Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 14:59:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082443.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_SRR3082443 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082443.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 14:59:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082443.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,553,991
Mapped reads	2,307,939 / 90.37%
Unmapped reads	246,052 / 9.63%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,889 / 0.74%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	83,381 / 3.26%
Duplication rate	2.69%
Clipped reads	990,419 / 38.78%

2.2. ACGT Content

Number/percentage of A's	43,872,883 / 28.16%
Number/percentage of C's	29,269,774 / 18.79%
Number/percentage of T's	48,335,476 / 31.03%
Number/percentage of G's	34,311,459 / 22.02%
Number/percentage of N's	3,219 / 0%
GC Percentage	40.81%

2.3. Coverage

Mean	0.0503

Standard Deviation	0.4196

2.4. Mapping Quality

Mean Mapping Quality	45.72

2.5. Mismatches and indels

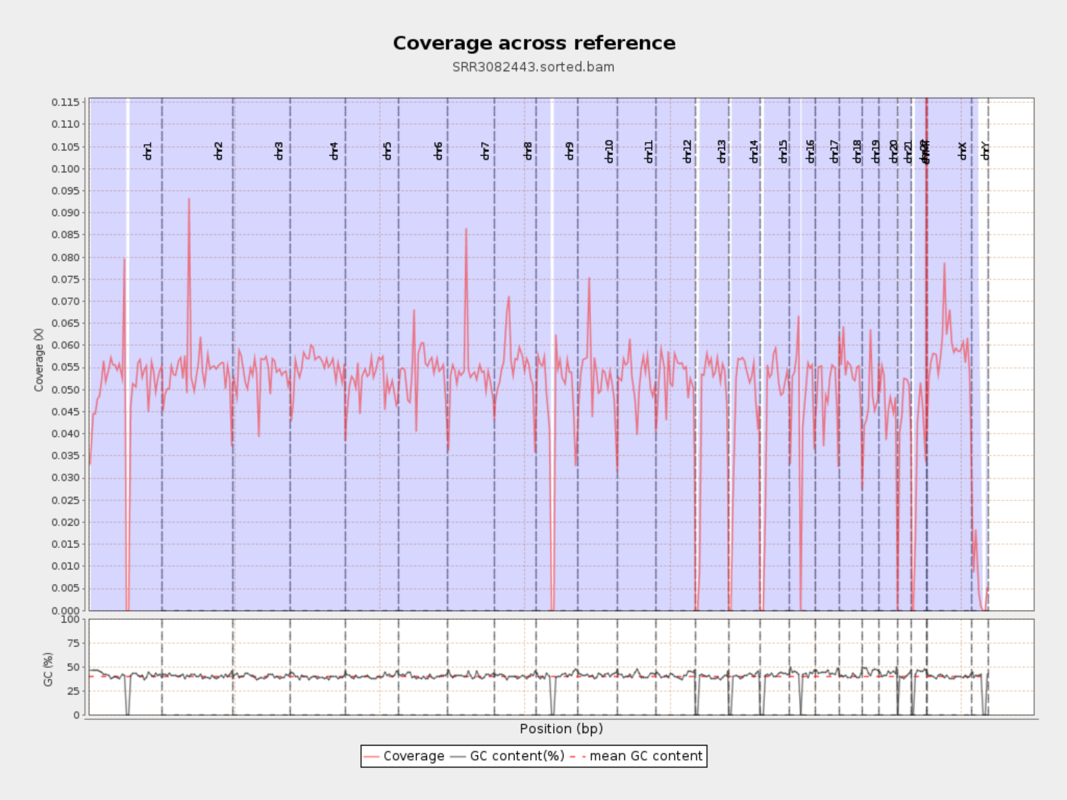
General error rate	0.84%
Mismatches	1,291,550
Insertions	12,507
Mapped reads with at least one insertion	0.54%
Deletions	34,655
Mapped reads with at least one deletion	1.49%
Homopolymer indels	47.05%

2.6. Chromosome stats

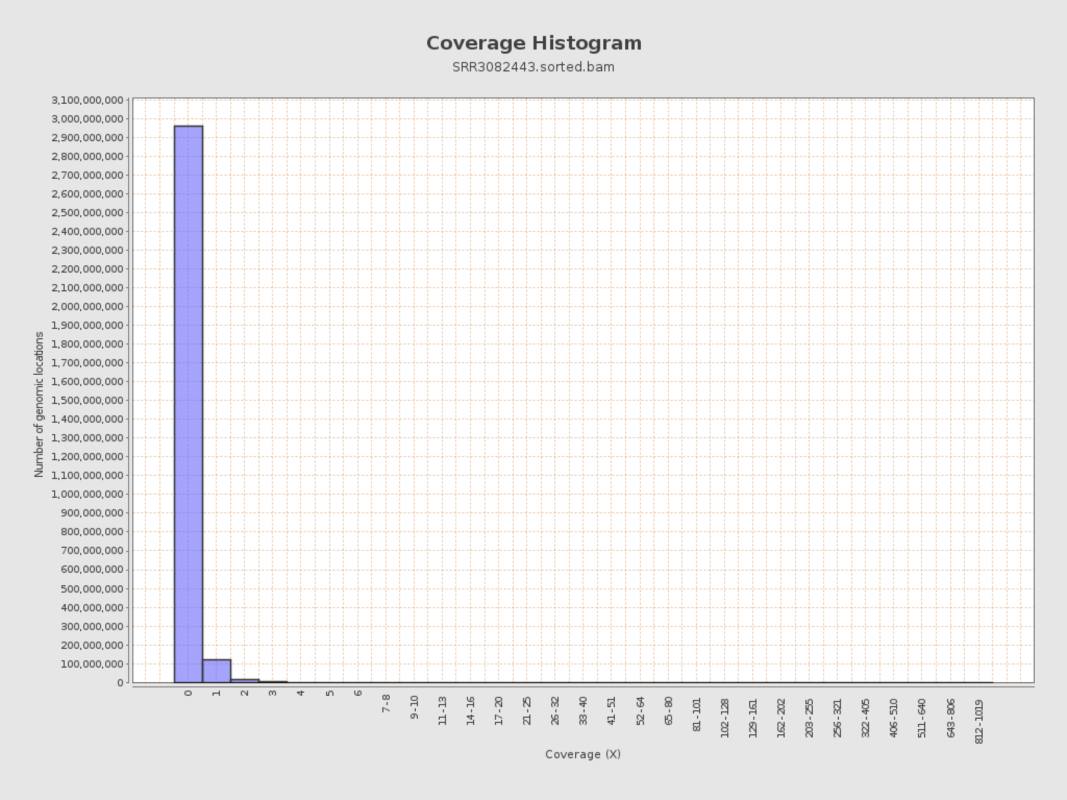
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12313158	0.0494	0.6917
chr2	243199373	13309593	0.0547	0.5392
chr3	198022430	10617287	0.0536	0.2566
chr4	191154276	10553656	0.0552	0.2699
chr5	180915260	9382598	0.0519	0.2542
chr6	171115067	9294561	0.0543	0.3093
chr7	159138663	8642596	0.0543	0.5866

chr8	146364022	8074115	0.0552	0.6816
chr9	141213431	6571643	0.0465	0.3817
chr10	135534747	7207343	0.0532	0.3725
chr11	135006516	7072214	0.0524	0.3617
chr12	133851895	7048675	0.0527	0.2591
chr13	115169878	5177303	0.045	0.2347
chr14	107349540	4758506	0.0443	0.2544
chr15	102531392	4445049	0.0434	0.2397
chr16	90354753	4249441	0.047	0.2769
chr17	81195210	3963077	0.0488	0.2745
chr18	78077248	4299429	0.0551	0.7068
chr19	59128983	2795784	0.0473	0.5207
chr20	63025520	2947047	0.0468	0.2509
chr21	48129895	2047791	0.0425	0.2456
chr22	51304566	1570003	0.0306	0.193
chrMT	16571	7897	0.4766	0.7645
chrX	155270560	9119649	0.0587	0.301
chrY	59373566	380389	0.0064	0.1307

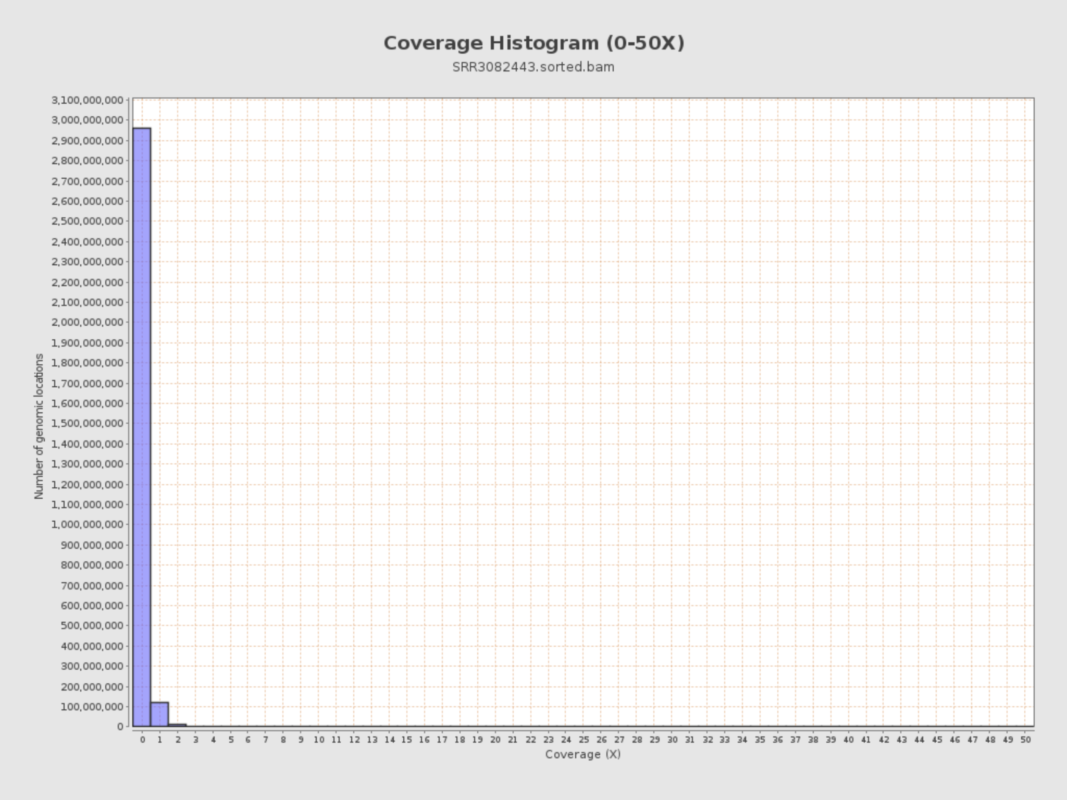
3. Results : Coverage across reference



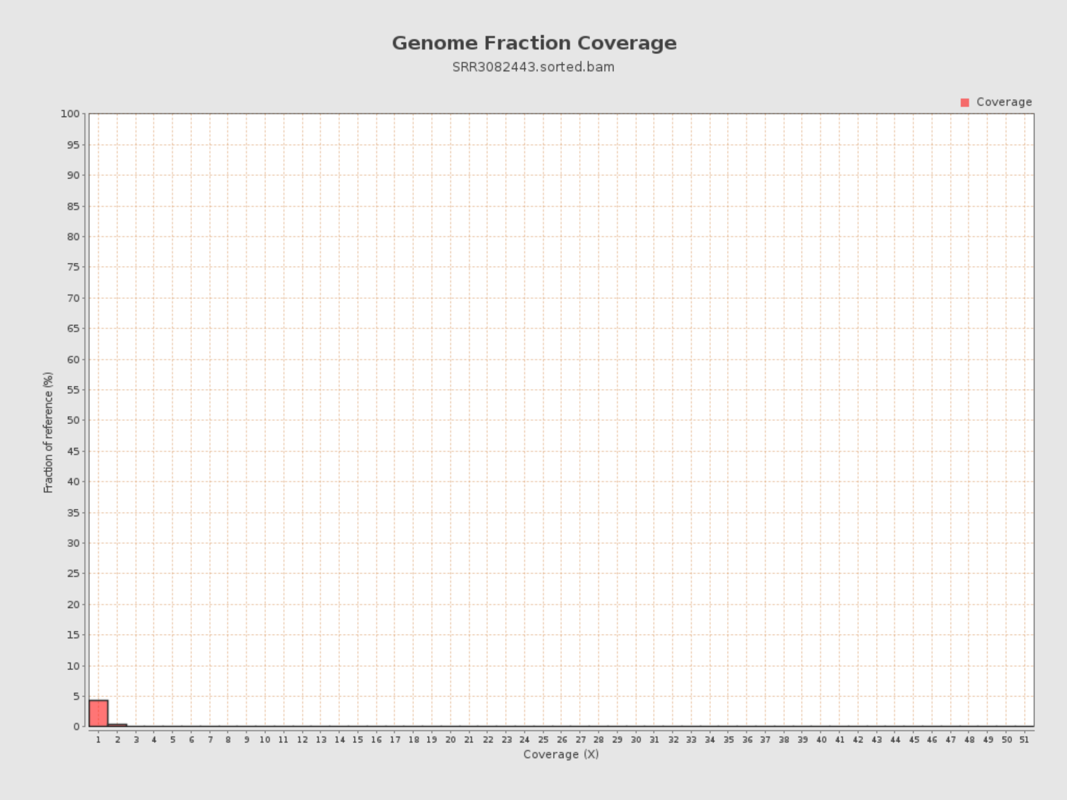
4. Results : Coverage Histogram



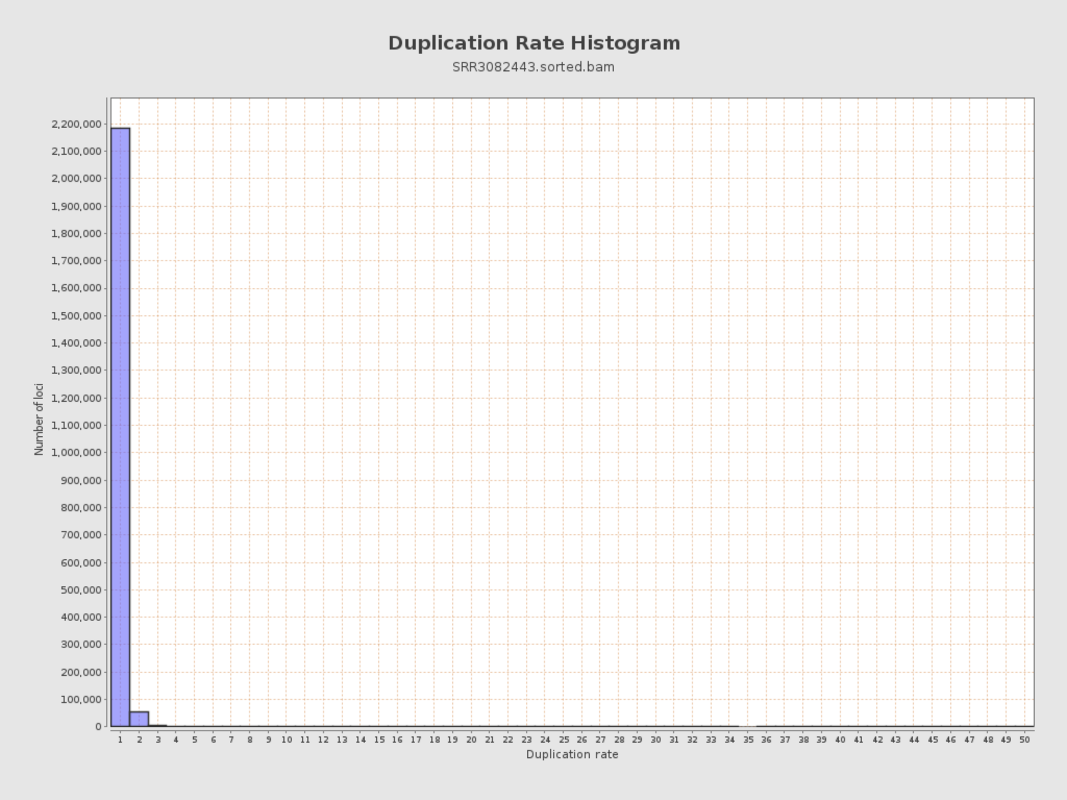
5. Results : Coverage Histogram (0-50X)



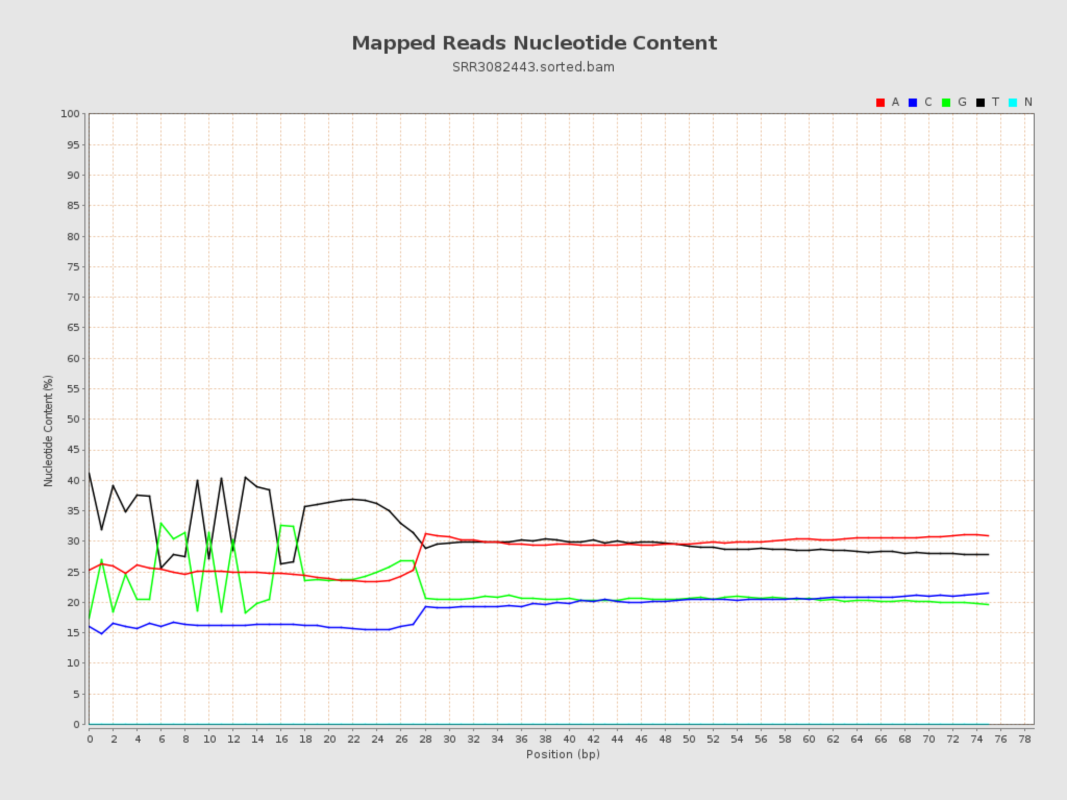
6. Results : Genome Fraction Coverage



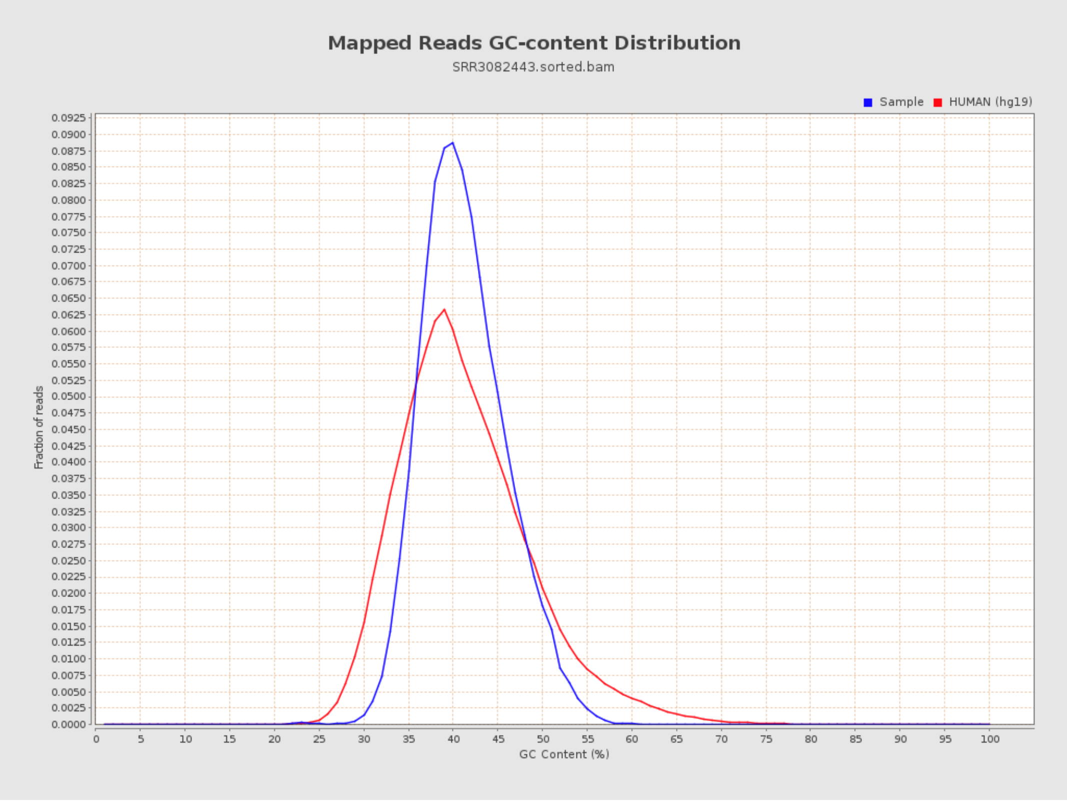
7. Results : Duplication Rate Histogram



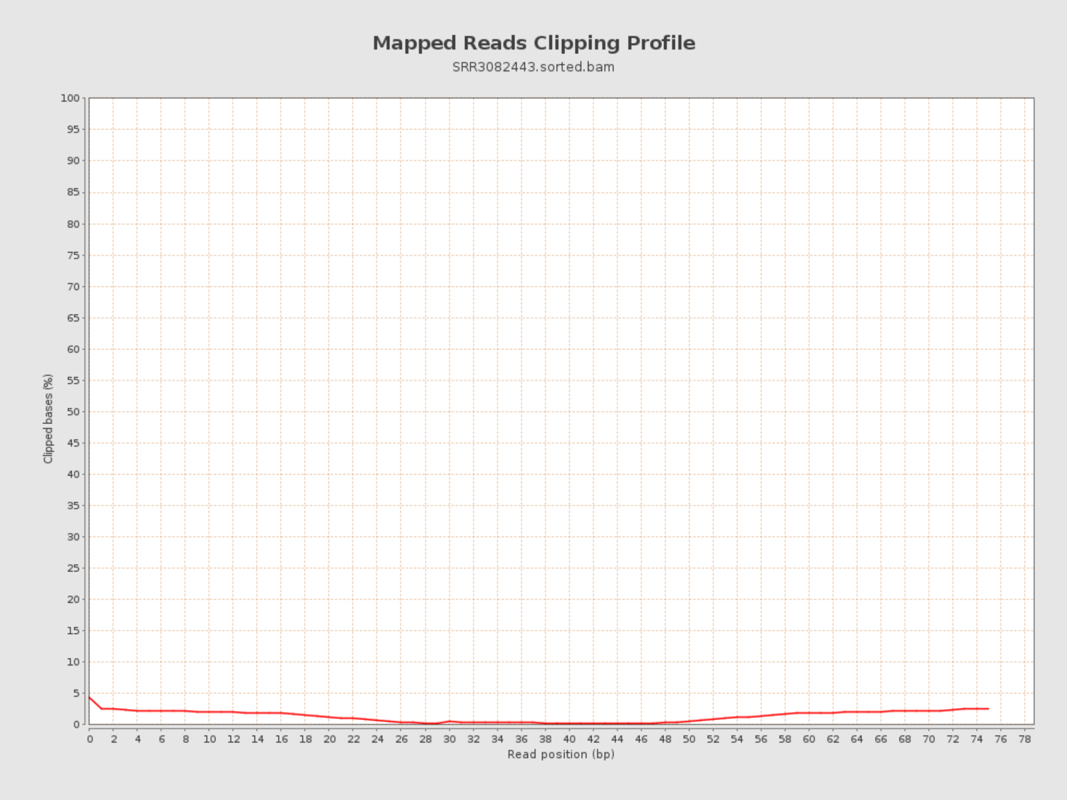
8. Results : Mapped Reads Nucleotide Content



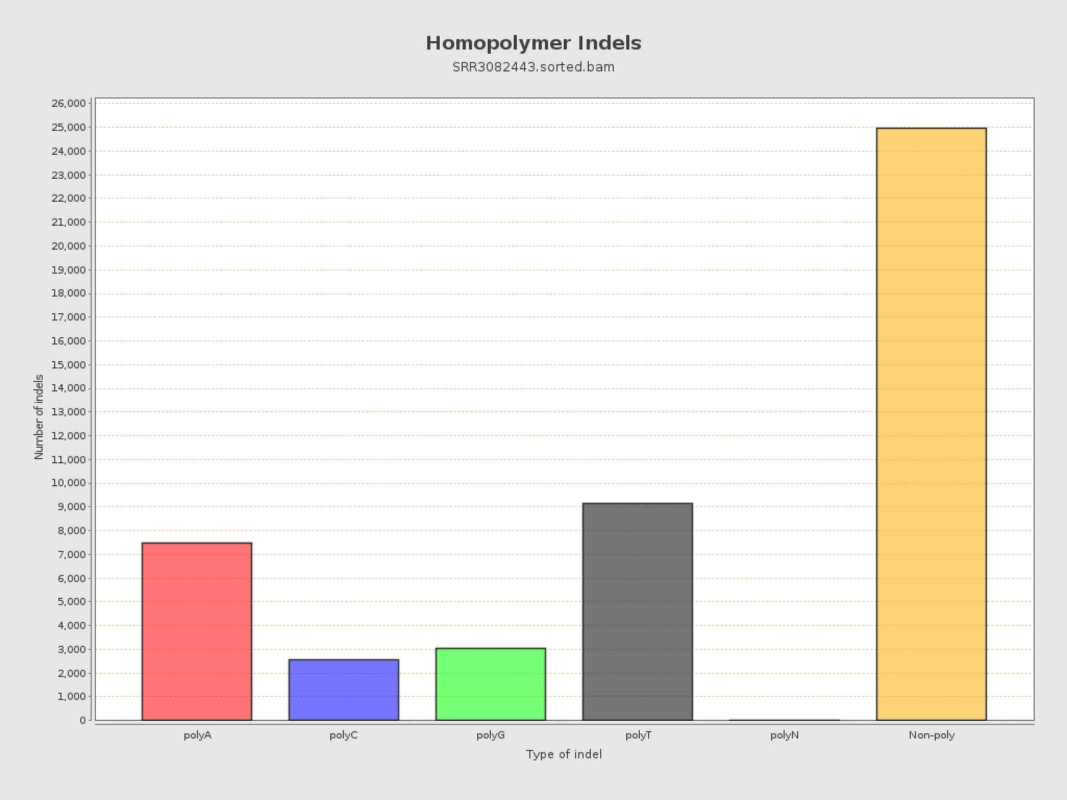
9. Results : Mapped Reads GC-content Distribution



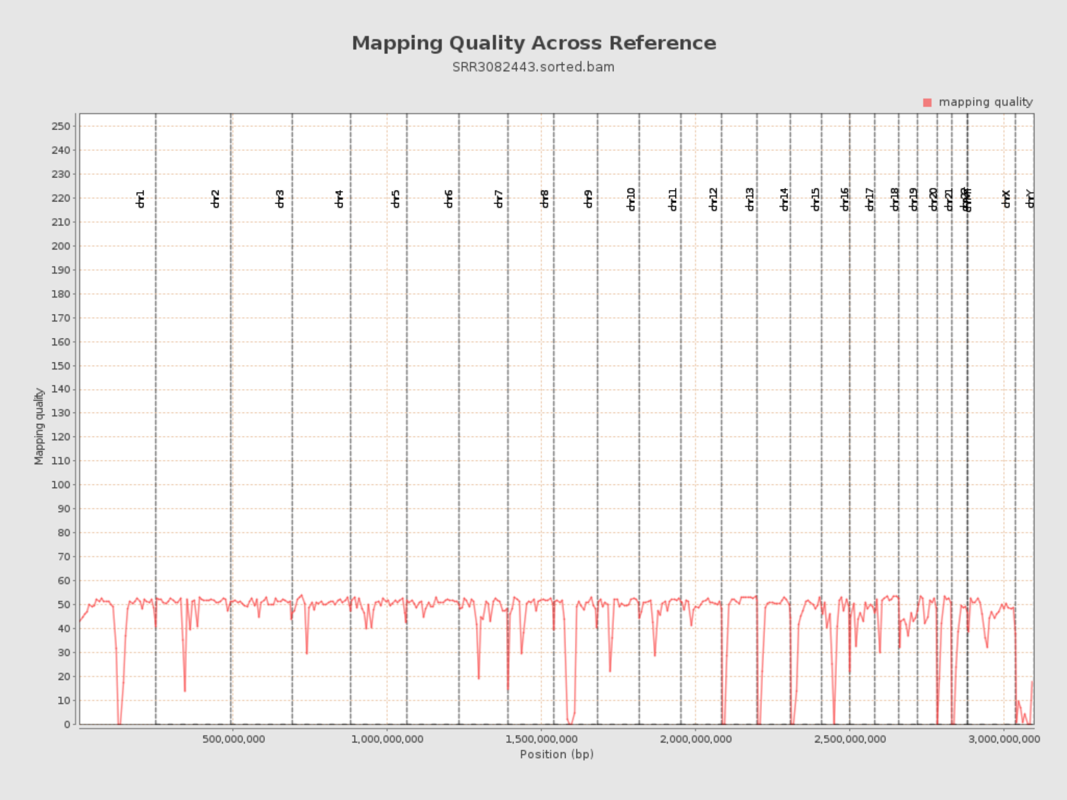
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram