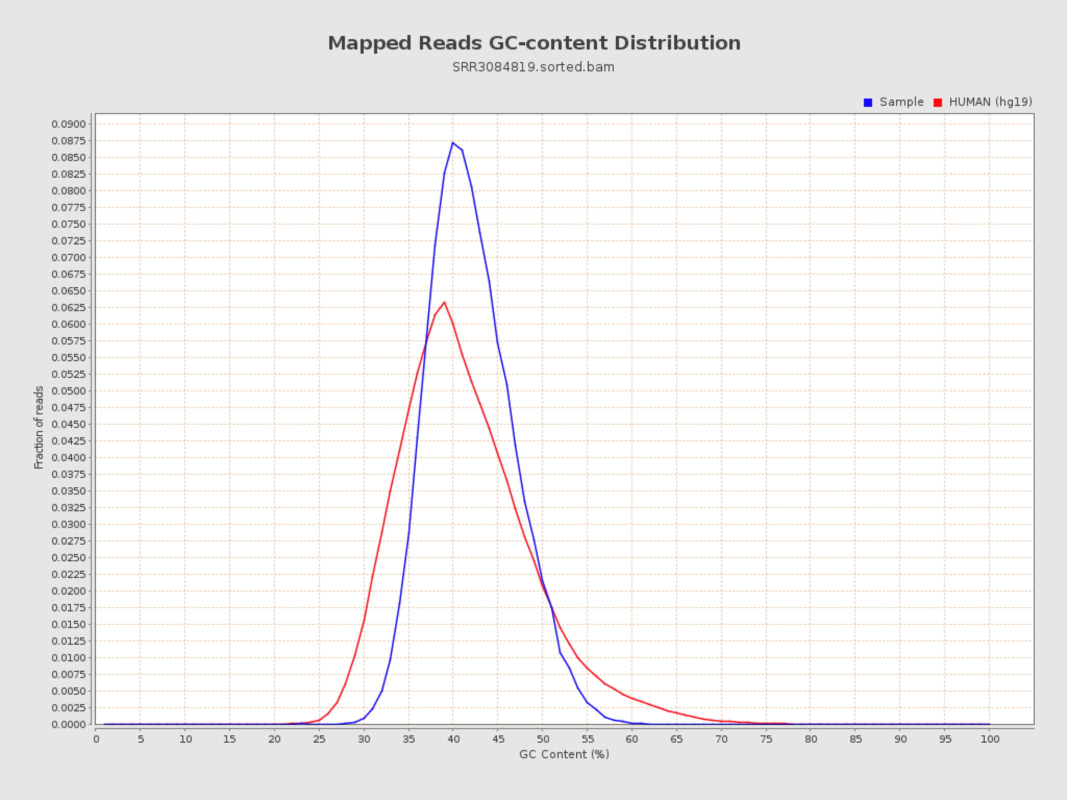
7. Results : Duplication Rate Histogram



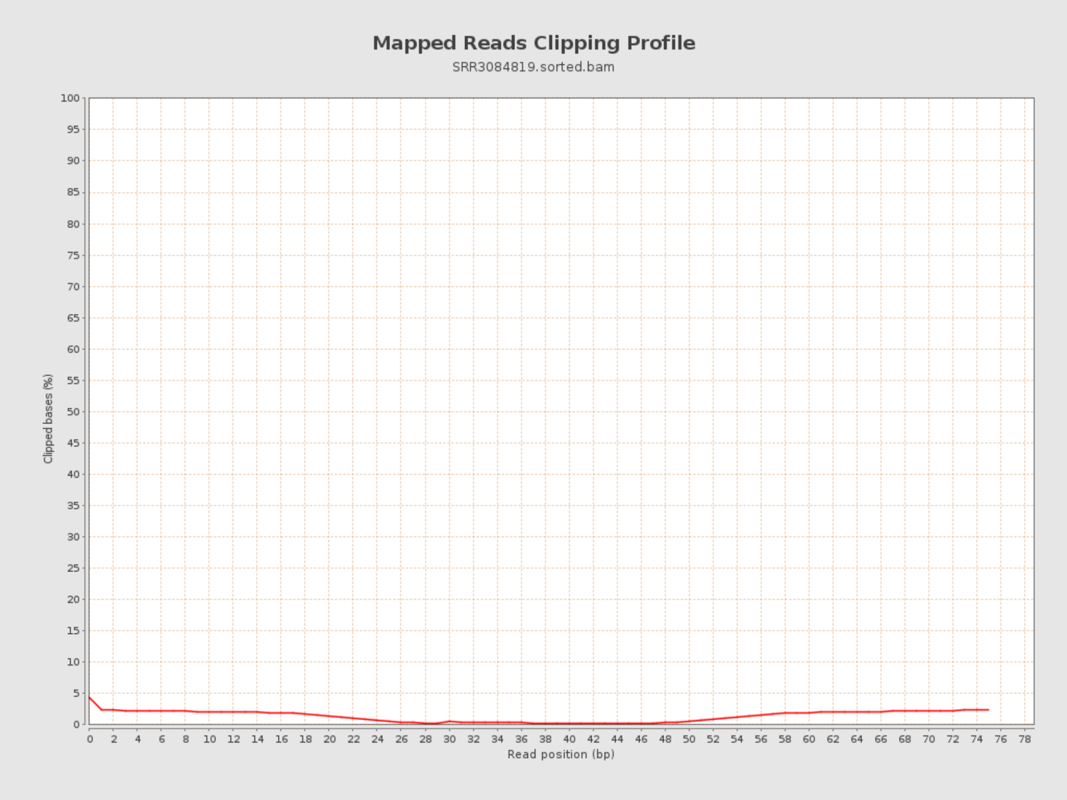
8. Results : Mapped Reads Nucleotide Content



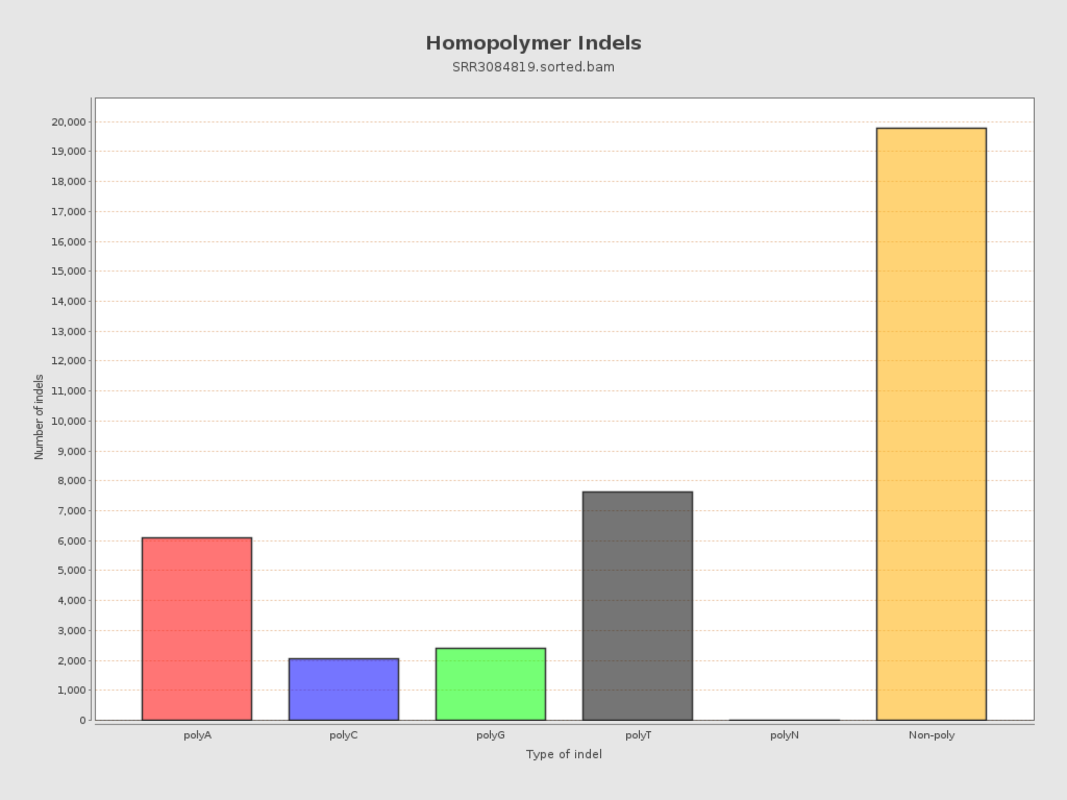
9. Results : Mapped Reads GC-content Distribution



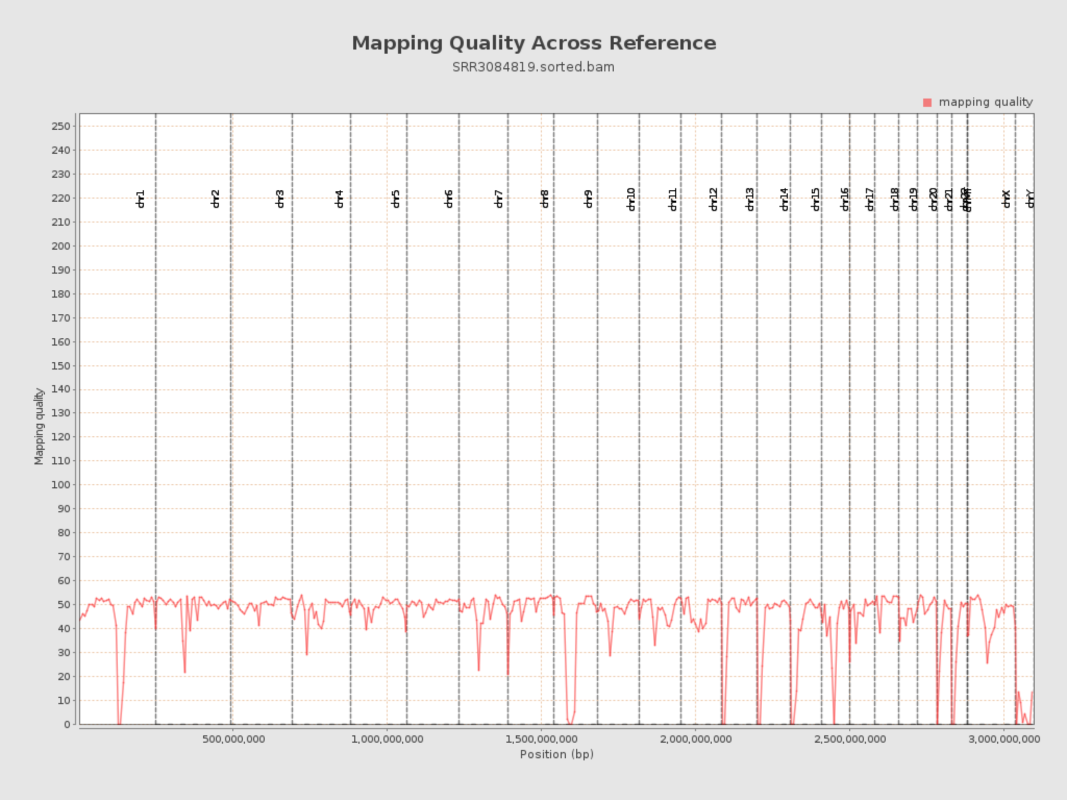
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram