Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 18:20:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084861.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_SRR3084861 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084861.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 18:20:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084861.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,356,000
Mapped reads	2,115,644 / 89.8%
Unmapped reads	240,356 / 10.2%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,685 / 0.62%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	101,081 / 4.29%
Duplication rate	4.27%
Clipped reads	775,759 / 32.93%

2.2. ACGT Content

Number/percentage of A's	41,279,922 / 28.52%
Number/percentage of C's	26,429,665 / 18.26%
Number/percentage of T's	46,500,636 / 32.12%
Number/percentage of G's	30,516,214 / 21.08%
Number/percentage of N's	22,646 / 0.02%
GC Percentage	39.34%

2.3. Coverage

Mean	0.0468

Standard Deviation	0.3022

2.4. Mapping Quality

Mean Mapping Quality	47.6

2.5. Mismatches and indels

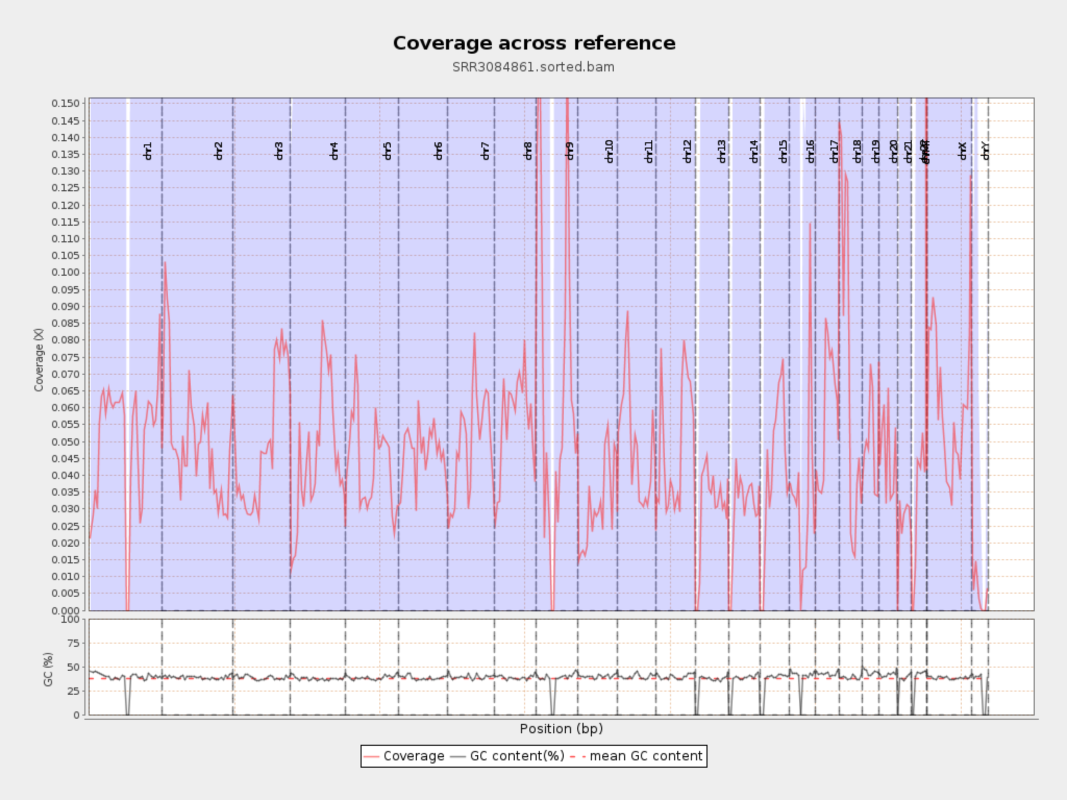
General error rate	0.8%
Mismatches	1,144,431
Insertions	11,238
Mapped reads with at least one insertion	0.53%
Deletions	31,547
Mapped reads with at least one deletion	1.48%
Homopolymer indels	49.21%

2.6. Chromosome stats

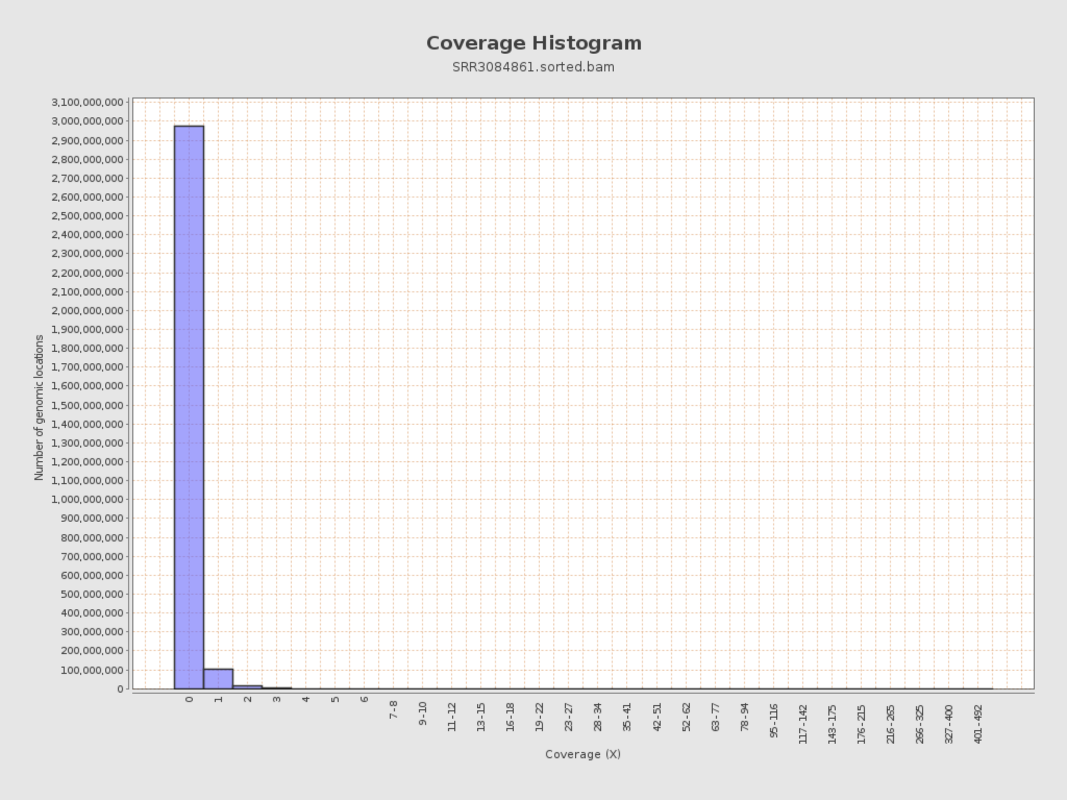
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12548594	0.0503	0.4364
chr2	243199373	12167991	0.05	0.3525
chr3	198022430	9844807	0.0497	0.2536
chr4	191154276	8783258	0.0459	0.2464
chr5	180915260	7943659	0.0439	0.2406
chr6	171115067	7970910	0.0466	0.2496
chr7	159138663	7934015	0.0499	0.3127

chr8	146364022	8158130	0.0557	0.4242
chr9	141213431	9332823	0.0661	0.3613
chr10	135534747	4133008	0.0305	0.2261
chr11	135006516	6679674	0.0495	0.2732
chr12	133851895	6531437	0.0488	0.2542
chr13	115169878	3429736	0.0298	0.1956
chr14	107349540	3113593	0.029	0.1977
chr15	102531392	4278781	0.0417	0.2322
chr16	90354753	3117460	0.0345	0.2239
chr17	81195210	4845546	0.0597	0.2824
chr18	78077248	5482408	0.0702	0.4918
chr19	59128983	2983936	0.0505	0.3419
chr20	63025520	2943493	0.0467	0.2502
chr21	48129895	1237480	0.0257	0.1893
chr22	51304566	1587074	0.0309	0.1986
chrMT	16571	90442	5.4578	3.4634
chrX	155270560	9354717	0.0602	0.2901
chrY	59373566	311724	0.0053	0.1161

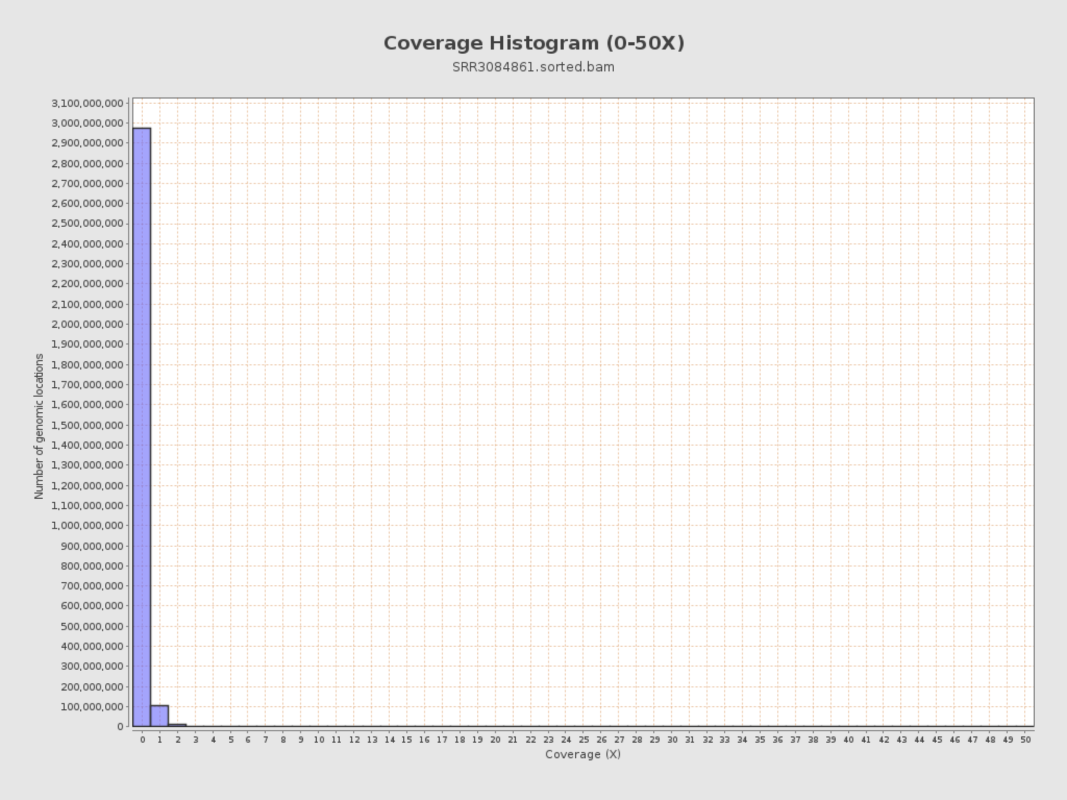
3. Results : Coverage across reference



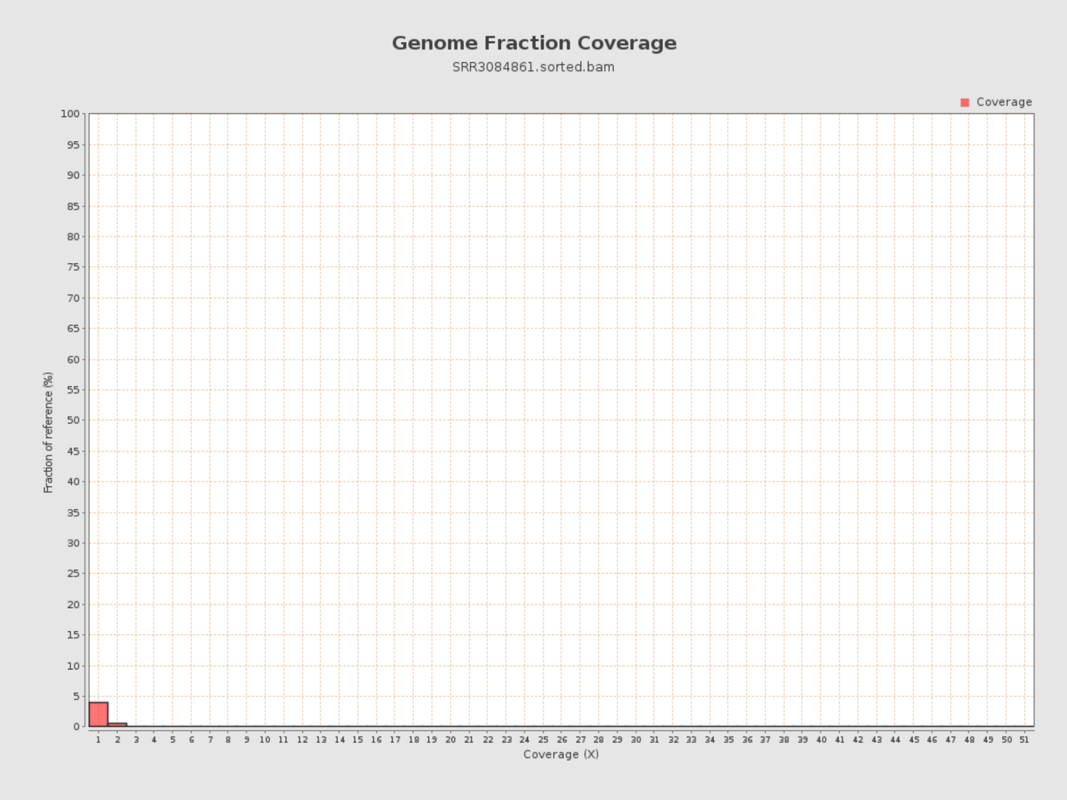
4. Results : Coverage Histogram



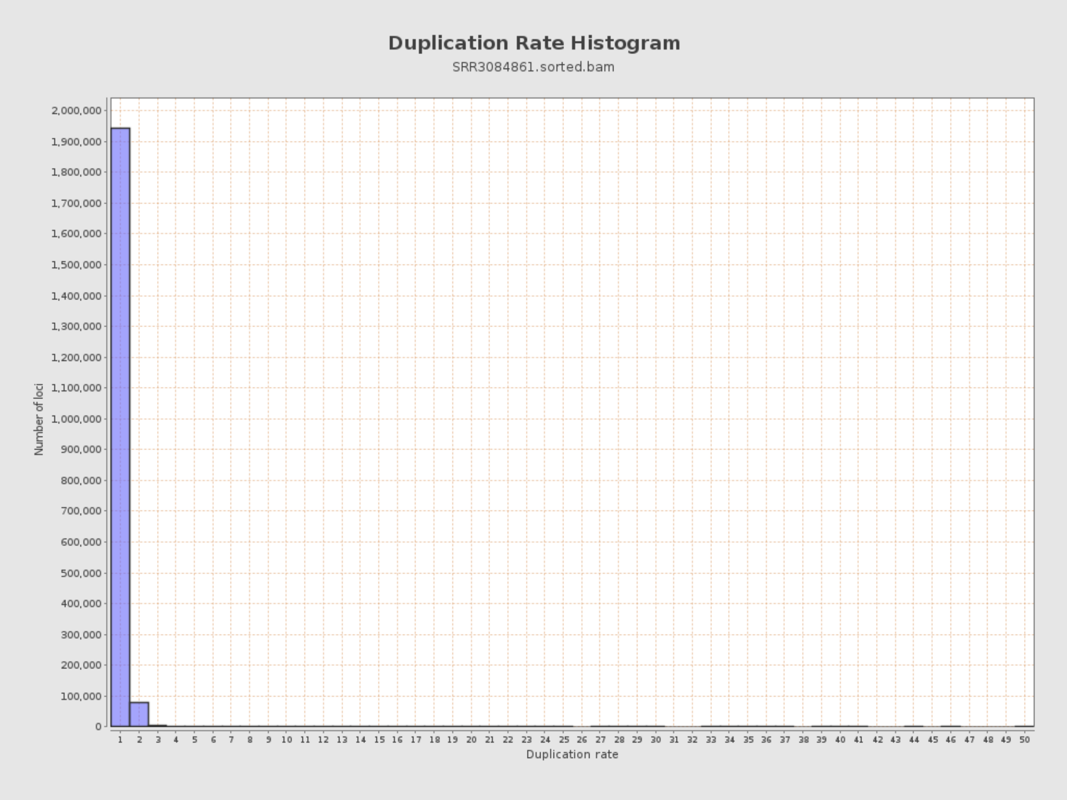
5. Results : Coverage Histogram (0-50X)



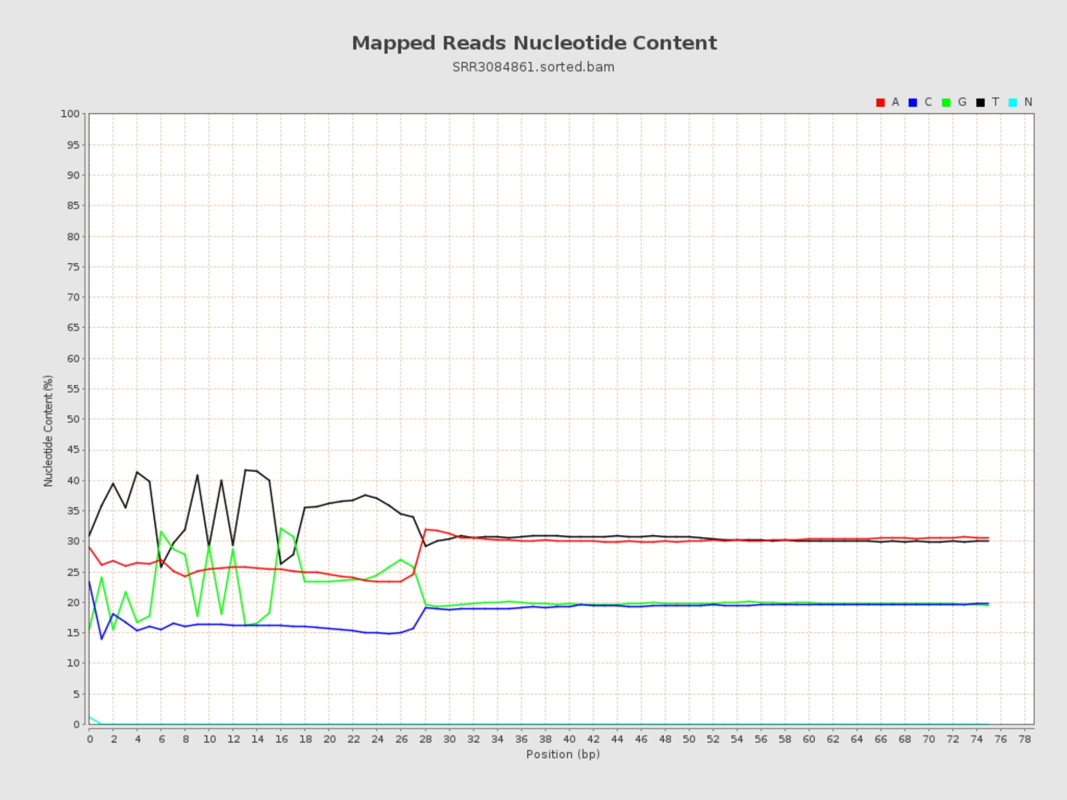
6. Results : Genome Fraction Coverage



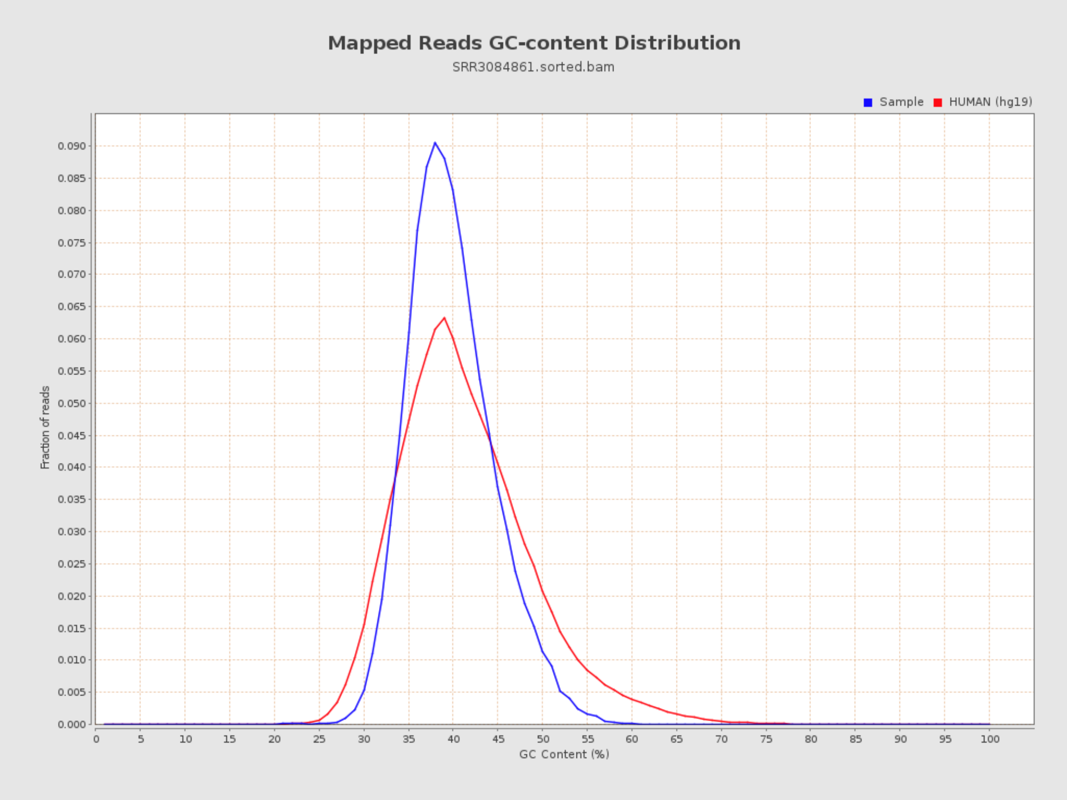
7. Results : Duplication Rate Histogram



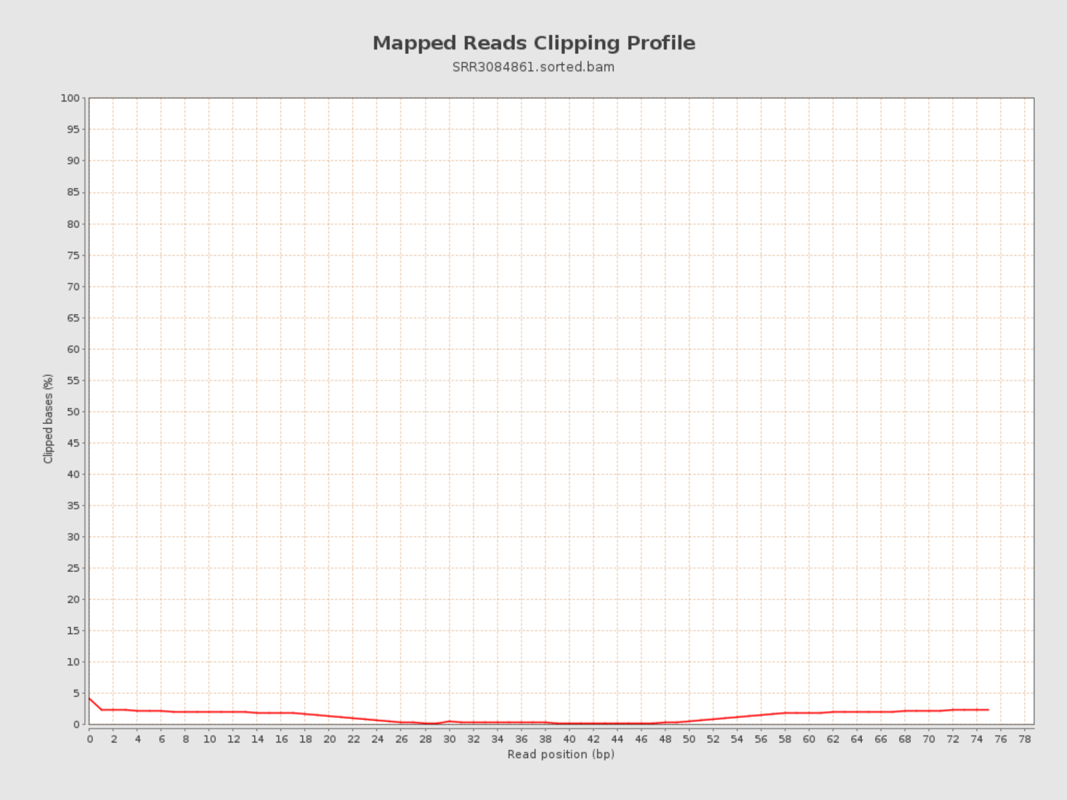
8. Results : Mapped Reads Nucleotide Content



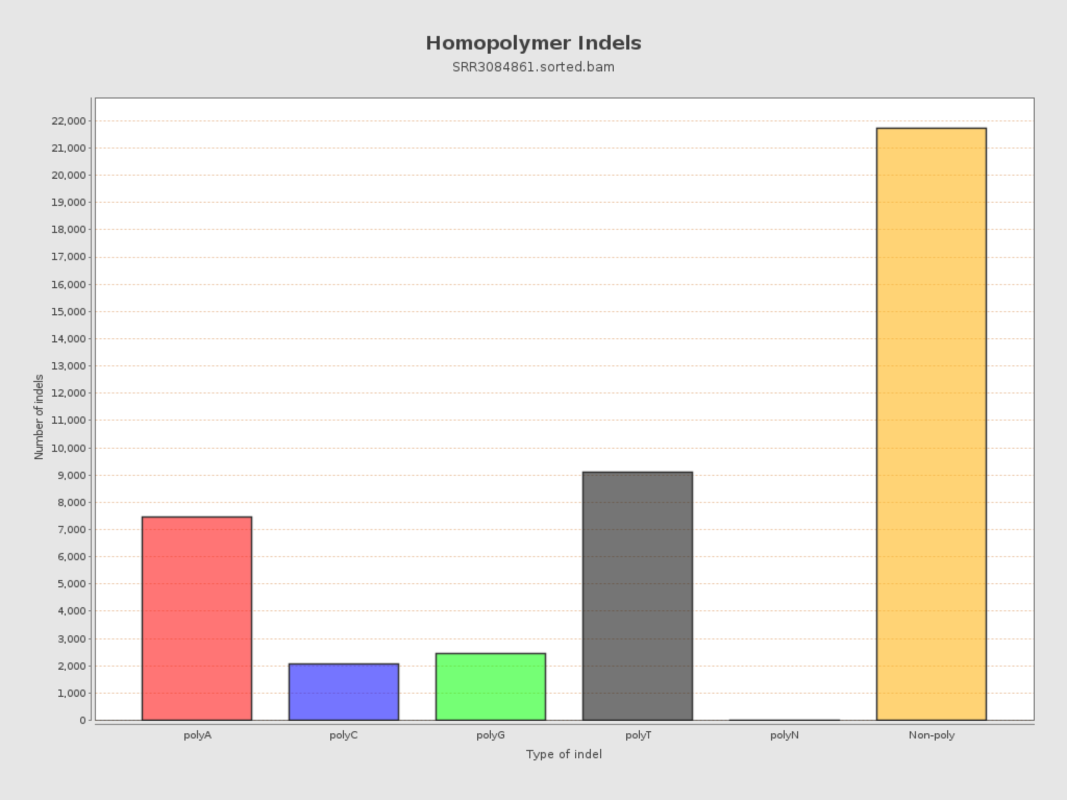
9. Results : Mapped Reads GC-content Distribution



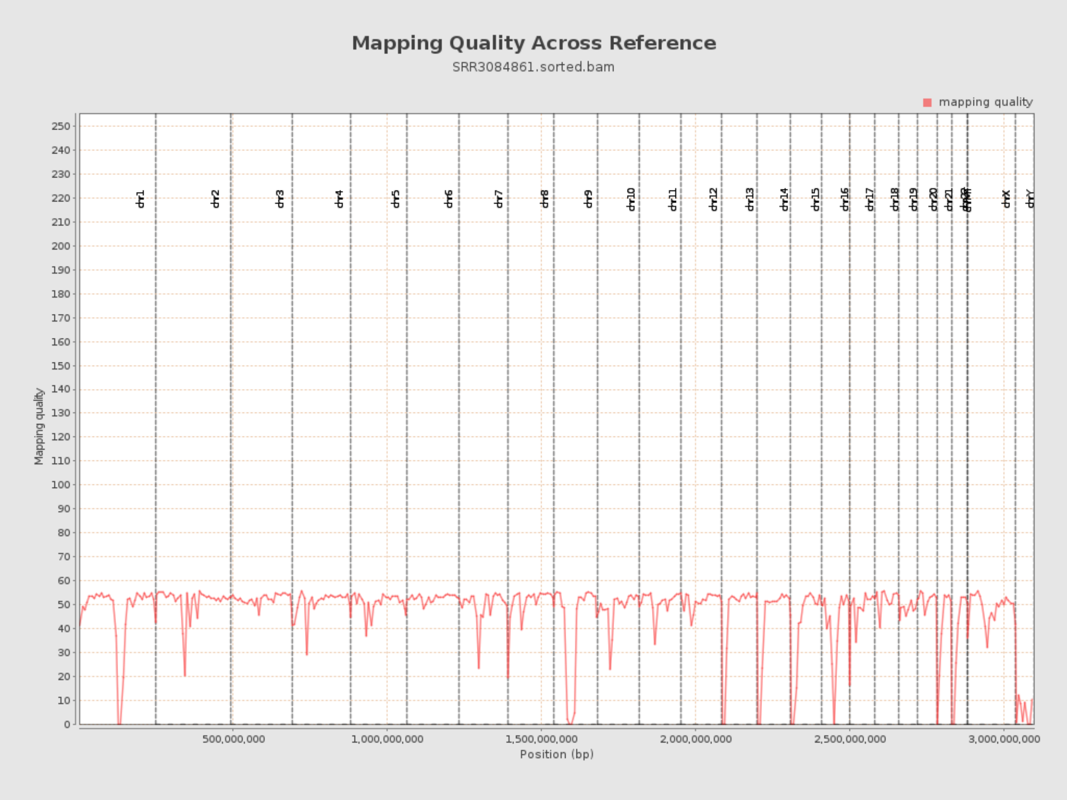
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram