Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 22:55:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524326.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_SRR10524326 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524326.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 22:55:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524326.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,949,006
Mapped reads	3,632,076 / 91.97%
Unmapped reads	316,930 / 8.03%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,723 / 0.42%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	187,327 / 4.74%
Duplication rate	3.65%
Clipped reads	3,641,777 / 92.22%

2.2. ACGT Content

Number/percentage of A's	49,396,991 / 23.37%
Number/percentage of C's	40,465,605 / 19.15%
Number/percentage of T's	67,071,457 / 31.73%
Number/percentage of G's	54,399,507 / 25.74%
Number/percentage of N's	29,233 / 0.01%
GC Percentage	44.88%

2.3. Coverage

Mean	0.0683

Standard Deviation	0.5531

2.4. Mapping Quality

Mean Mapping Quality	43.73

2.5. Mismatches and indels

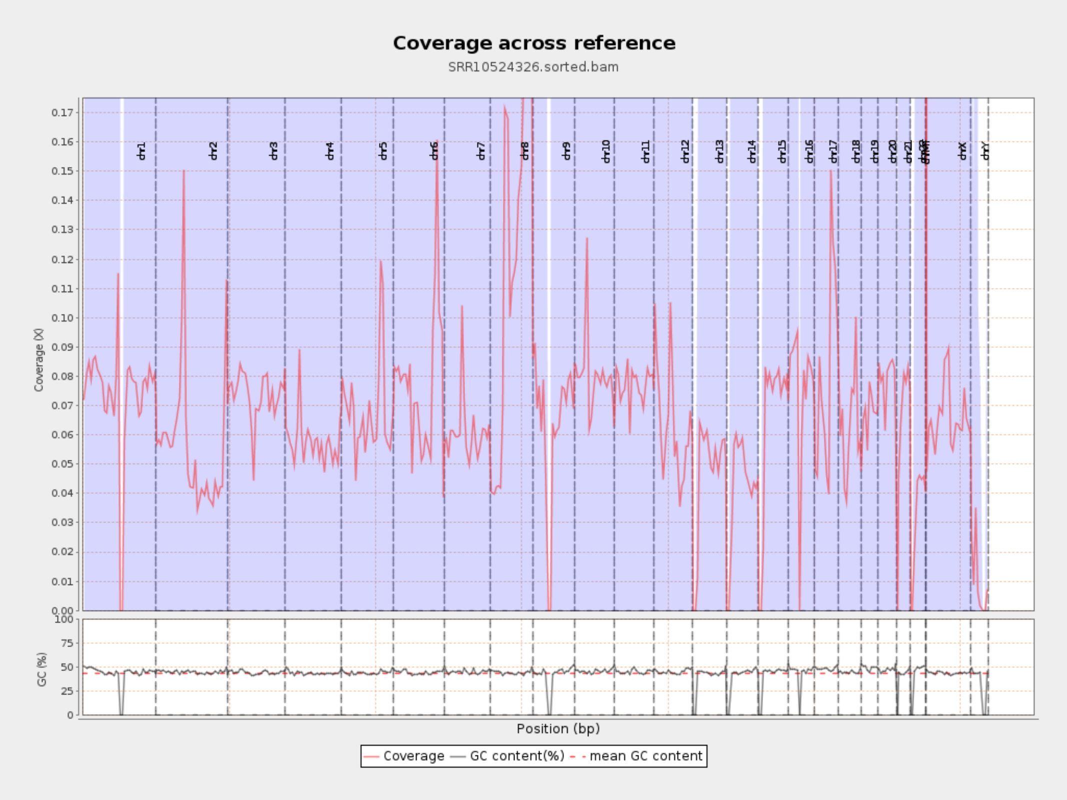
General error rate	0.51%
Mismatches	1,048,487
Insertions	12,927
Mapped reads with at least one insertion	0.35%
Deletions	34,013
Mapped reads with at least one deletion	0.93%
Homopolymer indels	42.88%

2.6. Chromosome stats

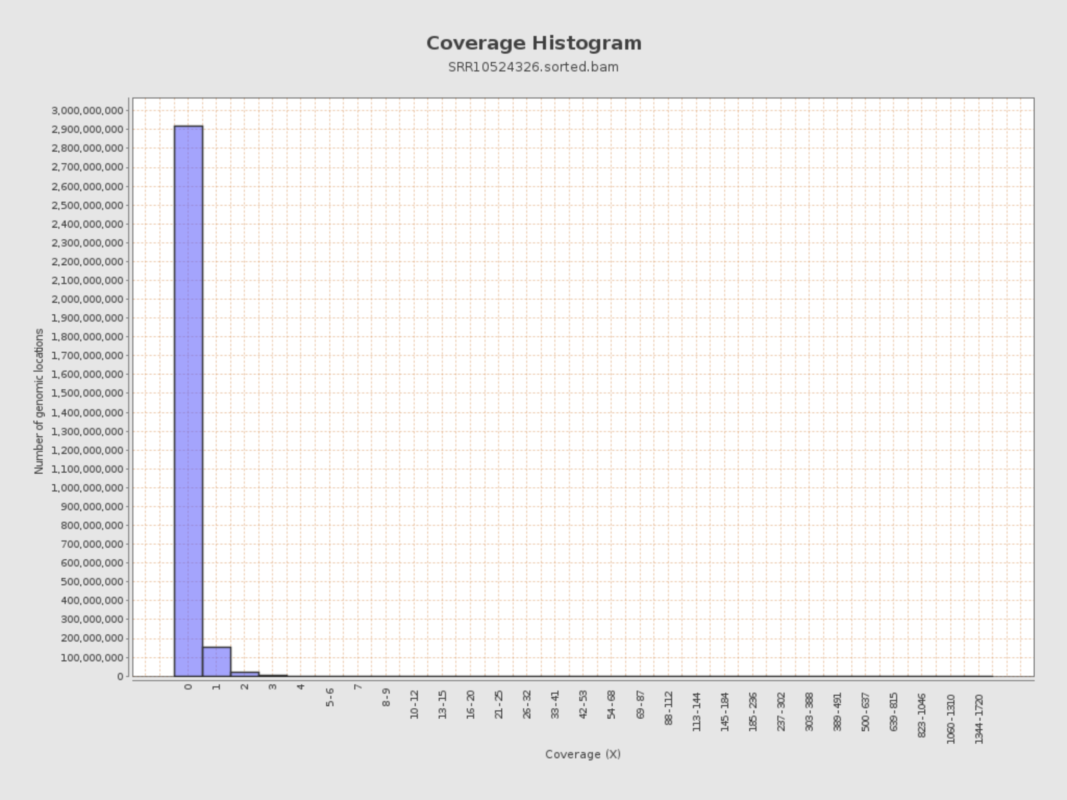
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	18288537	0.0734	1.0985
chr2	243199373	13714608	0.0564	0.7693
chr3	198022430	14534242	0.0734	0.3209
chr4	191154276	11028897	0.0577	0.3321
chr5	180915260	12413382	0.0686	0.3078
chr6	171115067	13379930	0.0782	0.376
chr7	159138663	9762549	0.0613	0.7225

chr8	146364022	20434283	0.1396	0.643
chr9	141213431	8896221	0.063	0.4158
chr10	135534747	10883151	0.0803	0.5336
chr11	135006516	10365042	0.0768	0.458
chr12	133851895	8581407	0.0641	0.3068
chr13	115169878	5369001	0.0466	0.2537
chr14	107349540	4501211	0.0419	0.2741
chr15	102531392	6489585	0.0633	0.3047
chr16	90354753	6753057	0.0747	0.354
chr17	81195210	6531316	0.0804	0.3932
chr18	78077248	4986457	0.0639	0.8005
chr19	59128983	3967642	0.0671	0.7462
chr20	63025520	4975703	0.0789	0.3389
chr21	48129895	3088048	0.0642	0.3373
chr22	51304566	1630946	0.0318	0.2086
chrMT	16571	18355	1.1077	1.2566
chrX	155270560	10238293	0.0659	0.3576
chrY	59373566	585248	0.0099	0.2553

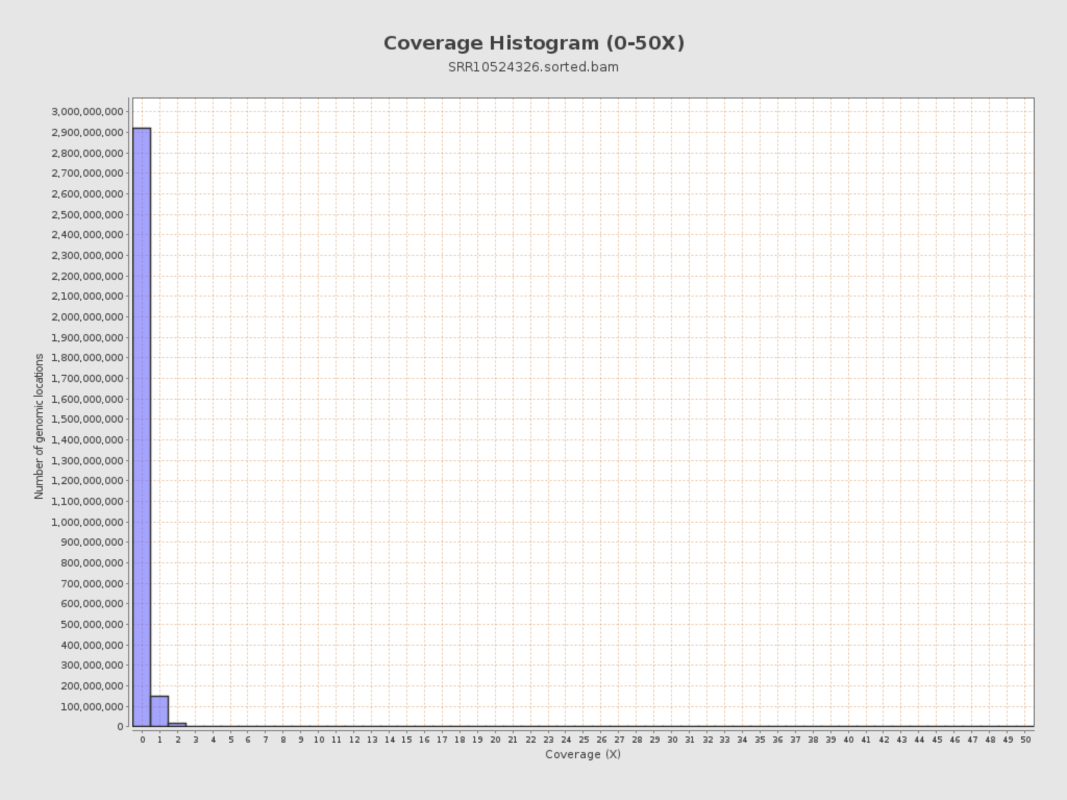
3. Results : Coverage across reference



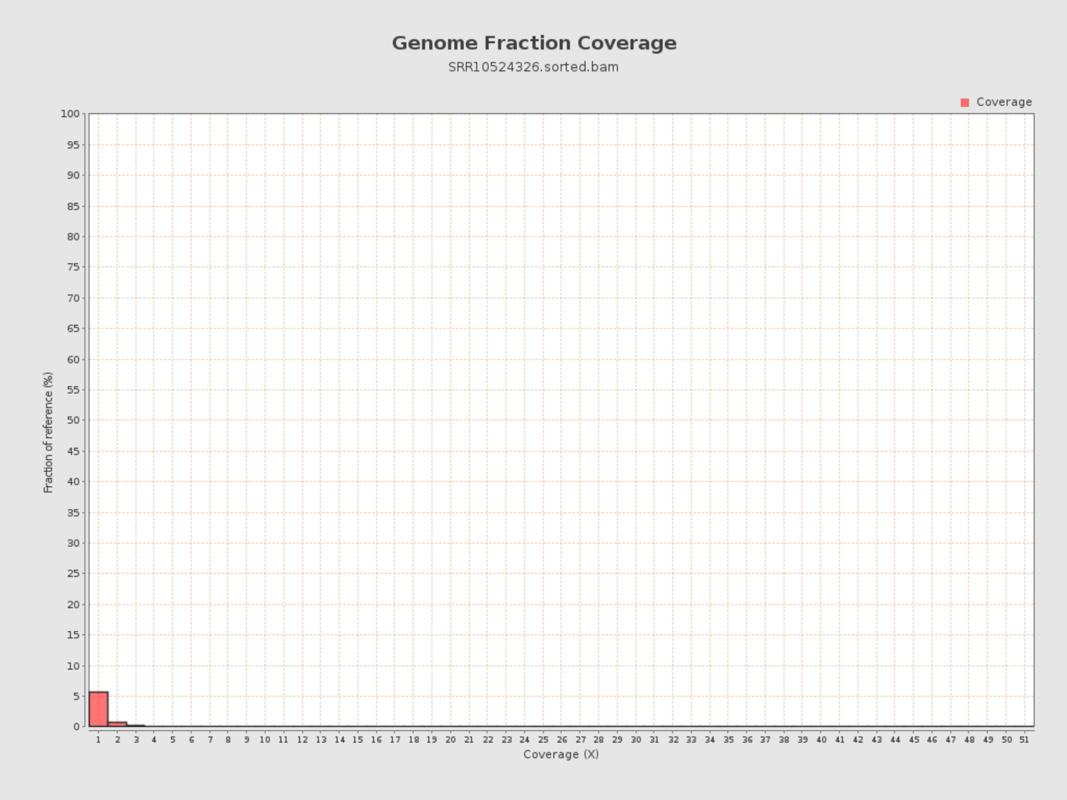
4. Results : Coverage Histogram



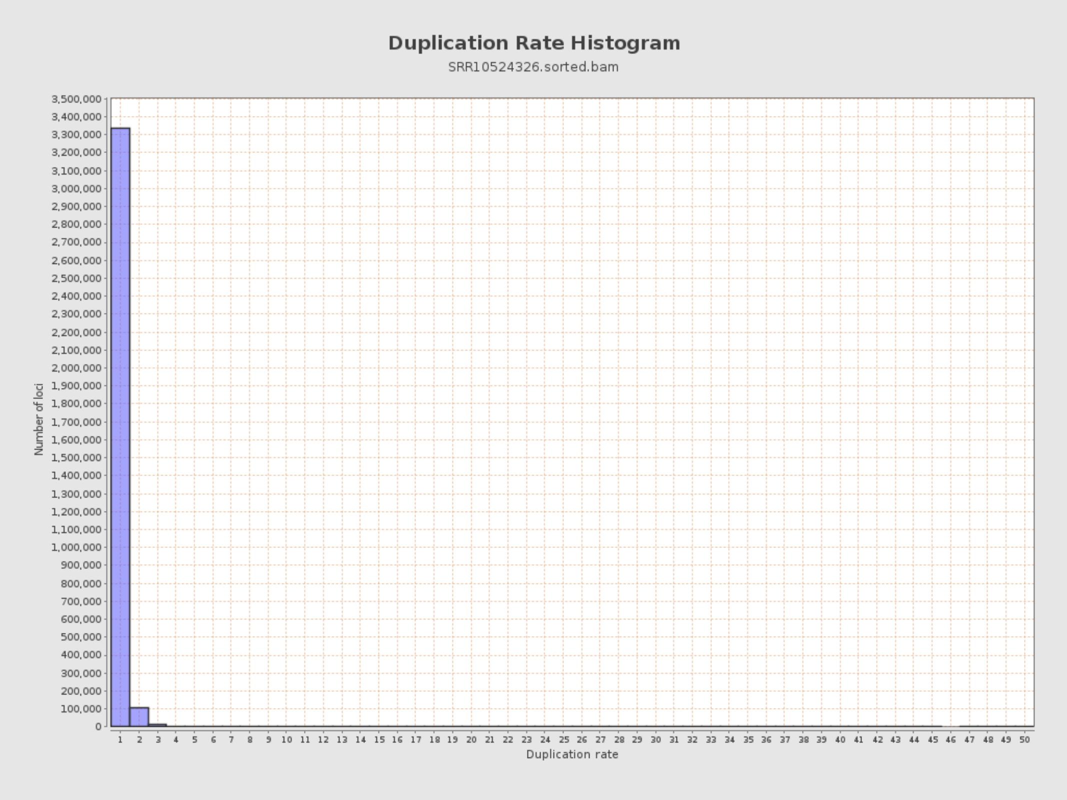
5. Results : Coverage Histogram (0-50X)



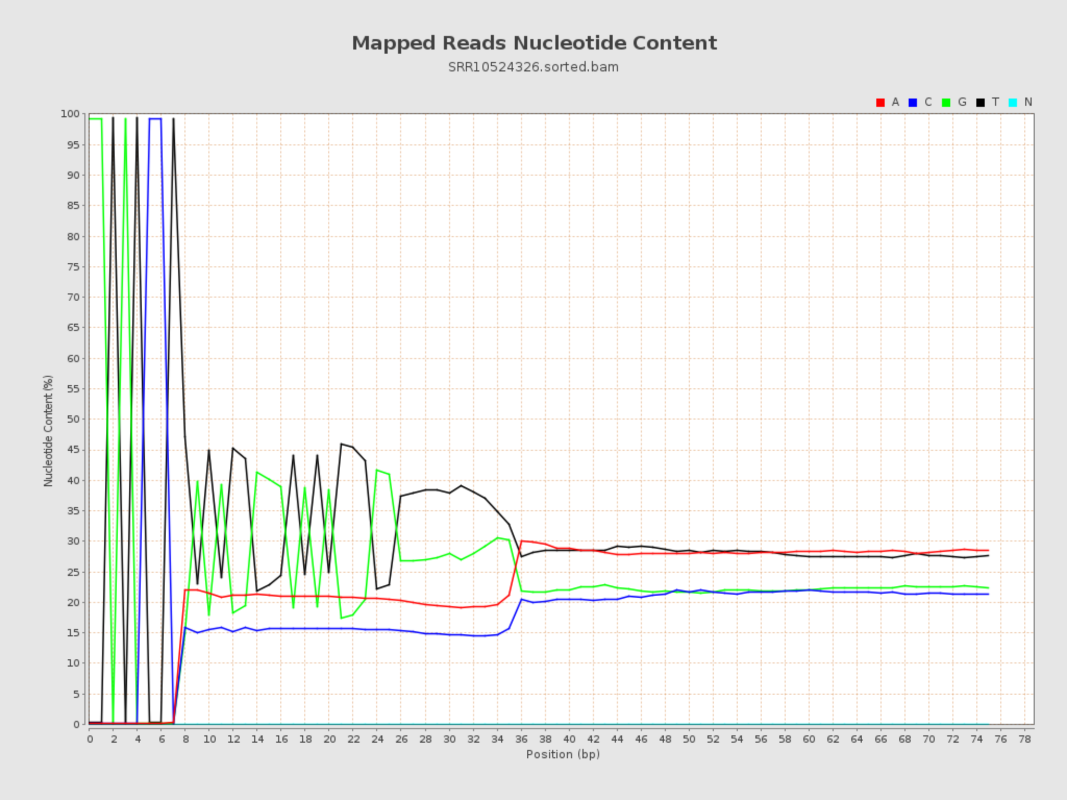
6. Results : Genome Fraction Coverage



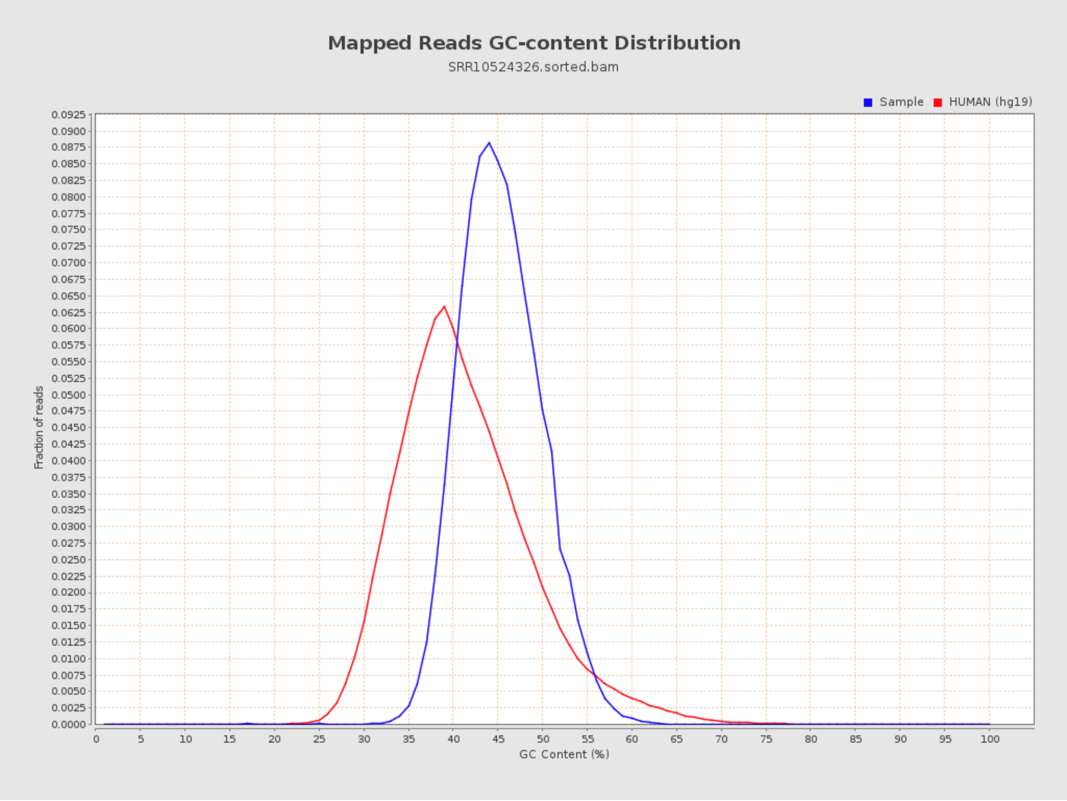
7. Results : Duplication Rate Histogram



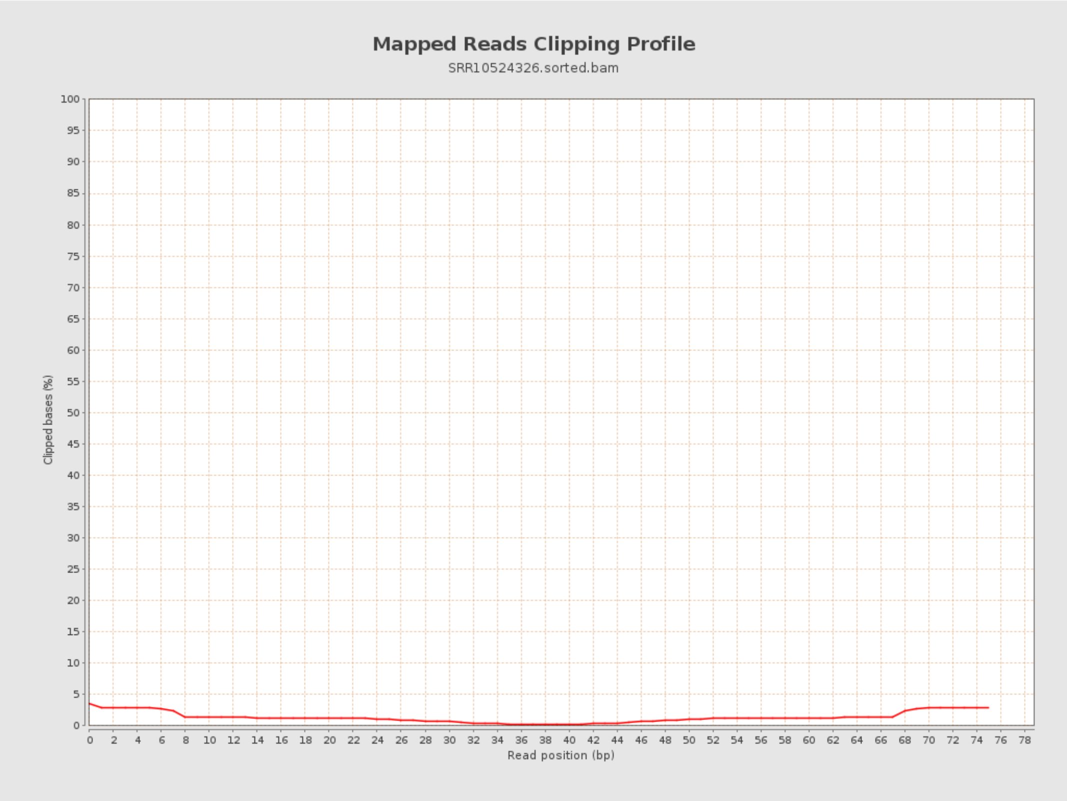
8. Results : Mapped Reads Nucleotide Content



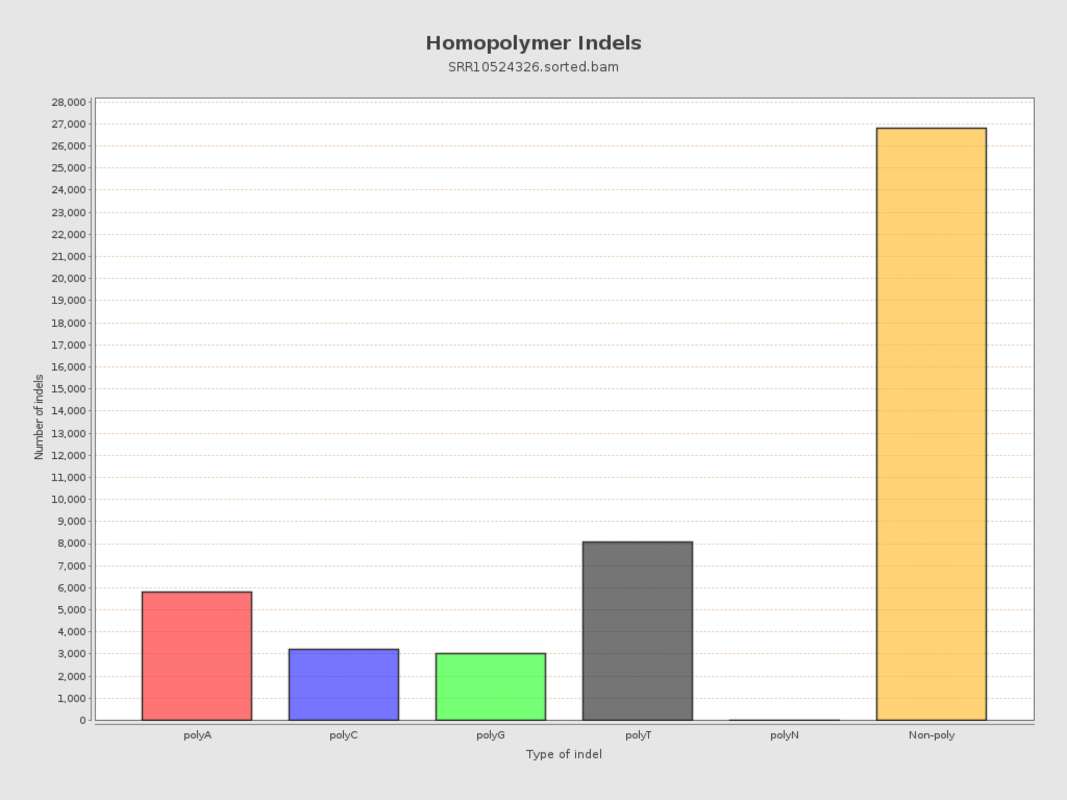
9. Results : Mapped Reads GC-content Distribution



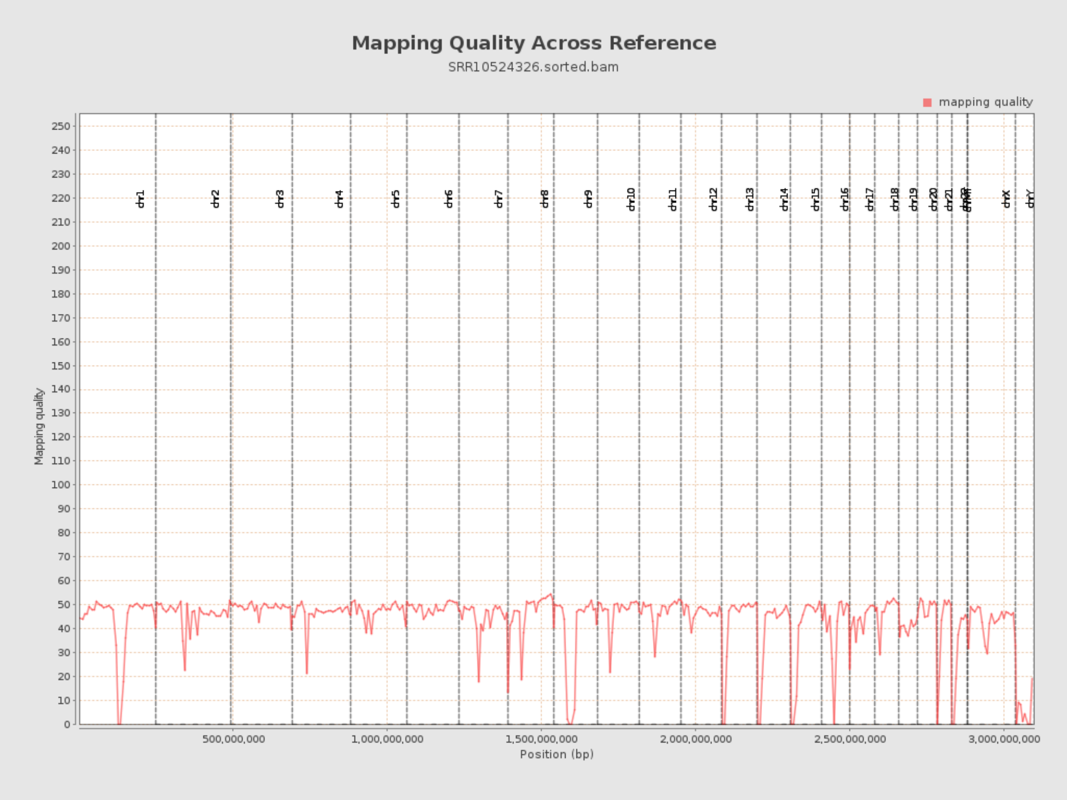
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram