Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 23:55:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524348.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_SRR10524348 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524348.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 23:55:15 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524348.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,197,549
Mapped reads	2,932,650 / 91.72%
Unmapped reads	264,899 / 8.28%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,284 / 0.42%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	157,970 / 4.94%
Duplication rate	3.88%
Clipped reads	2,934,215 / 91.76%

2.2. ACGT Content

Number/percentage of A's	40,466,751 / 23.61%
Number/percentage of C's	33,915,176 / 19.79%
Number/percentage of T's	56,231,375 / 32.81%
Number/percentage of G's	40,747,550 / 23.78%
Number/percentage of N's	23,269 / 0.01%
GC Percentage	43.56%

2.3. Coverage

Mean	0.0554

Standard Deviation	0.4802

2.4. Mapping Quality

Mean Mapping Quality	44.45

2.5. Mismatches and indels

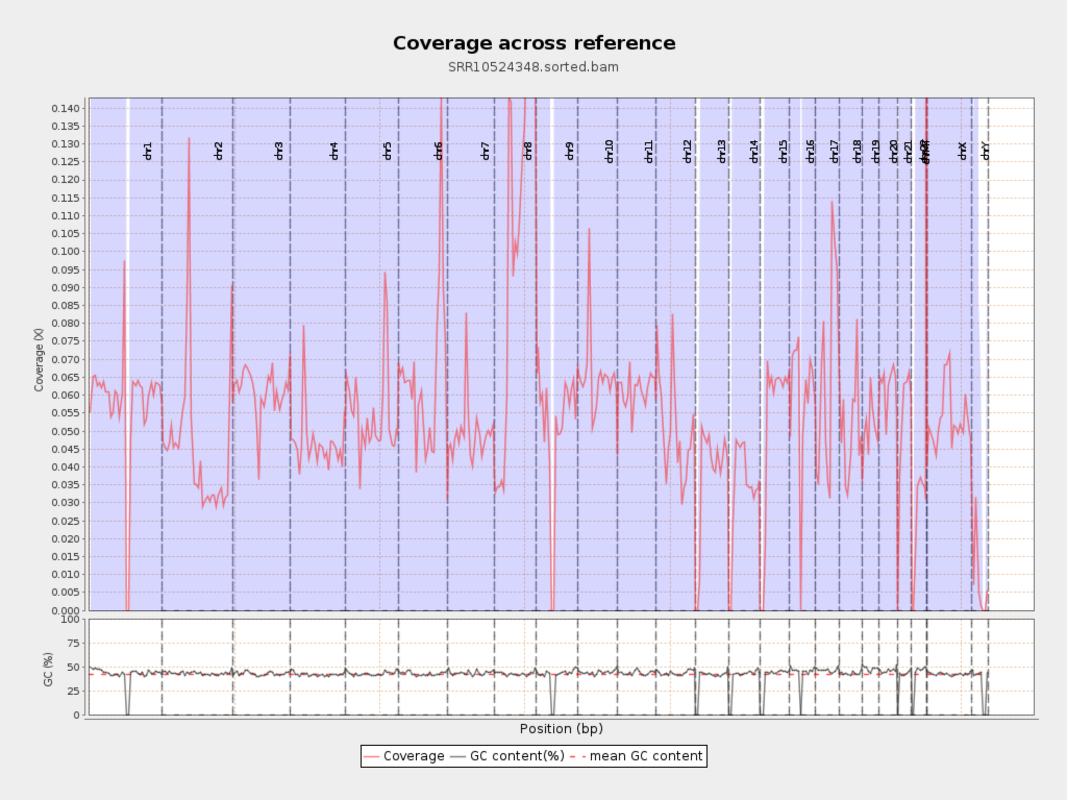
General error rate	0.53%
Mismatches	878,132
Insertions	12,908
Mapped reads with at least one insertion	0.44%
Deletions	31,176
Mapped reads with at least one deletion	1.06%
Homopolymer indels	41.78%

2.6. Chromosome stats

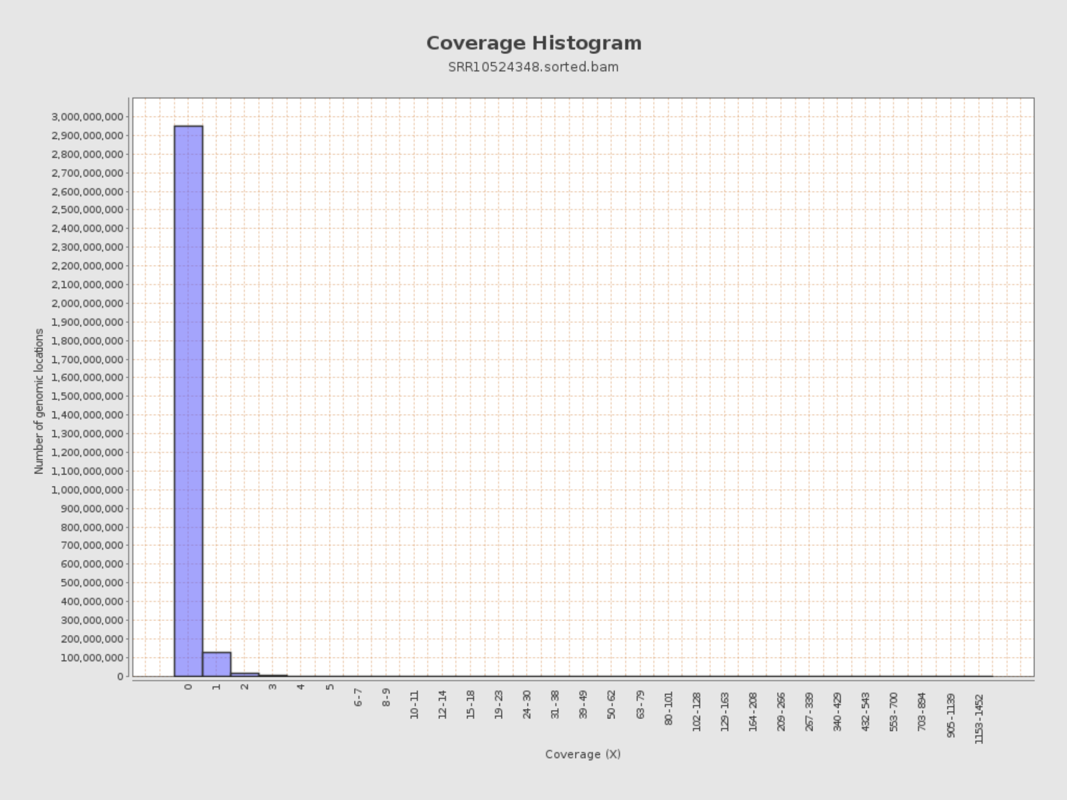
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14363147	0.0576	0.9577
chr2	243199373	11143620	0.0458	0.6616
chr3	198022430	12070369	0.061	0.2878
chr4	191154276	8871370	0.0464	0.3092
chr5	180915260	9982248	0.0552	0.2715
chr6	171115067	11070791	0.0647	0.3321
chr7	159138663	7863302	0.0494	0.5704

chr8	146364022	17684890	0.1208	0.5954
chr9	141213431	7152831	0.0507	0.3624
chr10	135534747	8829852	0.0651	0.4629
chr11	135006516	8259633	0.0612	0.3932
chr12	133851895	6727448	0.0503	0.2655
chr13	115169878	4280690	0.0372	0.2244
chr14	107349540	3595819	0.0335	0.233
chr15	102531392	5304646	0.0517	0.2622
chr16	90354753	5377376	0.0595	0.3101
chr17	81195210	5324149	0.0656	0.3367
chr18	78077248	4008173	0.0513	0.7201
chr19	59128983	3053549	0.0516	0.6108
chr20	63025520	3953794	0.0627	0.2951
chr21	48129895	2472848	0.0514	0.2982
chr22	51304566	1275887	0.0249	0.1828
chrMT	16571	13632	0.8226	1.0828
chrX	155270560	8250564	0.0531	0.3112
chrY	59373566	501809	0.0085	0.247

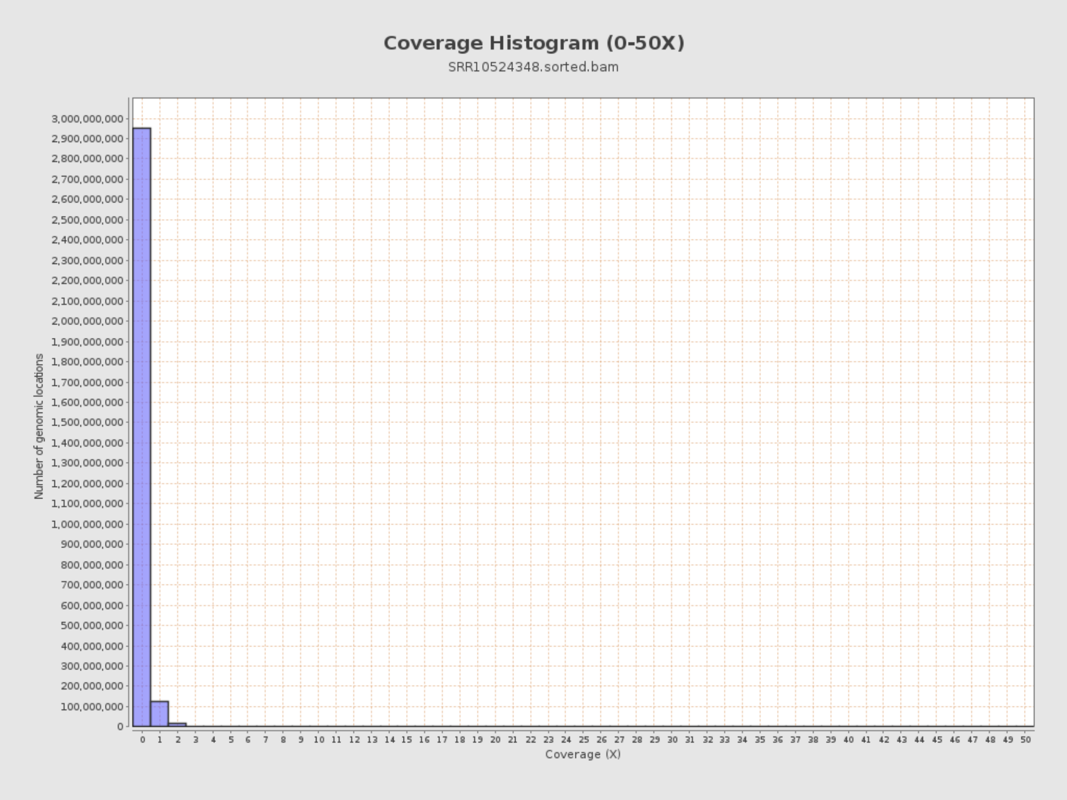
3. Results : Coverage across reference



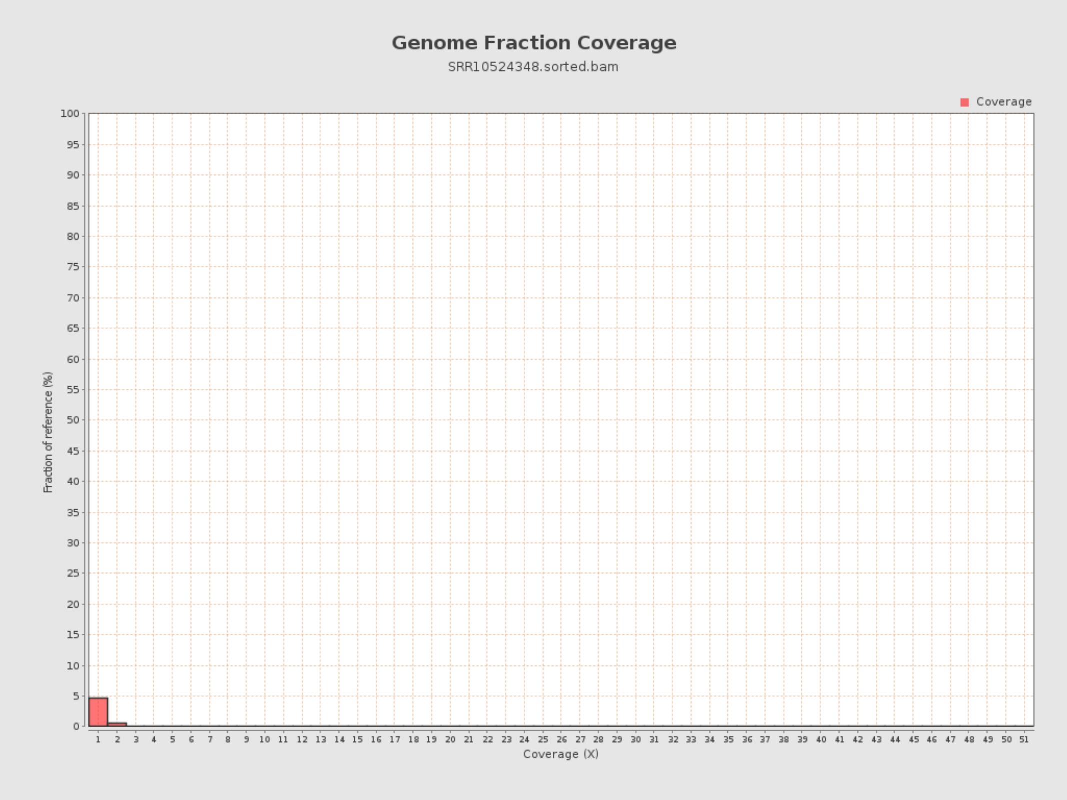
4. Results : Coverage Histogram



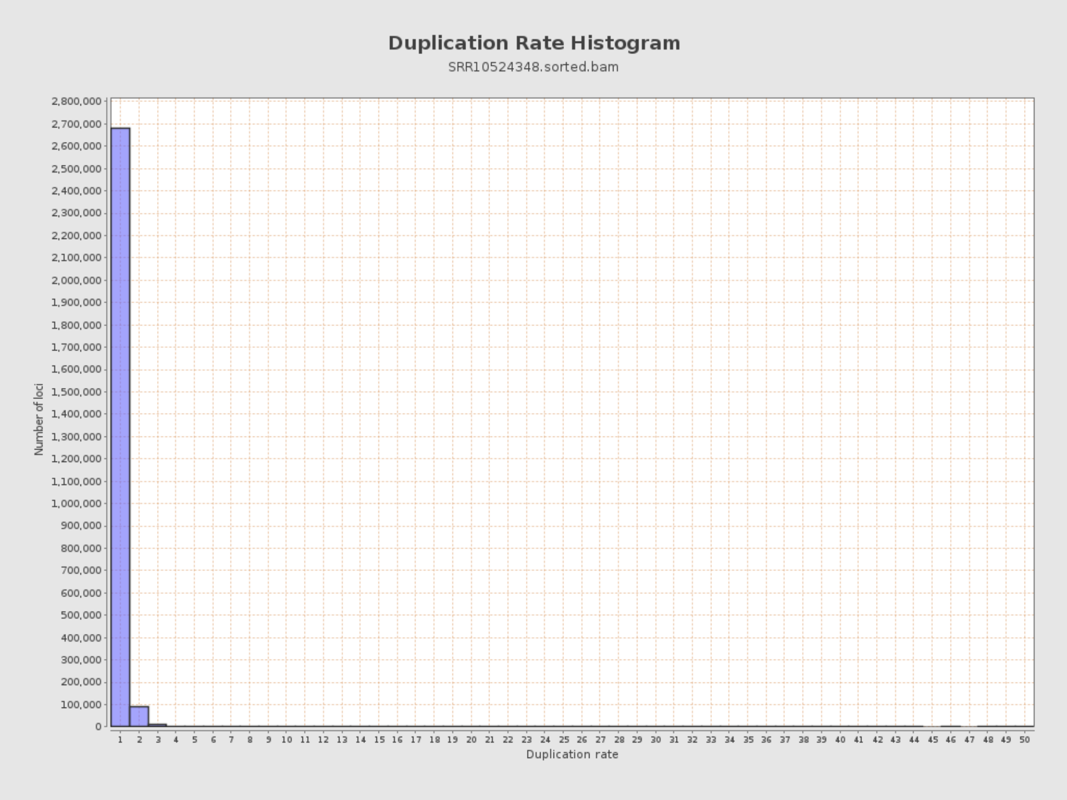
5. Results : Coverage Histogram (0-50X)



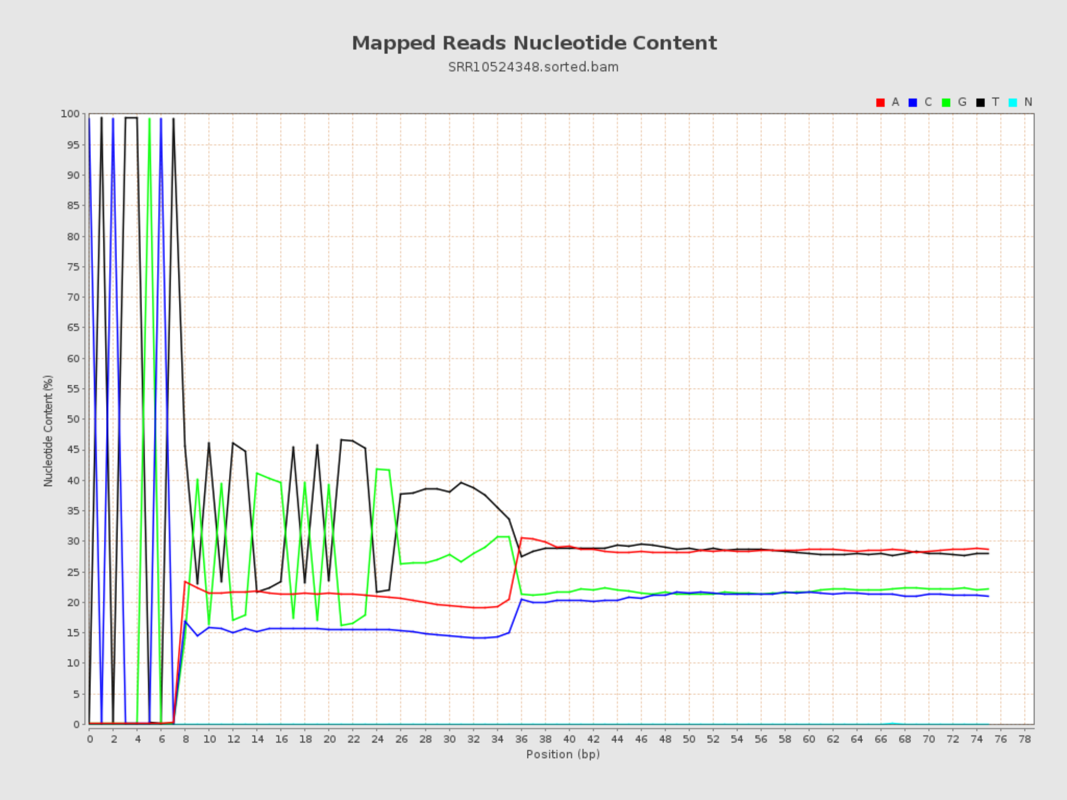
6. Results : Genome Fraction Coverage



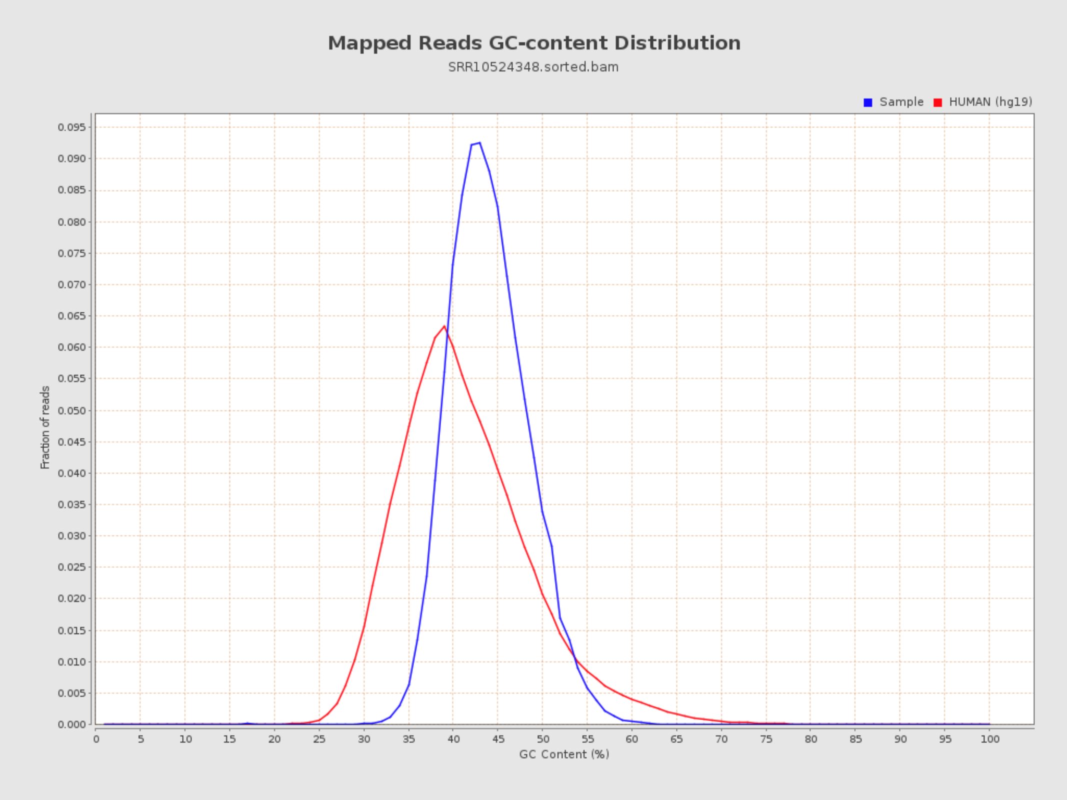
7. Results : Duplication Rate Histogram



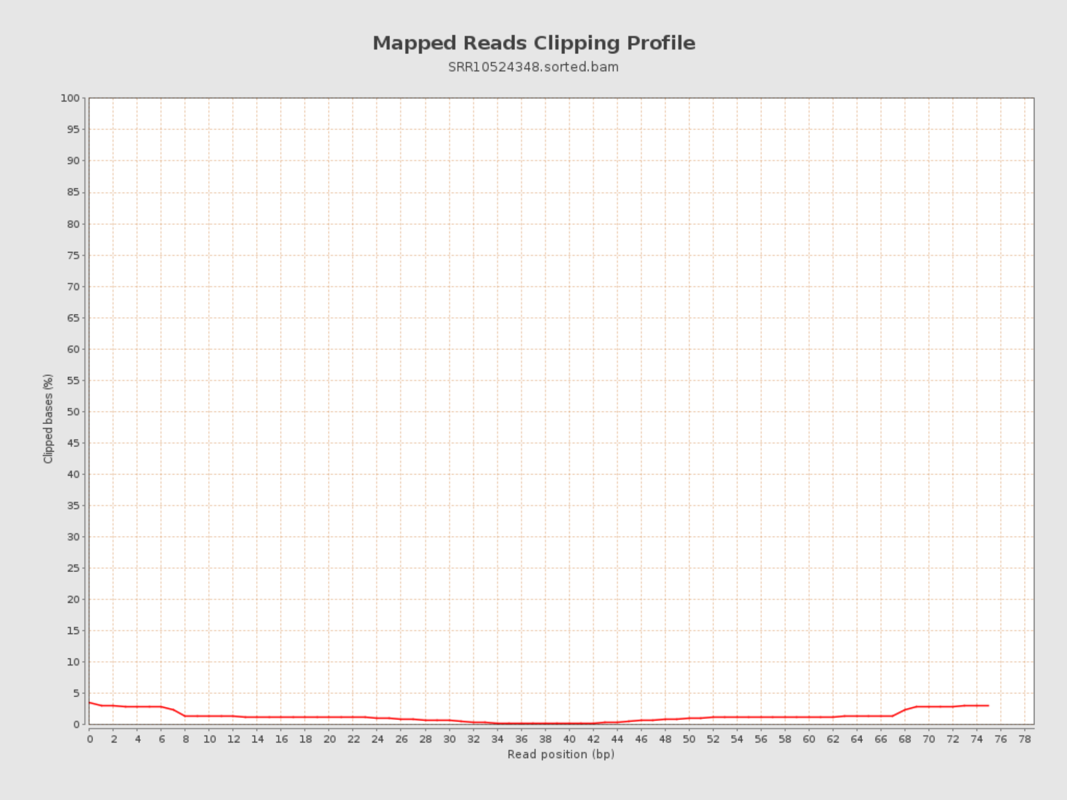
8. Results : Mapped Reads Nucleotide Content



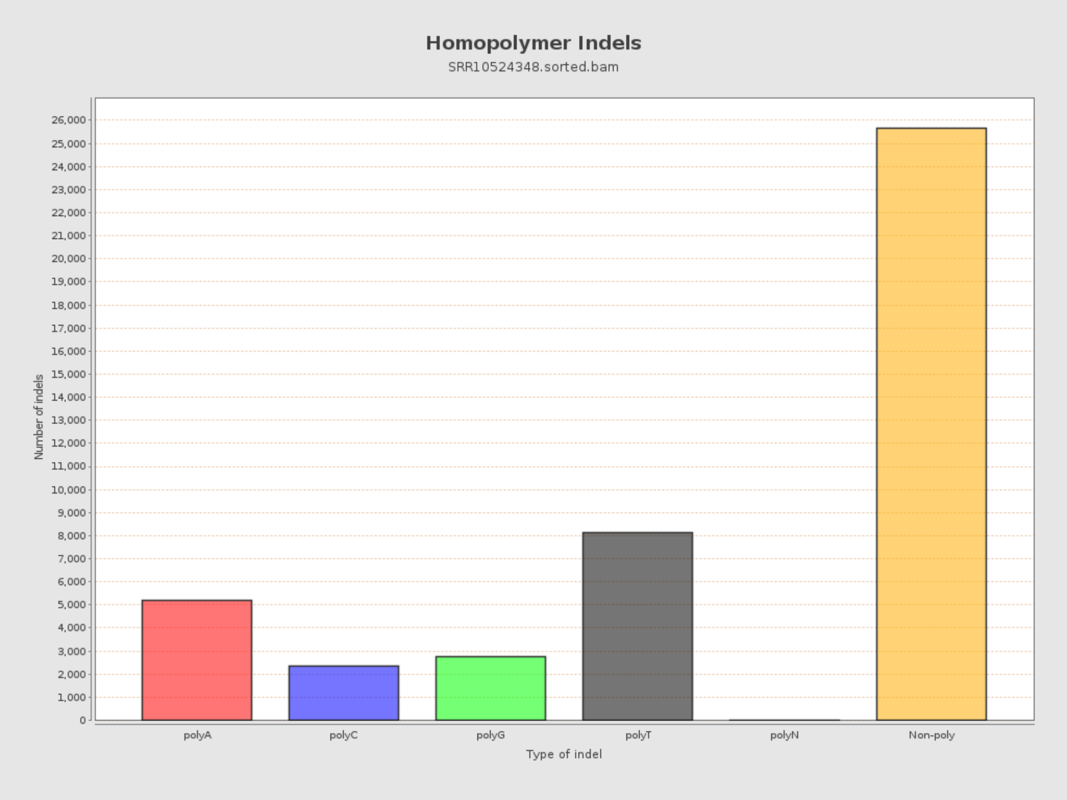
9. Results : Mapped Reads GC-content Distribution



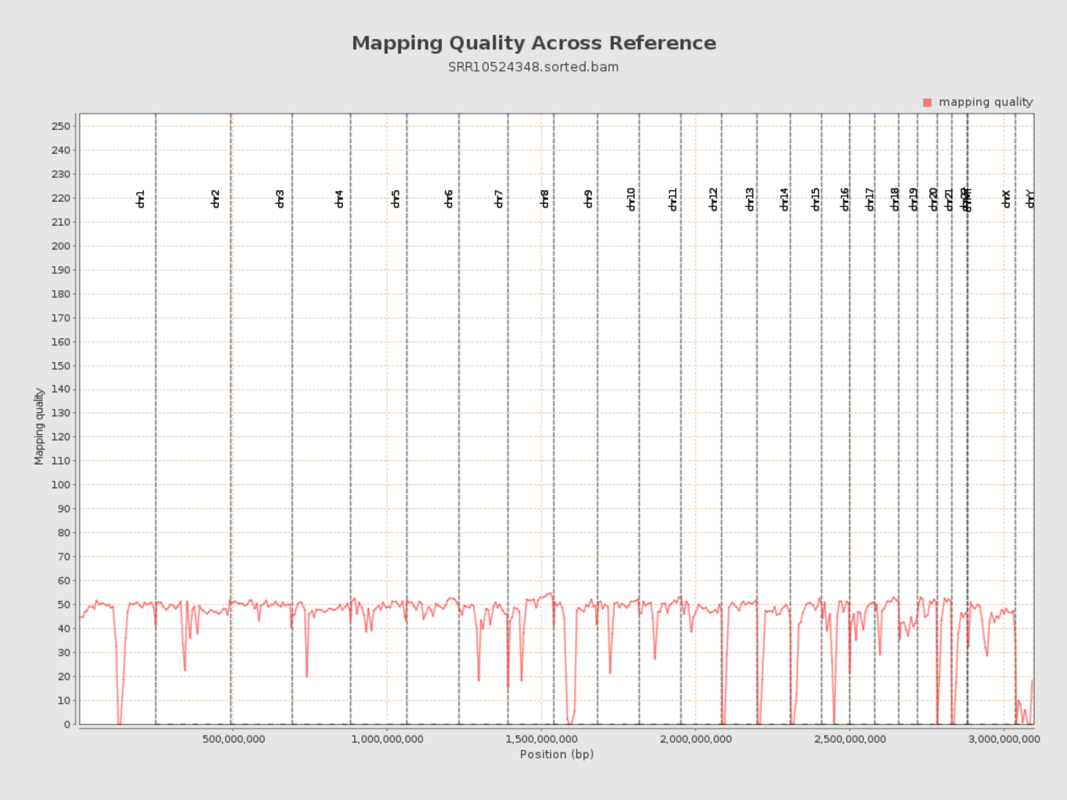
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram