Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 18:11:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084860.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_SRR3084860 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084860.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 18:11:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084860.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,388,337
Mapped reads	2,097,630 / 87.83%
Unmapped reads	290,707 / 12.17%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,117 / 0.76%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	127,956 / 5.36%
Duplication rate	5.3%
Clipped reads	840,546 / 35.19%

2.2. ACGT Content

Number/percentage of A's	40,476,261 / 28.49%
Number/percentage of C's	25,609,926 / 18.02%
Number/percentage of T's	45,966,462 / 32.35%
Number/percentage of G's	30,019,788 / 21.13%
Number/percentage of N's	21,703 / 0.02%
GC Percentage	39.15%

2.3. Coverage

Mean	0.0459

Standard Deviation	0.3516

2.4. Mapping Quality

Mean Mapping Quality	47.69

2.5. Mismatches and indels

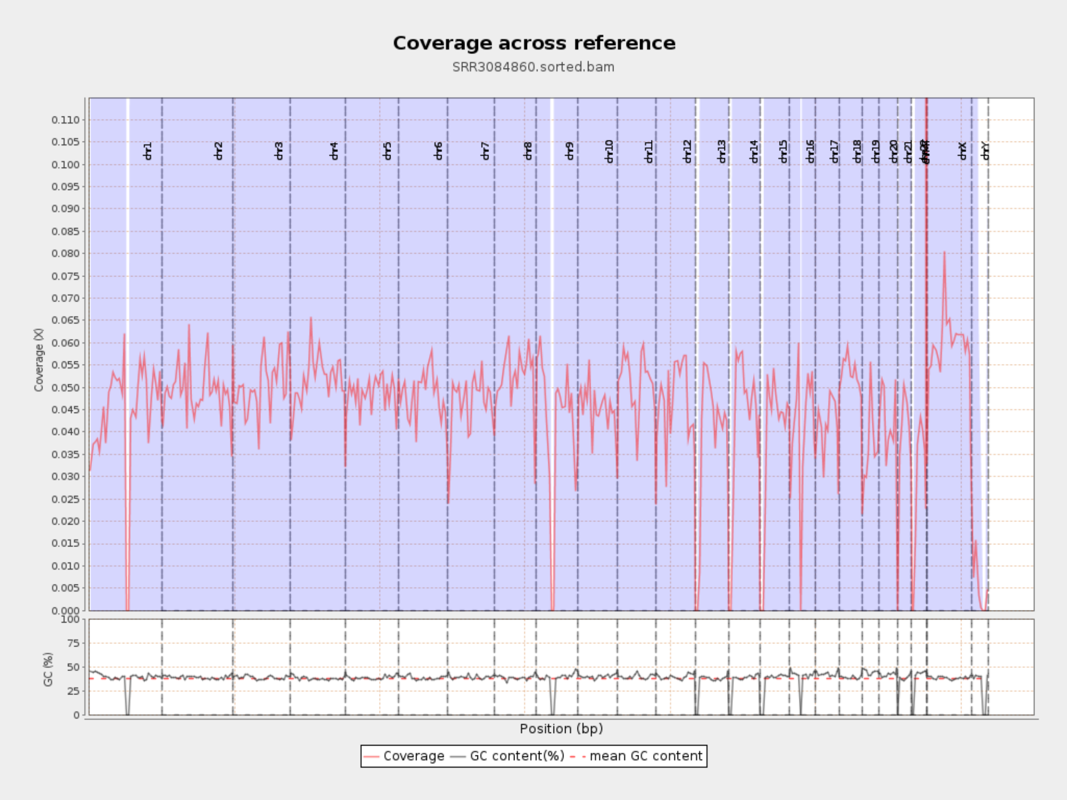
General error rate	0.84%
Mismatches	1,172,739
Insertions	10,946
Mapped reads with at least one insertion	0.52%
Deletions	31,022
Mapped reads with at least one deletion	1.46%
Homopolymer indels	48.83%

2.6. Chromosome stats

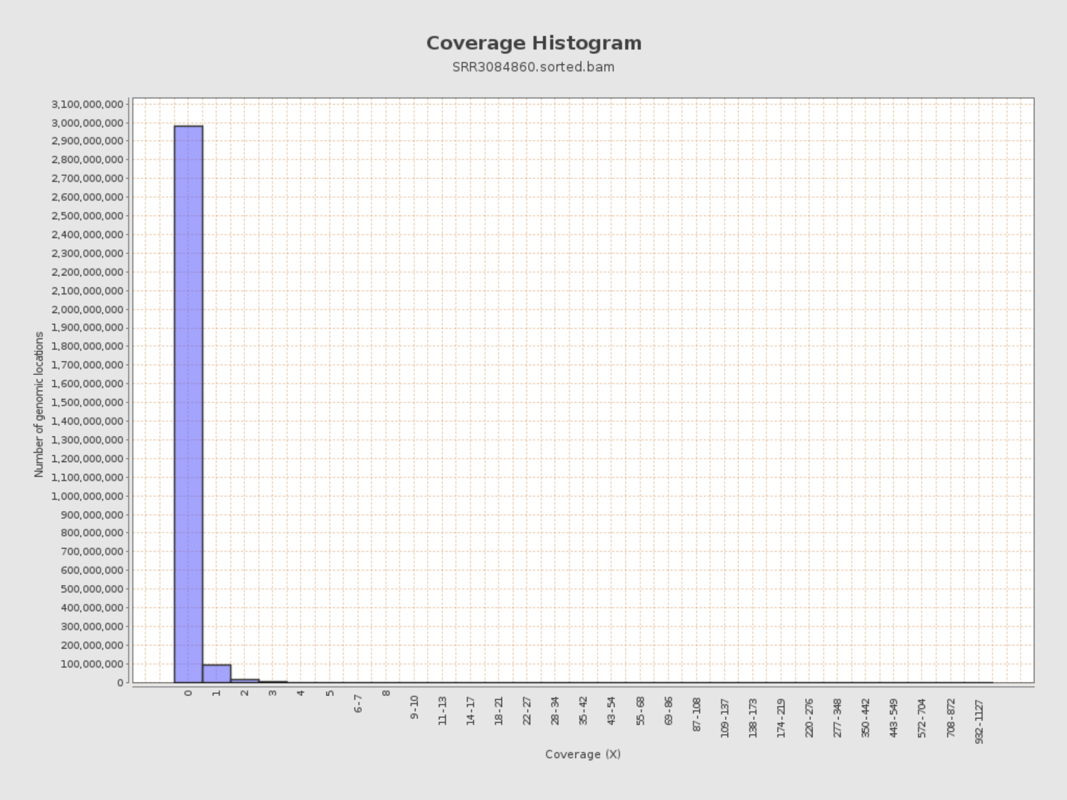
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11023201	0.0442	0.4865
chr2	243199373	11977154	0.0492	0.3427
chr3	198022430	10021816	0.0506	0.2675
chr4	191154276	9924567	0.0519	0.2788
chr5	180915260	8808751	0.0487	0.2641
chr6	171115067	8310568	0.0486	0.2669
chr7	159138663	7443951	0.0468	0.322

chr8	146364022	7663537	0.0524	0.7508
chr9	141213431	5895041	0.0417	0.3286
chr10	135534747	6203748	0.0458	0.3032
chr11	135006516	6872143	0.0509	0.305
chr12	133851895	6322069	0.0472	0.2628
chr13	115169878	4403736	0.0382	0.2321
chr14	107349540	4469427	0.0416	0.2541
chr15	102531392	3938524	0.0384	0.2313
chr16	90354753	3694942	0.0409	0.2551
chr17	81195210	3349521	0.0413	0.2577
chr18	78077248	4176771	0.0535	0.626
chr19	59128983	2198885	0.0372	0.3584
chr20	63025520	2672150	0.0424	0.2475
chr21	48129895	1819636	0.0378	0.2439
chr22	51304566	1378914	0.0269	0.1906
chrMT	16571	37550	2.266	1.8454
chrX	155270560	9215643	0.0594	0.3113
chrY	59373566	325957	0.0055	0.1103

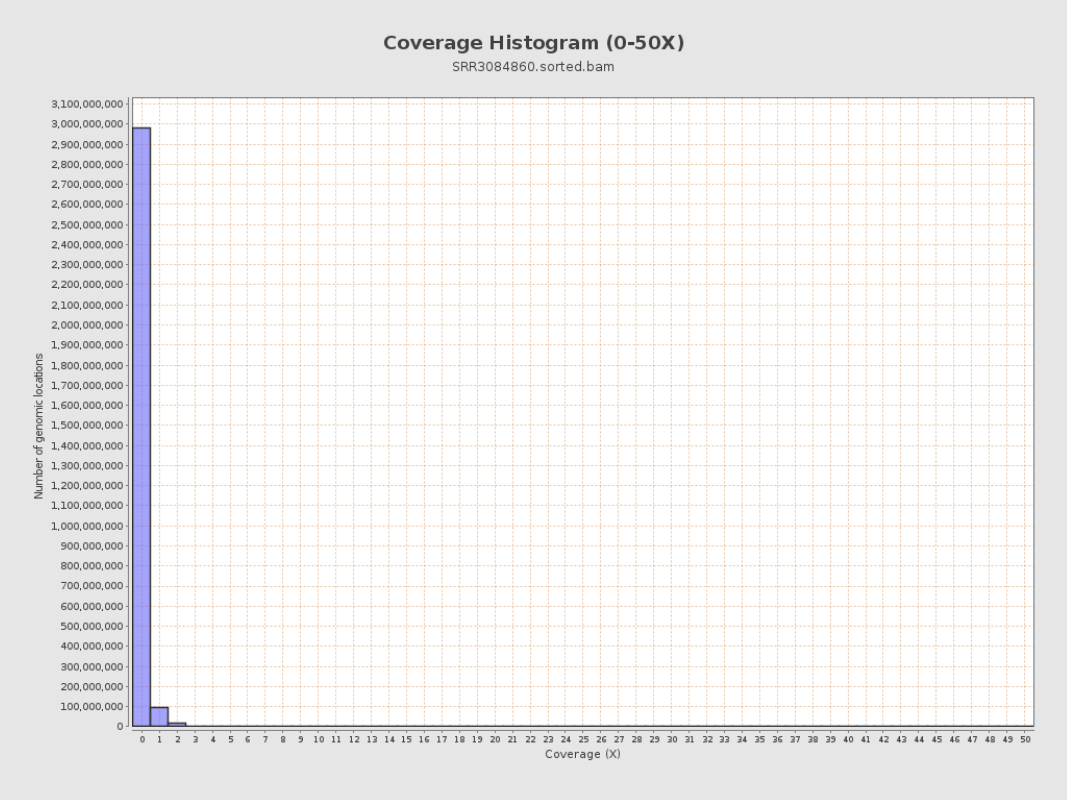
3. Results : Coverage across reference



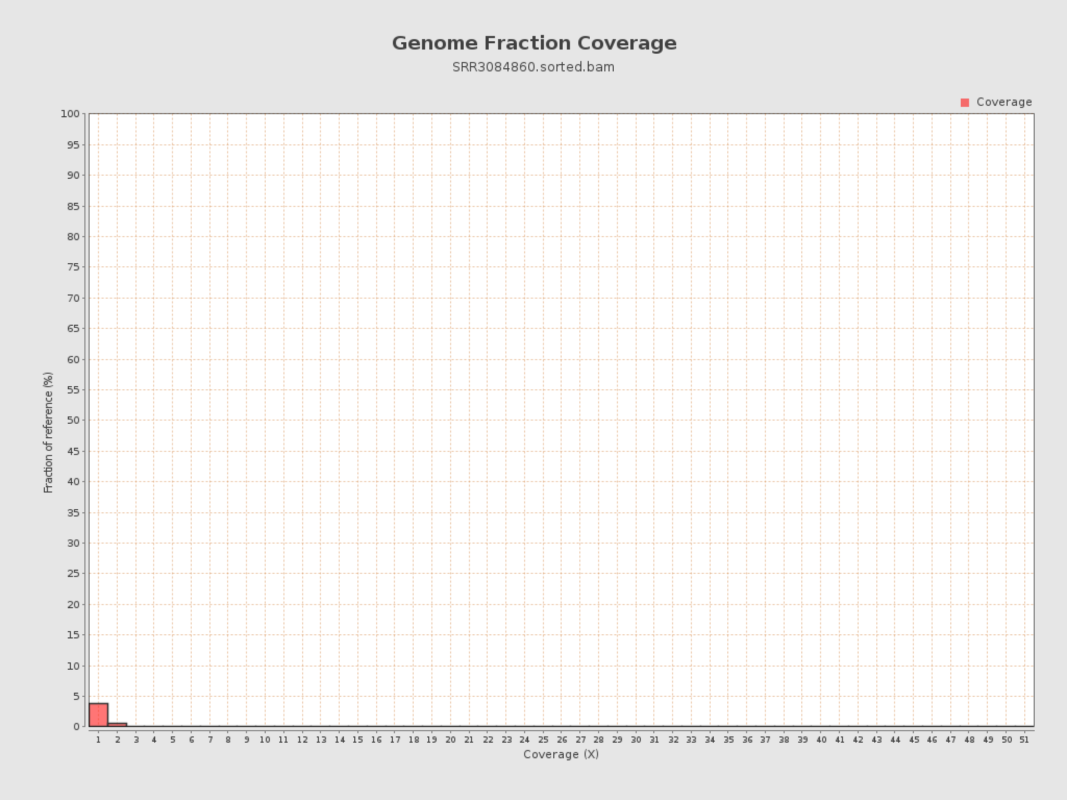
4. Results : Coverage Histogram



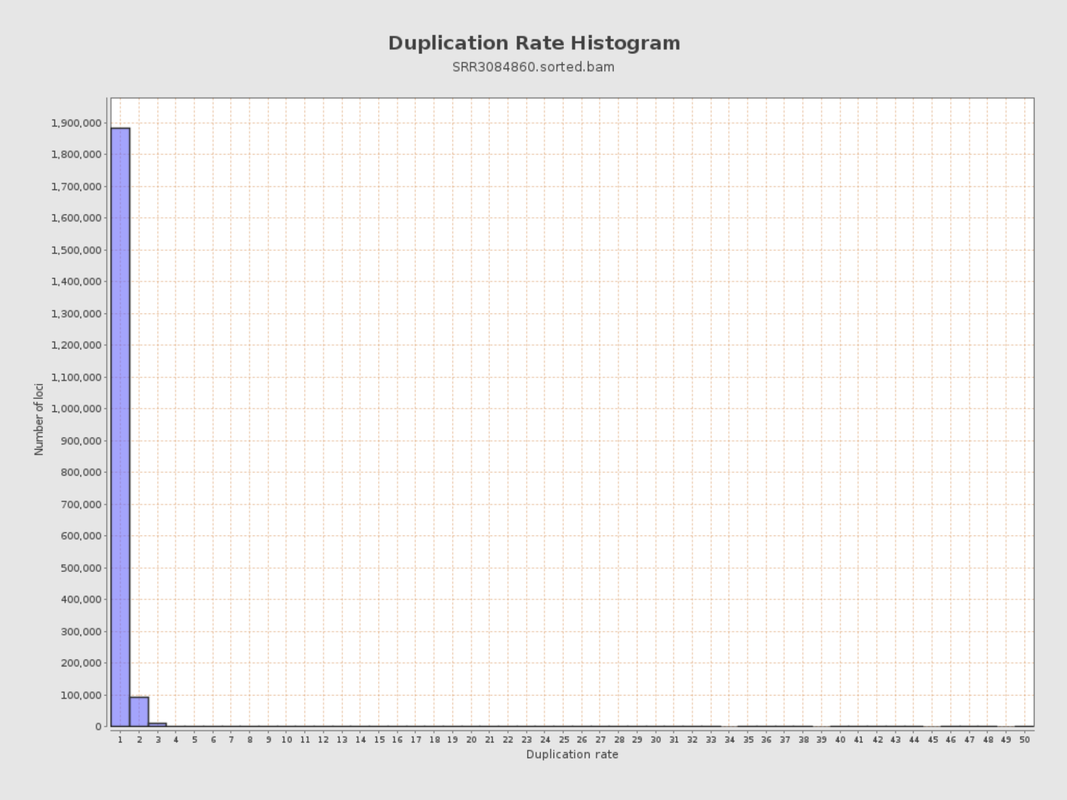
5. Results : Coverage Histogram (0-50X)



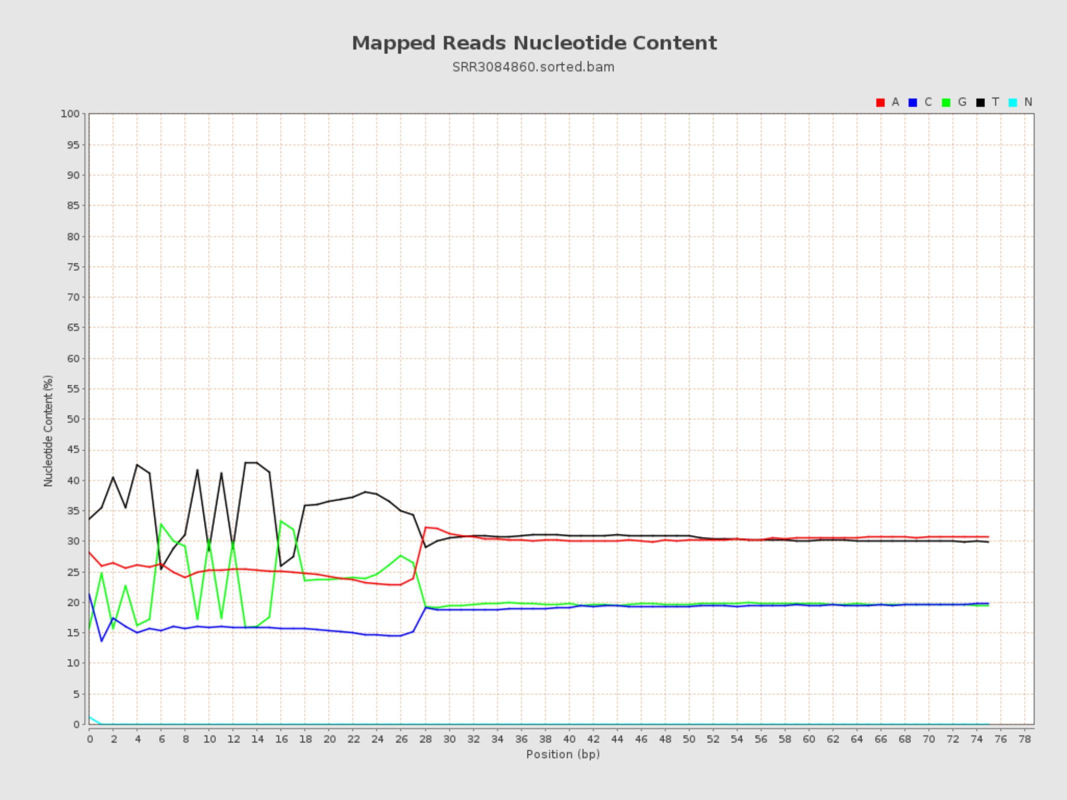
6. Results : Genome Fraction Coverage



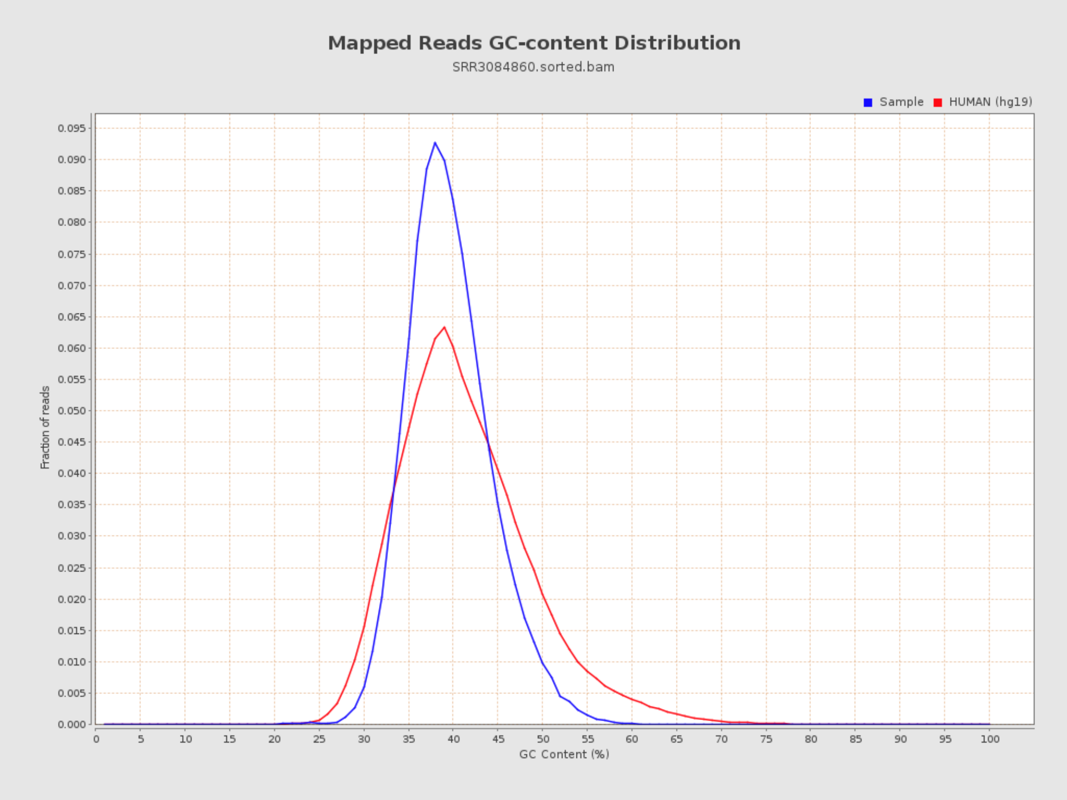
7. Results : Duplication Rate Histogram



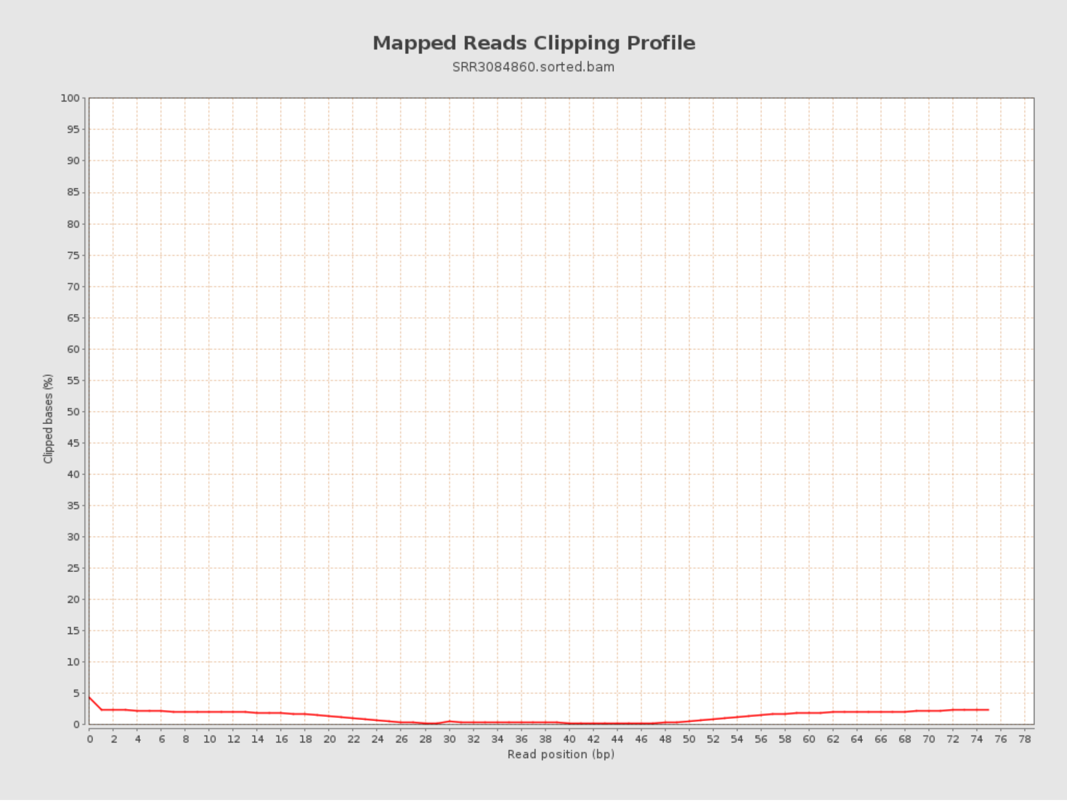
8. Results : Mapped Reads Nucleotide Content



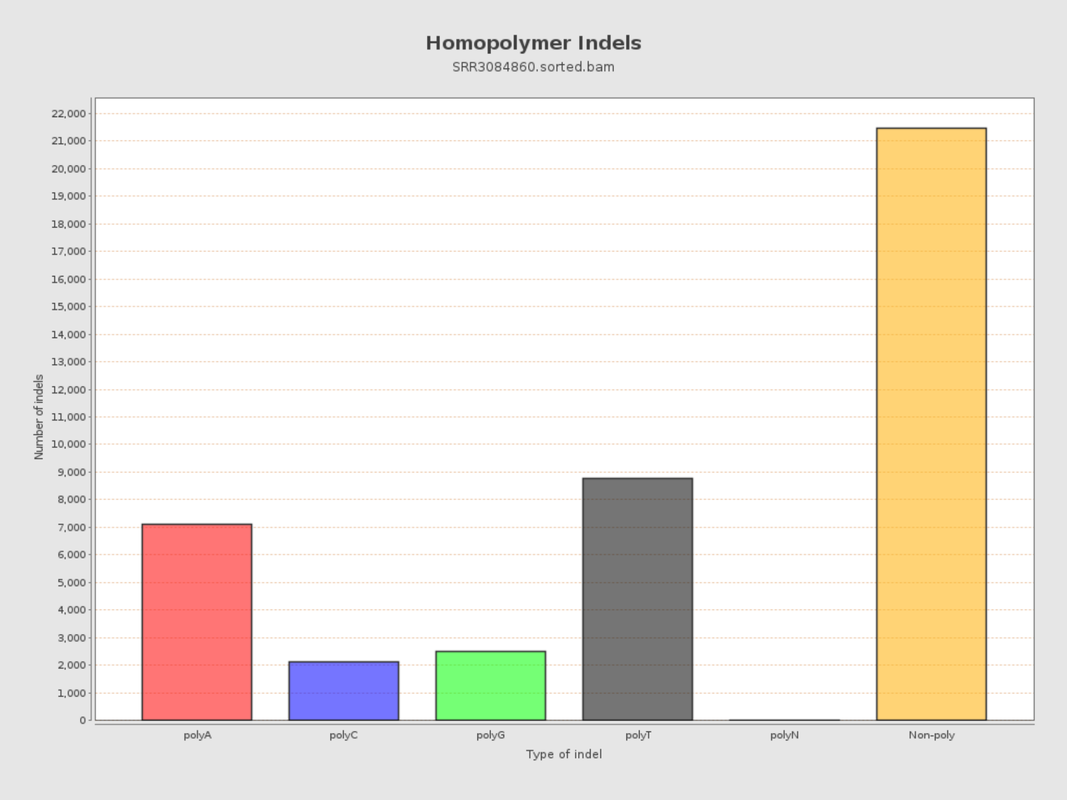
9. Results : Mapped Reads GC-content Distribution



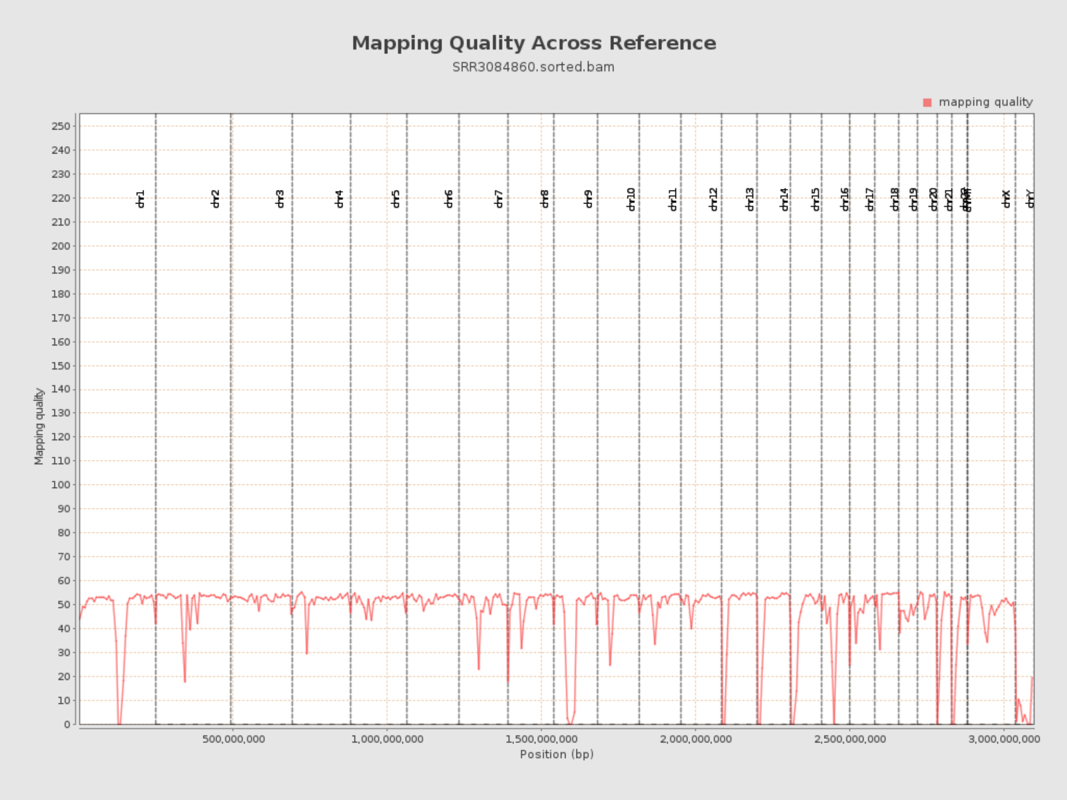
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram