Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 01:48:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524394.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_SRR10524394 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524394.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 01:48:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524394.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,780,831
Mapped reads	3,471,158 / 91.81%
Unmapped reads	309,673 / 8.19%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,785 / 0.31%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	217,032 / 5.74%
Duplication rate	4.57%
Clipped reads	3,473,110 / 91.86%

2.2. ACGT Content

Number/percentage of A's	48,761,164 / 24.07%
Number/percentage of C's	36,012,833 / 17.78%
Number/percentage of T's	66,422,286 / 32.79%
Number/percentage of G's	51,349,753 / 25.35%
Number/percentage of N's	25,605 / 0.01%
GC Percentage	43.13%

2.3. Coverage

Mean	0.0655

Standard Deviation	0.602

2.4. Mapping Quality

Mean Mapping Quality	45.5

2.5. Mismatches and indels

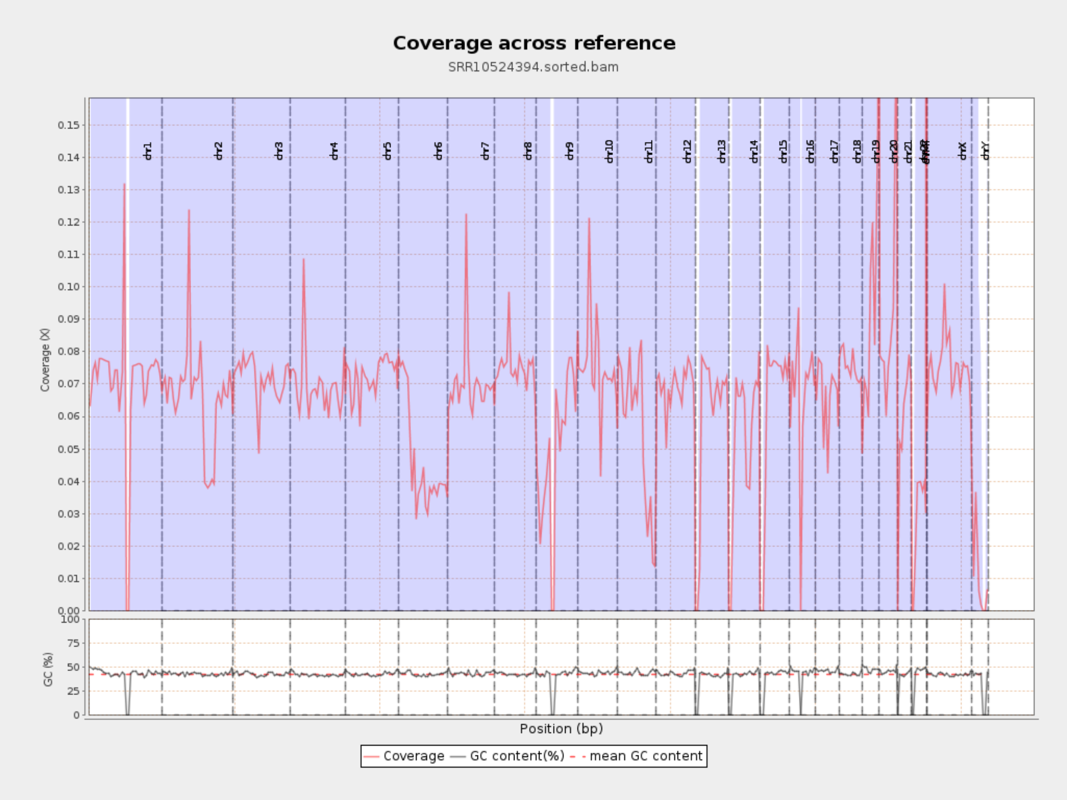
General error rate	0.5%
Mismatches	989,052
Insertions	14,182
Mapped reads with at least one insertion	0.41%
Deletions	36,286
Mapped reads with at least one deletion	1.04%
Homopolymer indels	44.21%

2.6. Chromosome stats

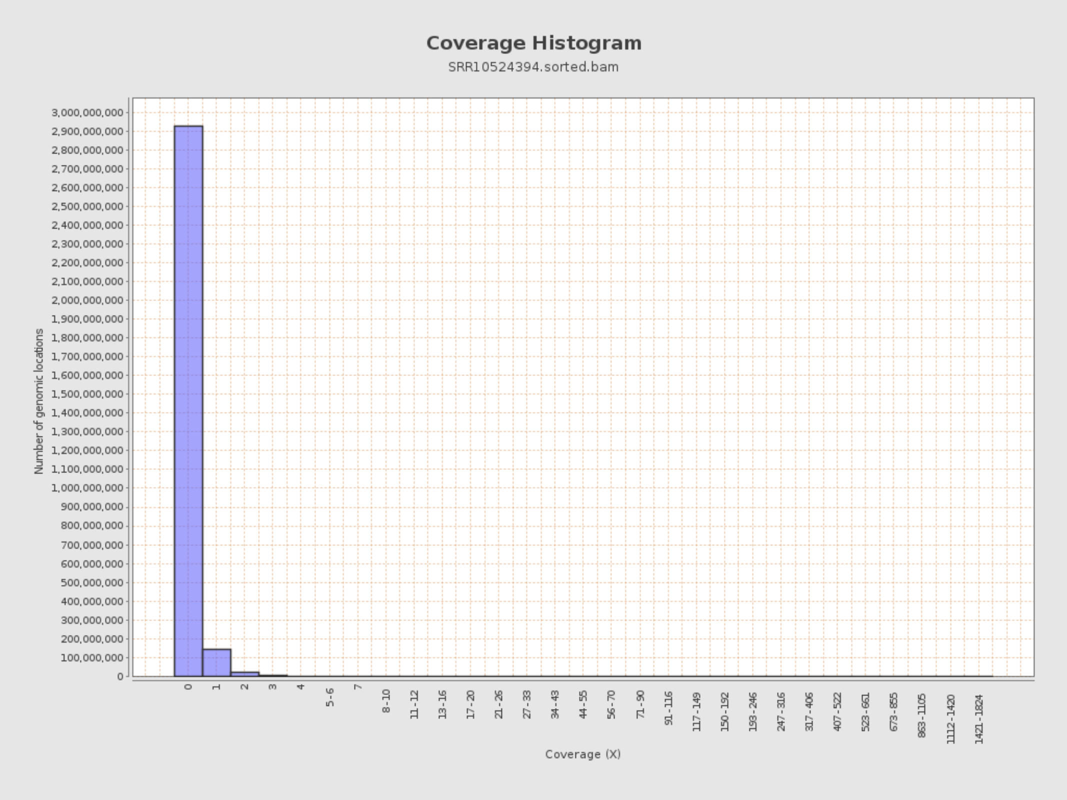
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	17536159	0.0704	1.3923
chr2	243199373	16152699	0.0664	0.6794
chr3	198022430	14189956	0.0717	0.3147
chr4	191154276	13252050	0.0693	0.3826
chr5	180915260	13115328	0.0725	0.3183
chr6	171115067	7945550	0.0464	0.3038
chr7	159138663	11261127	0.0708	0.8659

chr8	146364022	11033030	0.0754	0.4994
chr9	141213431	6910859	0.0489	0.4085
chr10	135534747	10239284	0.0755	0.5209
chr11	135006516	7523367	0.0557	0.4314
chr12	133851895	9257008	0.0692	0.3253
chr13	115169878	6769180	0.0588	0.2854
chr14	107349540	5603622	0.0522	0.29
chr15	102531392	6380695	0.0622	0.2947
chr16	90354753	6060991	0.0671	0.3363
chr17	81195210	5316392	0.0655	0.3456
chr18	78077248	5918660	0.0758	0.7784
chr19	59128983	5723116	0.0968	0.9042
chr20	63025520	5886450	0.0934	0.3953
chr21	48129895	2798127	0.0581	0.3418
chr22	51304566	1402227	0.0273	0.1925
chrMT	16571	20666	1.2471	1.4518
chrX	155270560	11707629	0.0754	0.3956
chrY	59373566	625240	0.0105	0.2662

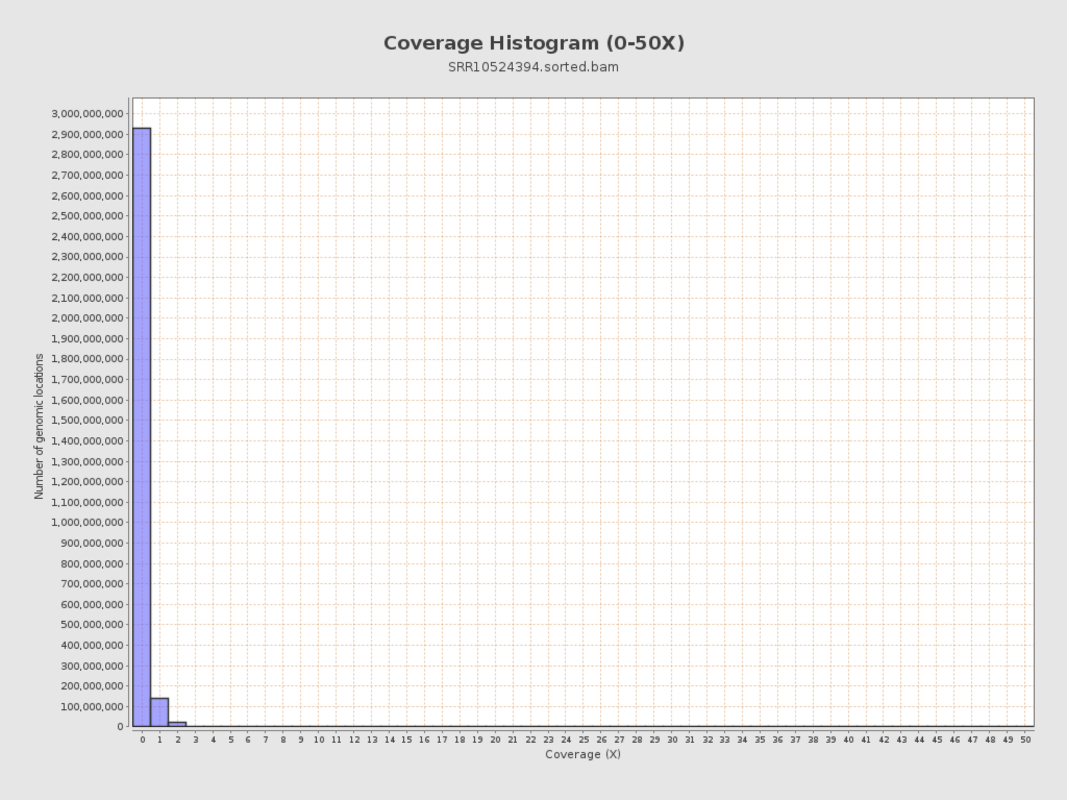
3. Results : Coverage across reference



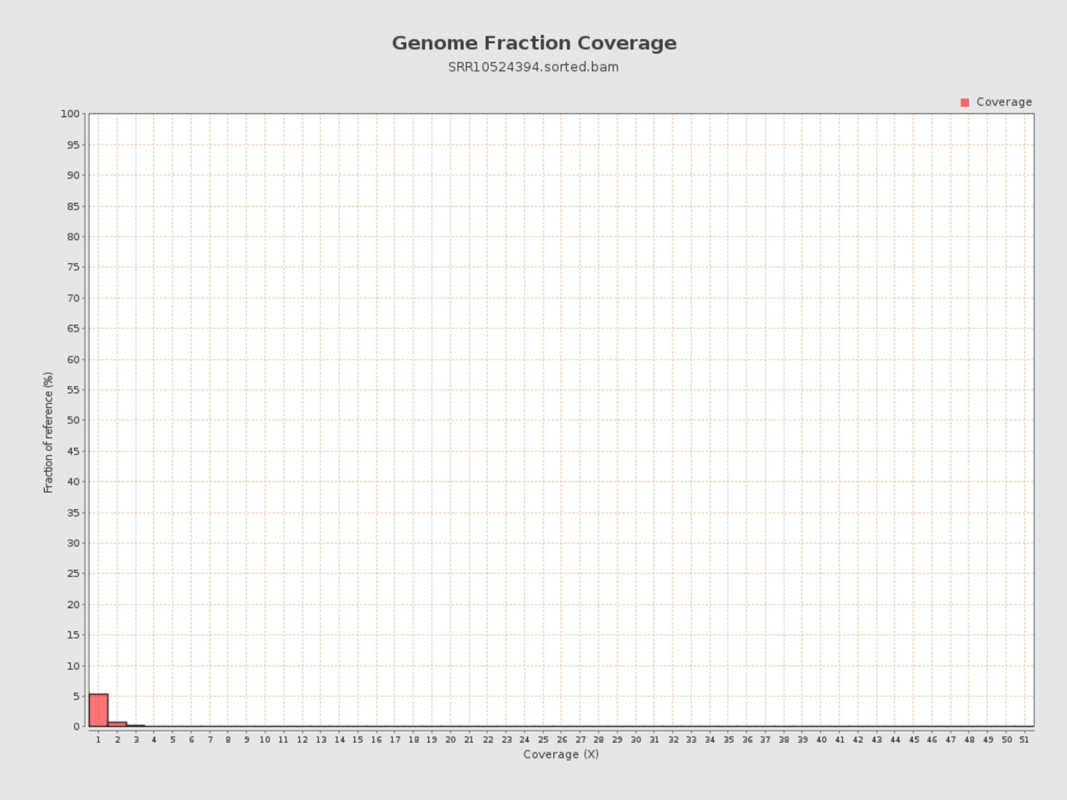
4. Results : Coverage Histogram



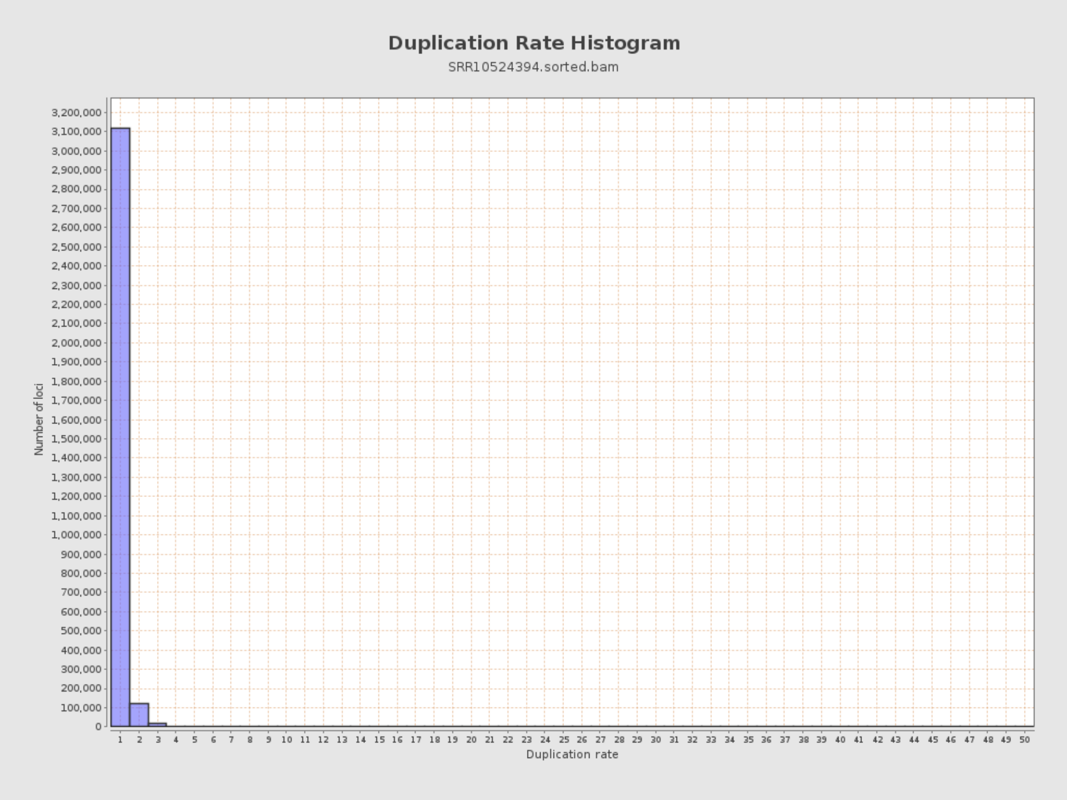
5. Results : Coverage Histogram (0-50X)



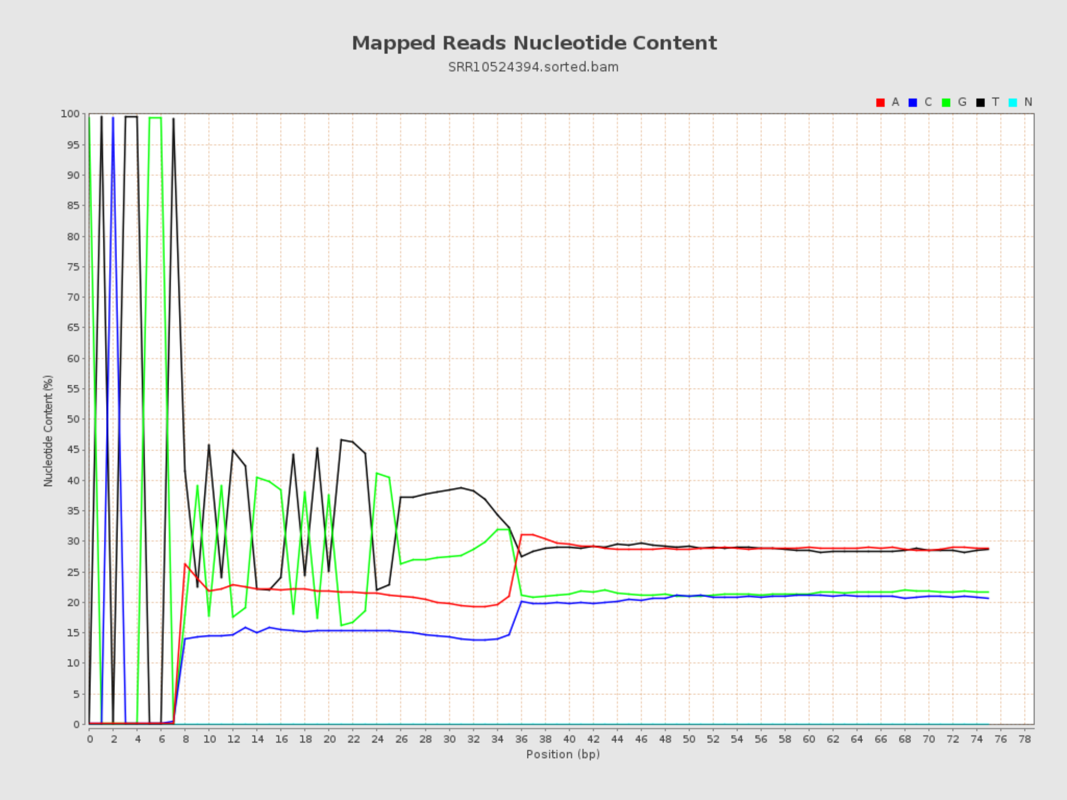
6. Results : Genome Fraction Coverage



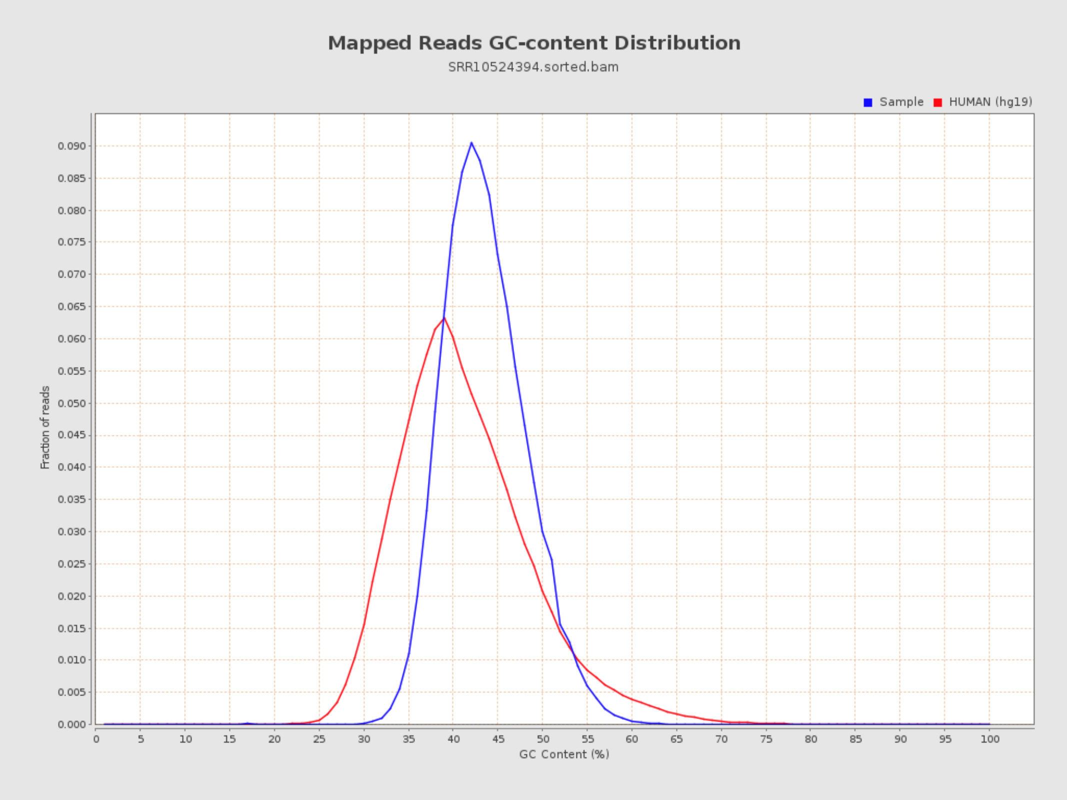
7. Results : Duplication Rate Histogram



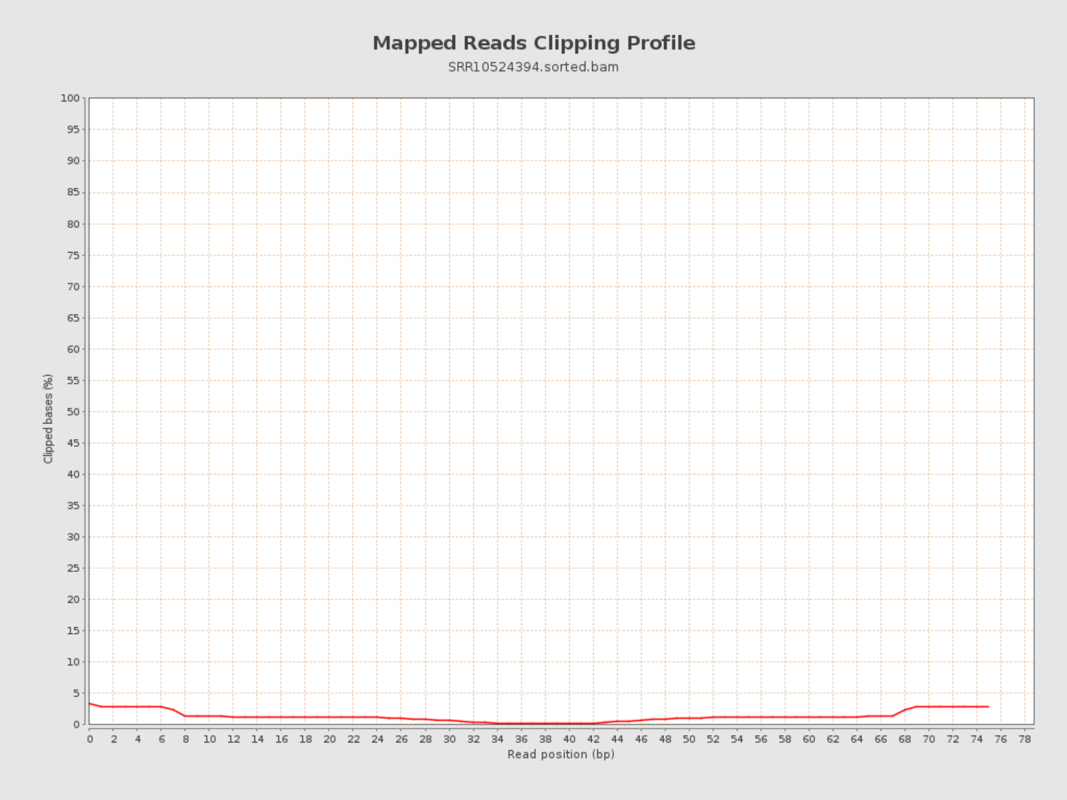
8. Results : Mapped Reads Nucleotide Content



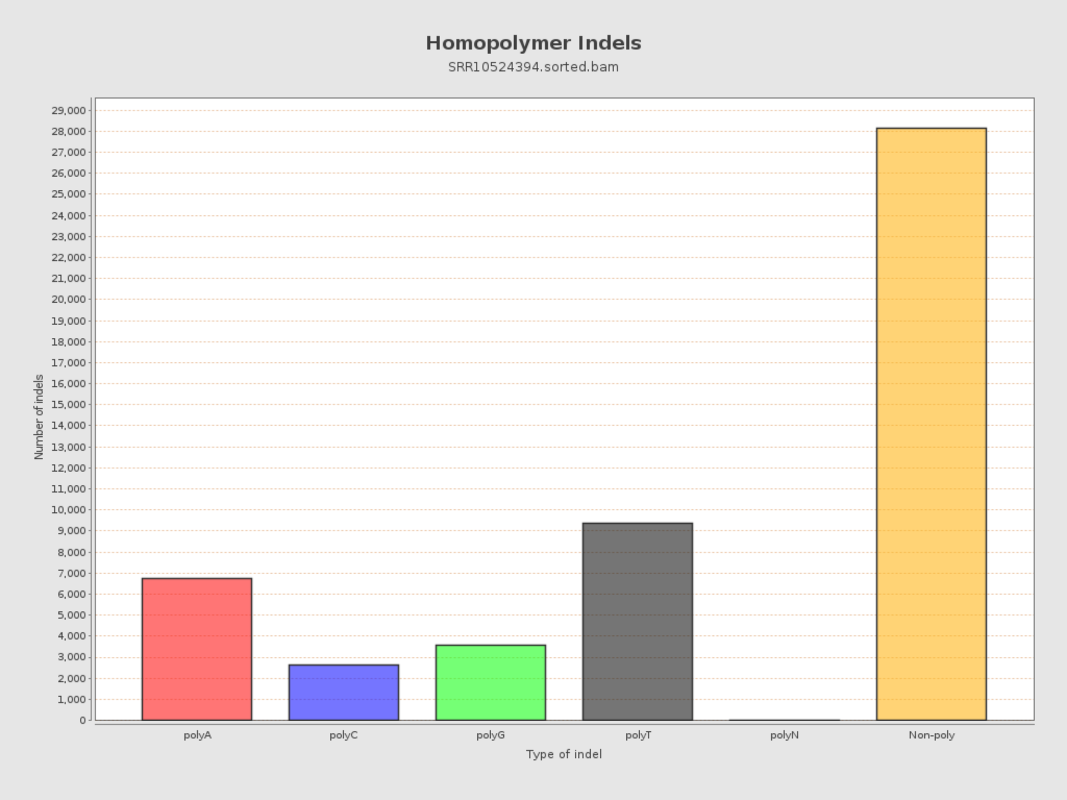
9. Results : Mapped Reads GC-content Distribution



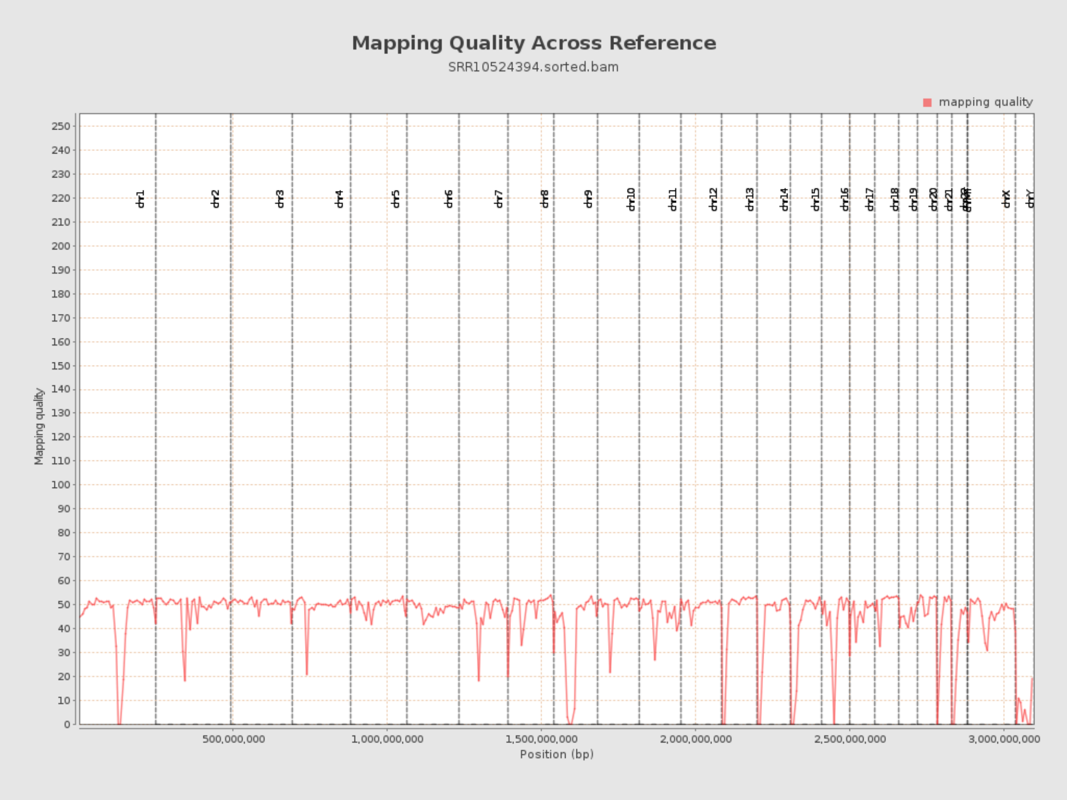
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram