Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 14:41:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082426.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_SRR3082426 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082426.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 14:41:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082426.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,759,095
Mapped reads	2,454,728 / 88.97%
Unmapped reads	304,367 / 11.03%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,203 / 0.7%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	100,102 / 3.63%
Duplication rate	2.95%
Clipped reads	1,091,926 / 39.58%

2.2. ACGT Content

Number/percentage of A's	46,174,705 / 28.08%
Number/percentage of C's	30,475,959 / 18.53%
Number/percentage of T's	51,383,262 / 31.24%
Number/percentage of G's	36,419,497 / 22.15%
Number/percentage of N's	3,204 / 0%
GC Percentage	40.68%

2.3. Coverage

Mean	0.0531

Standard Deviation	0.4832

2.4. Mapping Quality

Mean Mapping Quality	45.36

2.5. Mismatches and indels

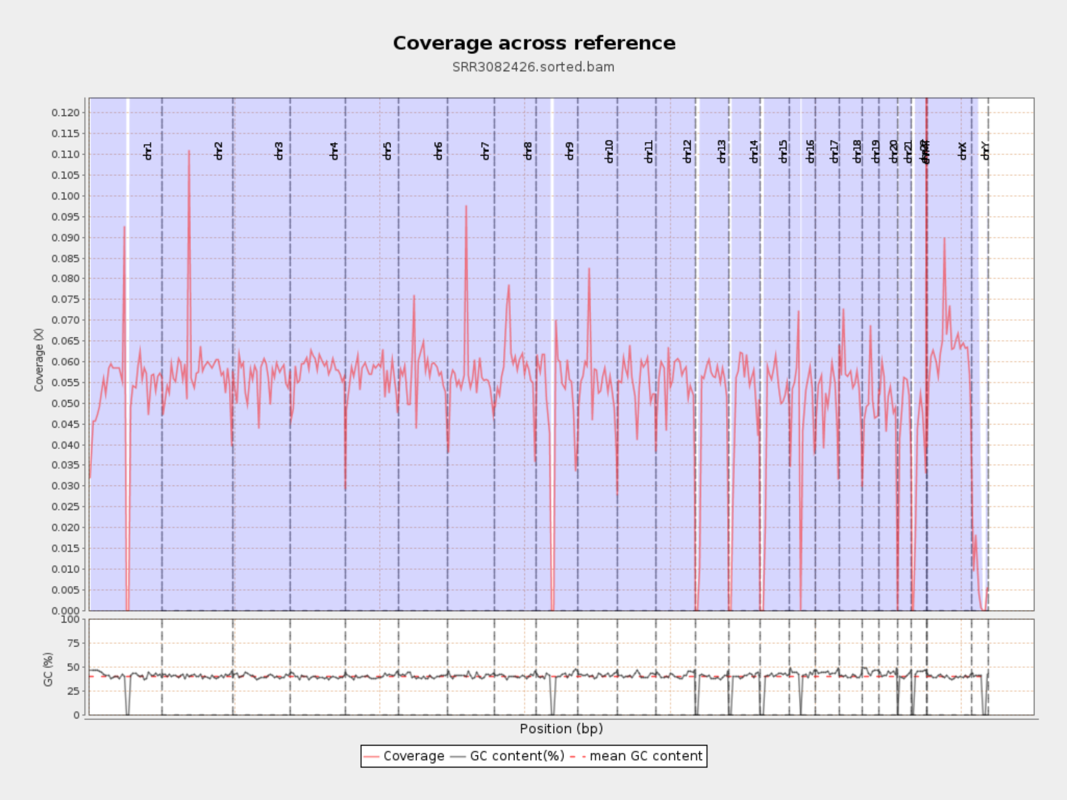
General error rate	0.86%
Mismatches	1,384,862
Insertions	13,480
Mapped reads with at least one insertion	0.55%
Deletions	36,384
Mapped reads with at least one deletion	1.47%
Homopolymer indels	47.12%

2.6. Chromosome stats

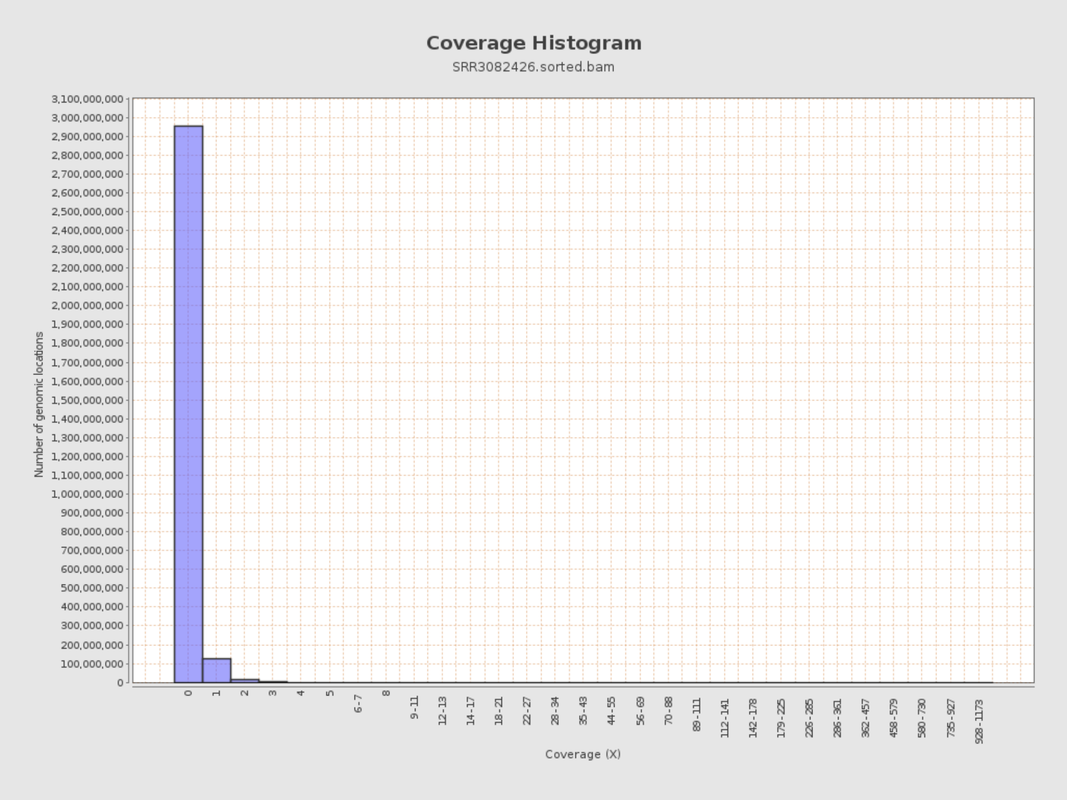
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12929553	0.0519	0.8574
chr2	243199373	14169546	0.0583	0.6231
chr3	198022430	11139318	0.0563	0.2655
chr4	191154276	11085466	0.058	0.2778
chr5	180915260	10276139	0.0568	0.2699
chr6	171115067	9813263	0.0573	0.3438
chr7	159138663	9086536	0.0571	0.6652

chr8	146364022	8549204	0.0584	0.7692
chr9	141213431	6960700	0.0493	0.4485
chr10	135534747	7544384	0.0557	0.4218
chr11	135006516	7430725	0.055	0.3935
chr12	133851895	7434372	0.0555	0.2701
chr13	115169878	5425940	0.0471	0.2417
chr14	107349540	5038527	0.0469	0.2671
chr15	102531392	4576114	0.0446	0.2503
chr16	90354753	4381724	0.0485	0.29
chr17	81195210	4067500	0.0501	0.2856
chr18	78077248	4470324	0.0573	0.8425
chr19	59128983	2967610	0.0502	0.6438
chr20	63025520	3184623	0.0505	0.2635
chr21	48129895	2146555	0.0446	0.2571
chr22	51304566	1615777	0.0315	0.1968
chrMT	16571	4179	0.2522	0.5378
chrX	155270560	9814594	0.0632	0.3319
chrY	59373566	402789	0.0068	0.1294

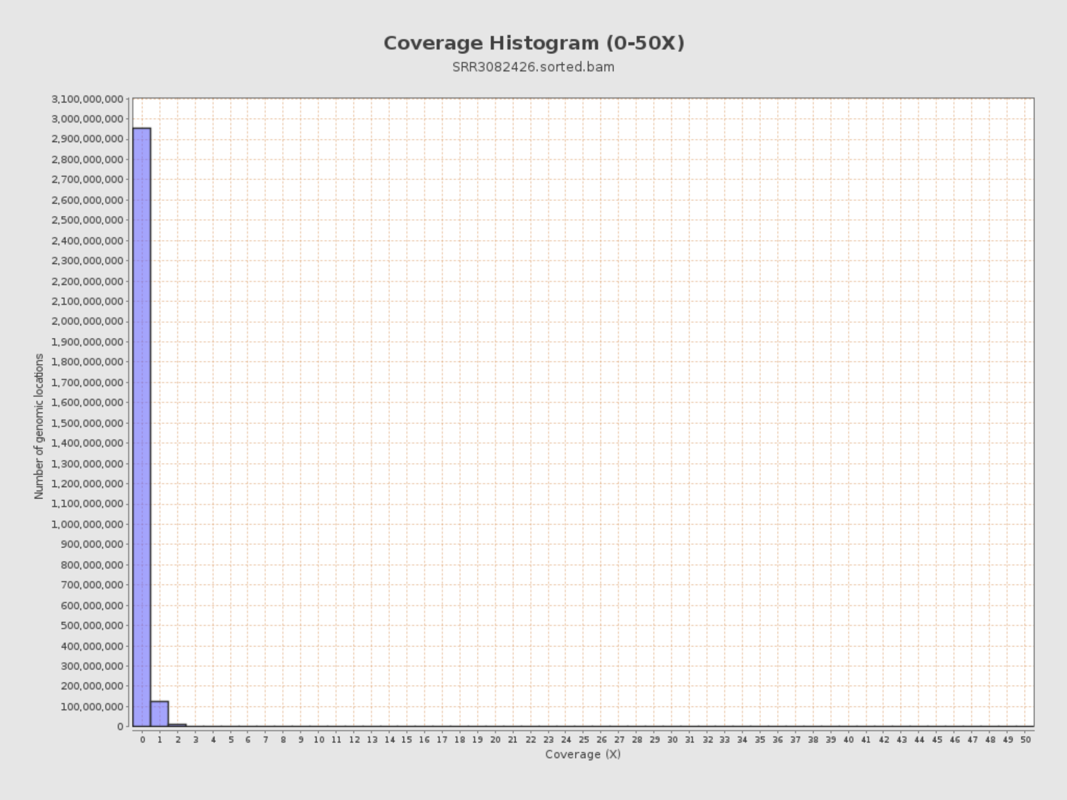
3. Results : Coverage across reference



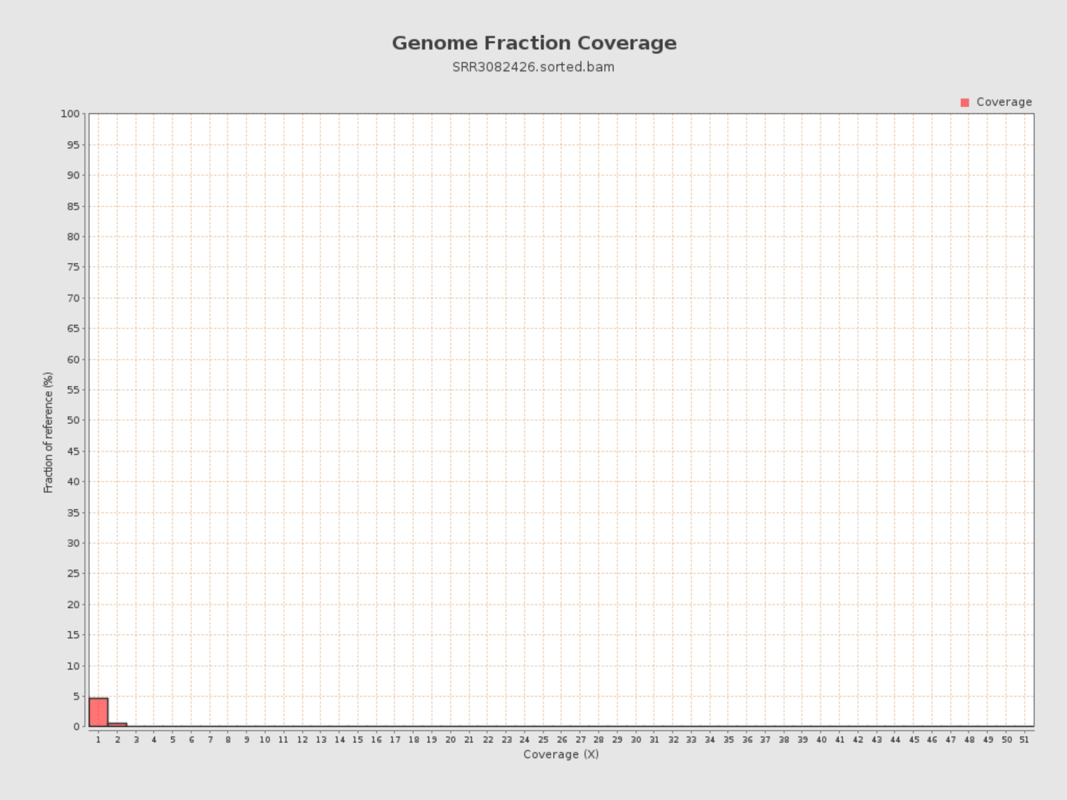
4. Results : Coverage Histogram



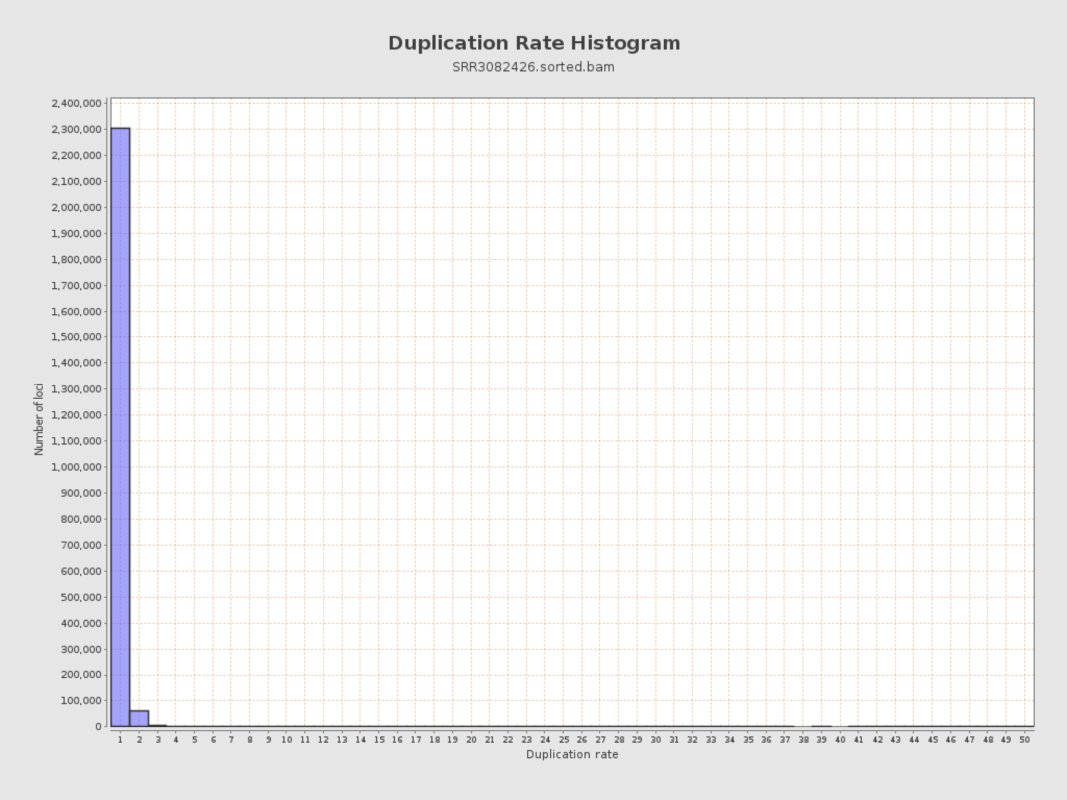
5. Results : Coverage Histogram (0-50X)



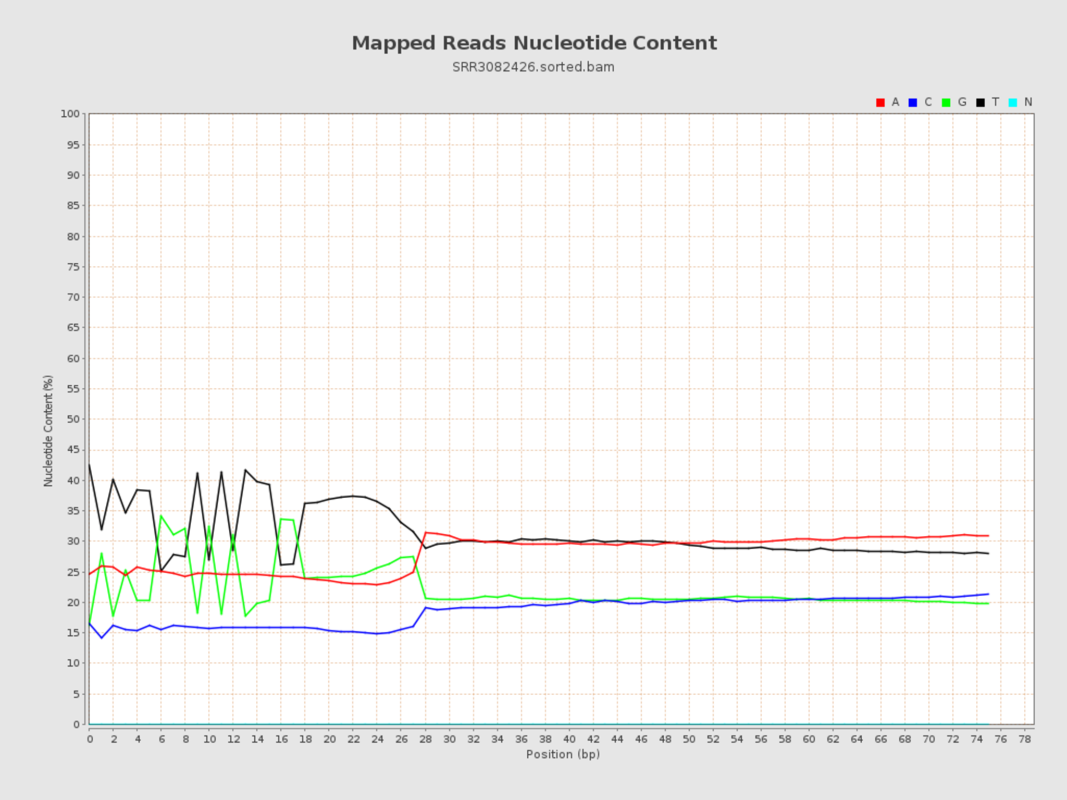
6. Results : Genome Fraction Coverage



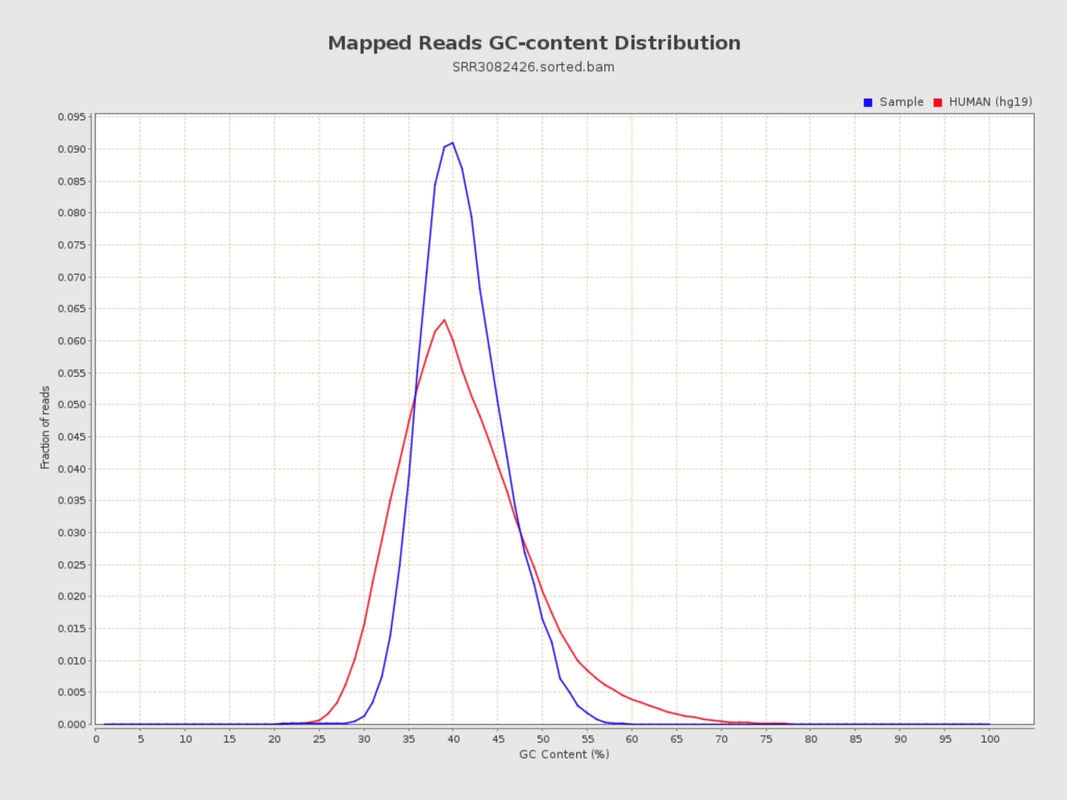
7. Results : Duplication Rate Histogram



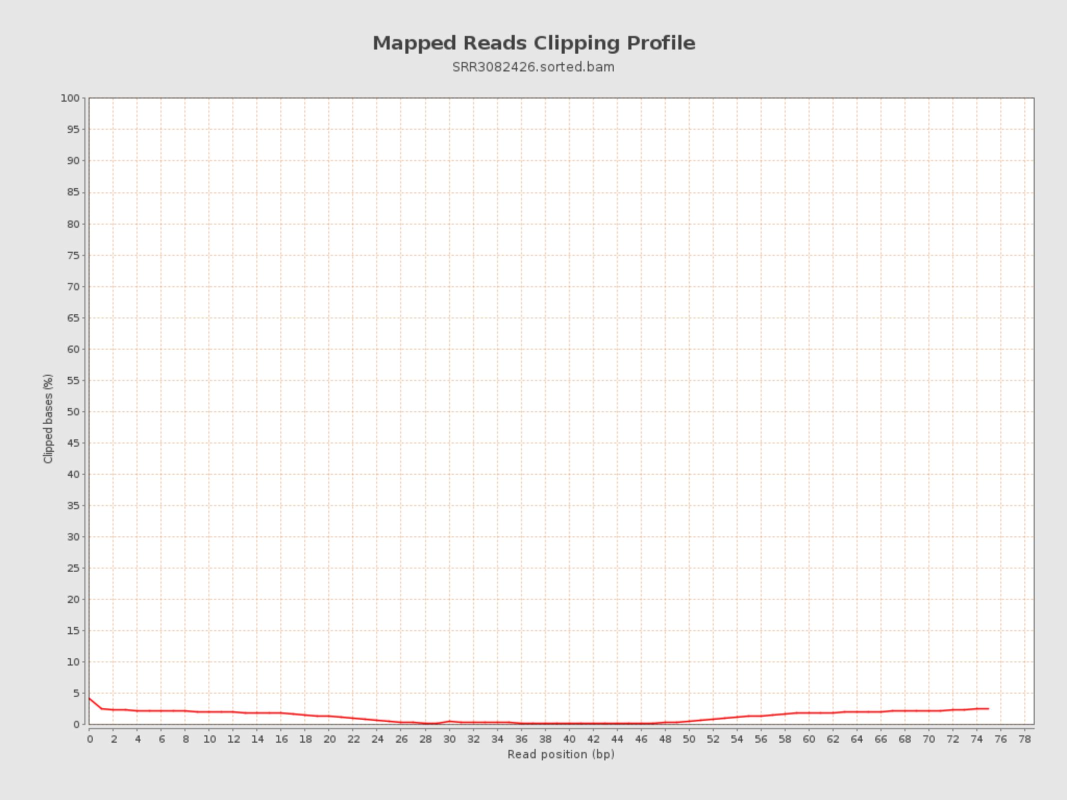
8. Results : Mapped Reads Nucleotide Content



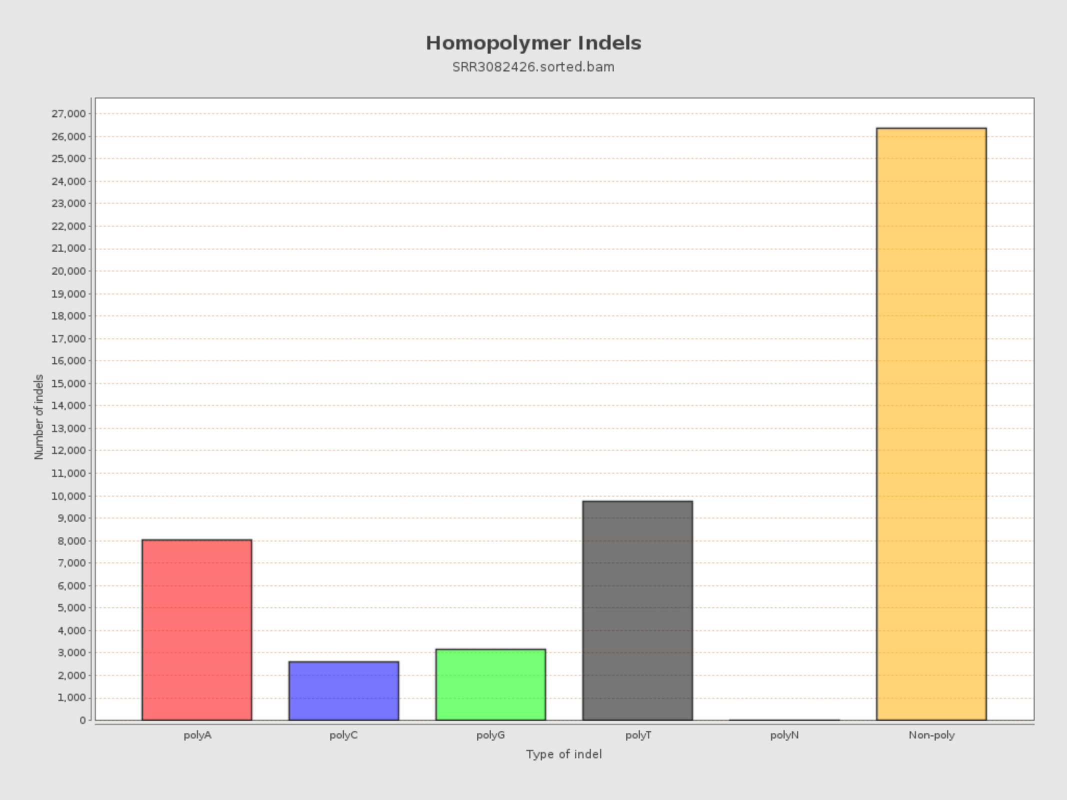
9. Results : Mapped Reads GC-content Distribution



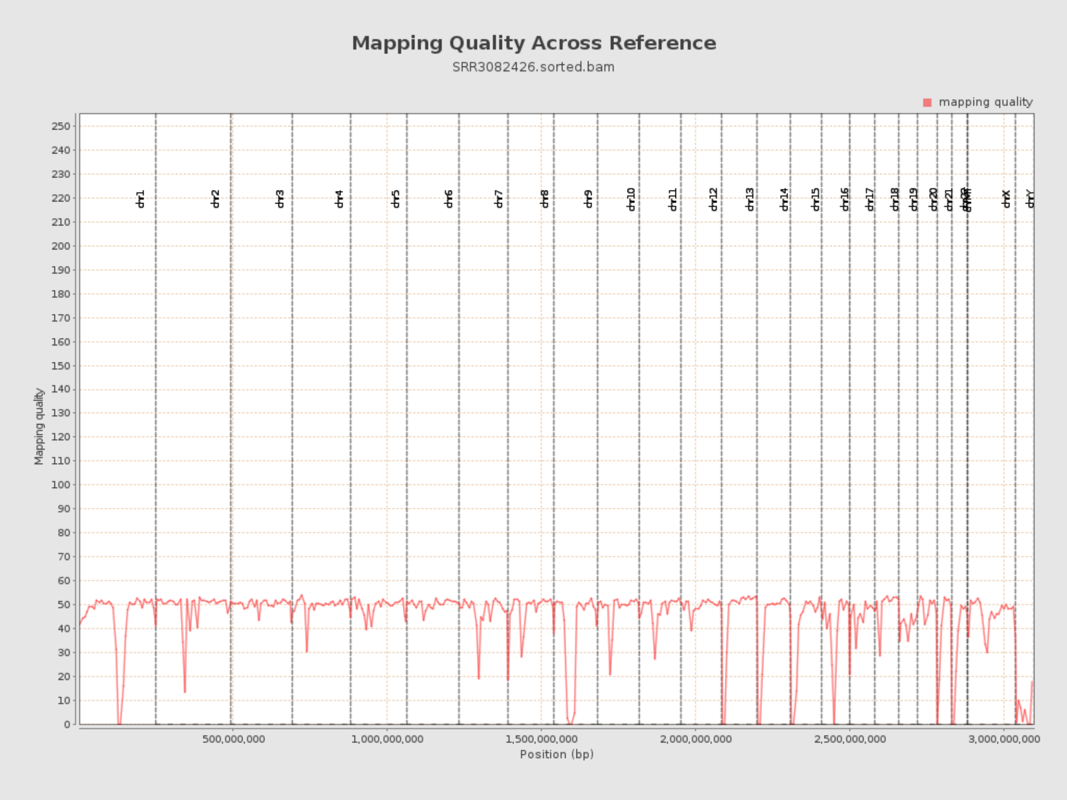
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram