Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 17:28:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525092.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_SRR10525092 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525092.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 17:28:00 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525092.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,984,239
Mapped reads	1,840,182 / 92.74%
Unmapped reads	144,057 / 7.26%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	46,562 / 2.35%
Read min/max/mean length	30 / 101 / 101.89
Duplicated reads (estimated)	63,746 / 3.21%
Duplication rate	1.98%
Clipped reads	1,885,202 / 95.01%

2.2. ACGT Content

Number/percentage of A's	38,275,414 / 26.56%
Number/percentage of C's	29,362,407 / 20.37%
Number/percentage of T's	43,180,613 / 29.96%
Number/percentage of G's	33,308,299 / 23.11%
Number/percentage of N's	5,738 / 0%
GC Percentage	43.48%

2.3. Coverage

Mean	0.0466

Standard Deviation	0.5066

2.4. Mapping Quality

Mean Mapping Quality	46.2

2.5. Mismatches and indels

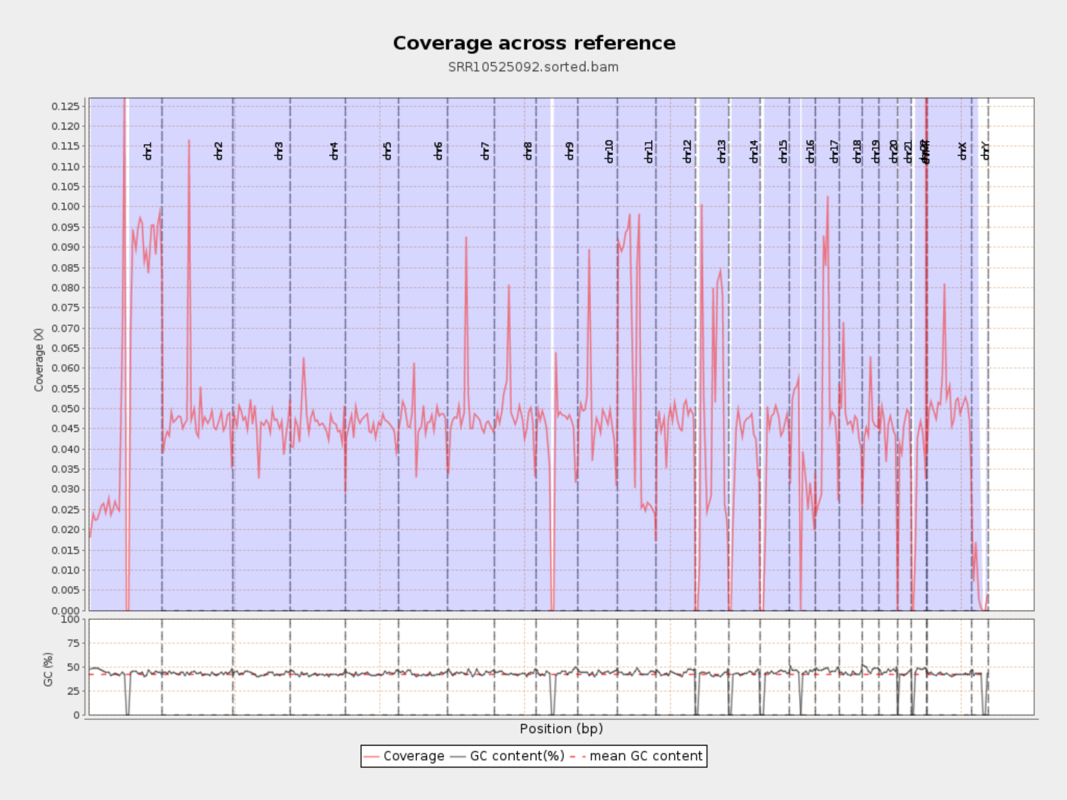
General error rate	0.76%
Mismatches	1,073,589
Insertions	12,326
Mapped reads with at least one insertion	0.66%
Deletions	32,312
Mapped reads with at least one deletion	1.73%
Homopolymer indels	42.69%

2.6. Chromosome stats

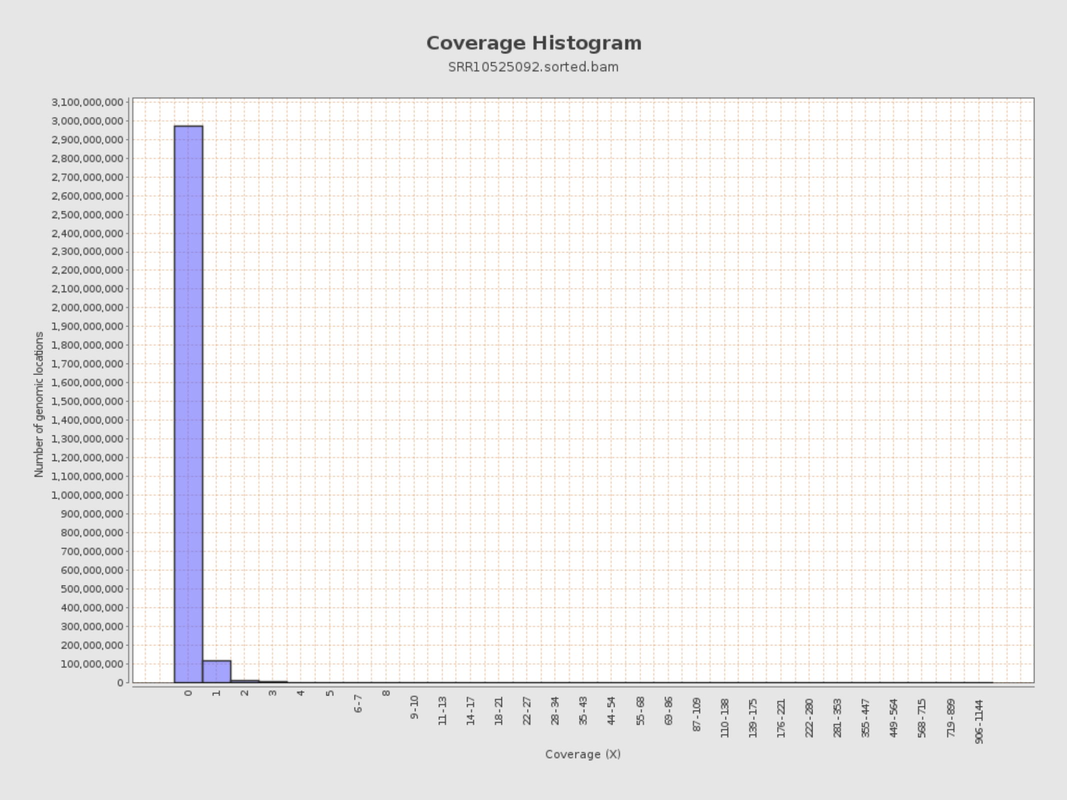
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14167388	0.0568	0.9624
chr2	243199373	11826407	0.0486	0.6698
chr3	198022430	9172394	0.0463	0.2392
chr4	191154276	8885946	0.0465	0.256
chr5	180915260	8299709	0.0459	0.2426
chr6	171115067	8086815	0.0473	0.2953
chr7	159138663	7784951	0.0489	0.7255

chr8	146364022	7227088	0.0494	0.6358
chr9	141213431	5907820	0.0418	0.441
chr10	135534747	6614583	0.0488	0.5135
chr11	135006516	8041325	0.0596	0.5777
chr12	133851895	6290056	0.047	0.2421
chr13	115169878	5202848	0.0452	0.2356
chr14	107349540	4024629	0.0375	0.2607
chr15	102531392	3940345	0.0384	0.2146
chr16	90354753	3218630	0.0356	0.2466
chr17	81195210	4321304	0.0532	0.3286
chr18	78077248	3846964	0.0493	0.8344
chr19	59128983	2755773	0.0466	0.6849
chr20	63025520	2780186	0.0441	0.2418
chr21	48129895	1900809	0.0395	0.2448
chr22	51304566	1514500	0.0295	0.1875
chrMT	16571	13405	0.8089	1.171
chrX	155270560	8038910	0.0518	0.3741
chrY	59373566	324671	0.0055	0.1309

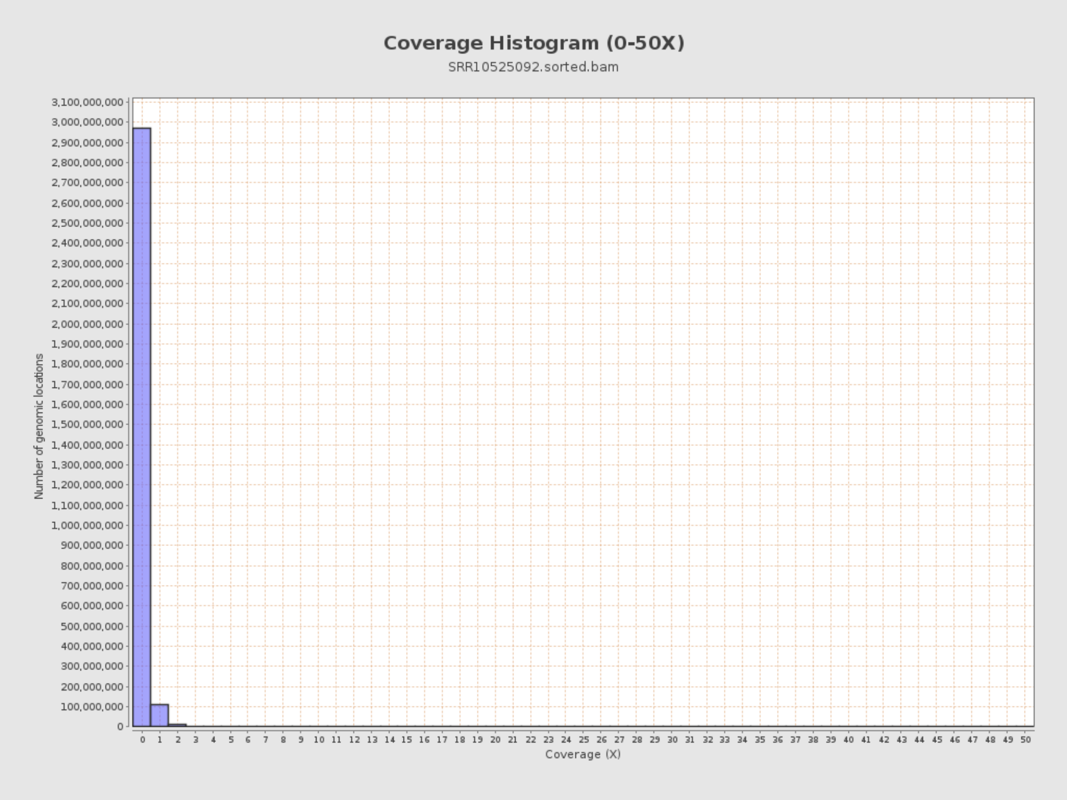
3. Results : Coverage across reference



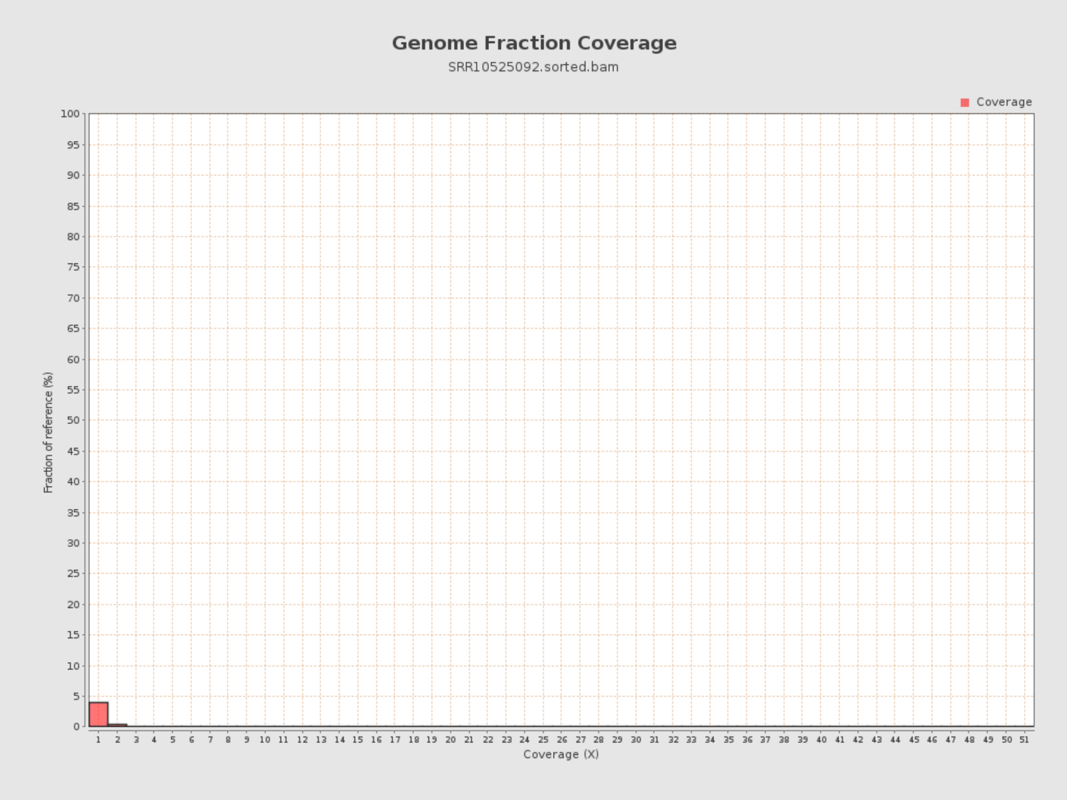
4. Results : Coverage Histogram



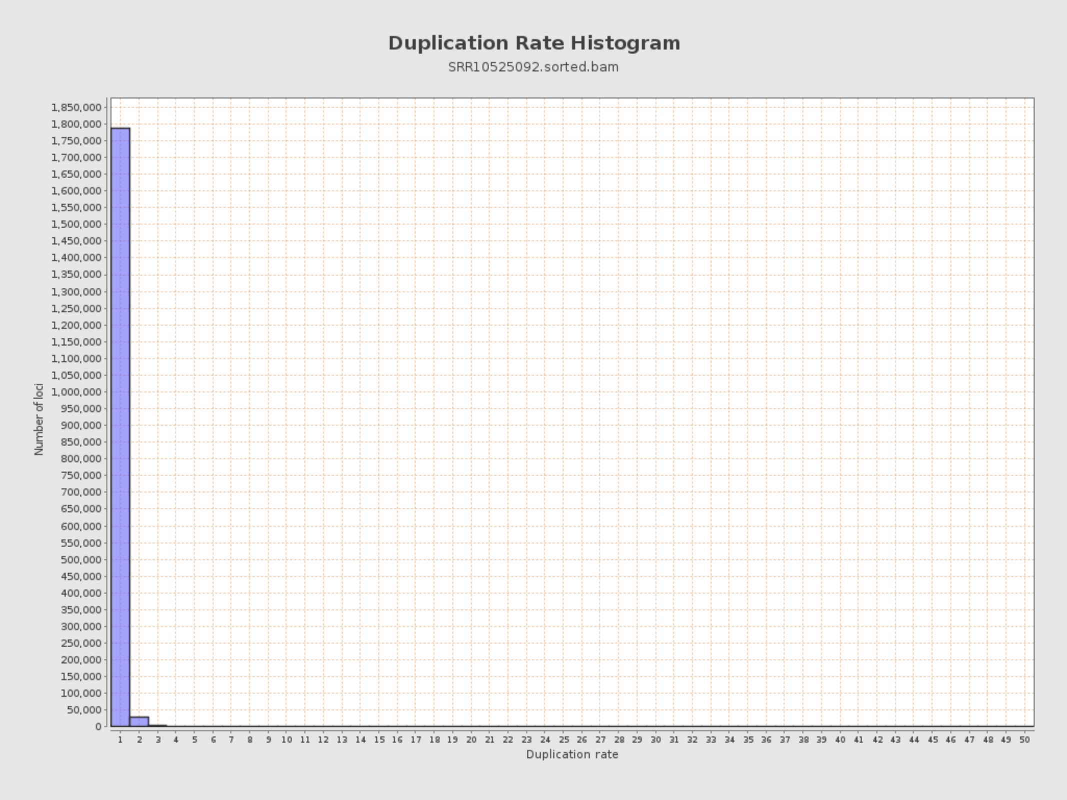
5. Results : Coverage Histogram (0-50X)



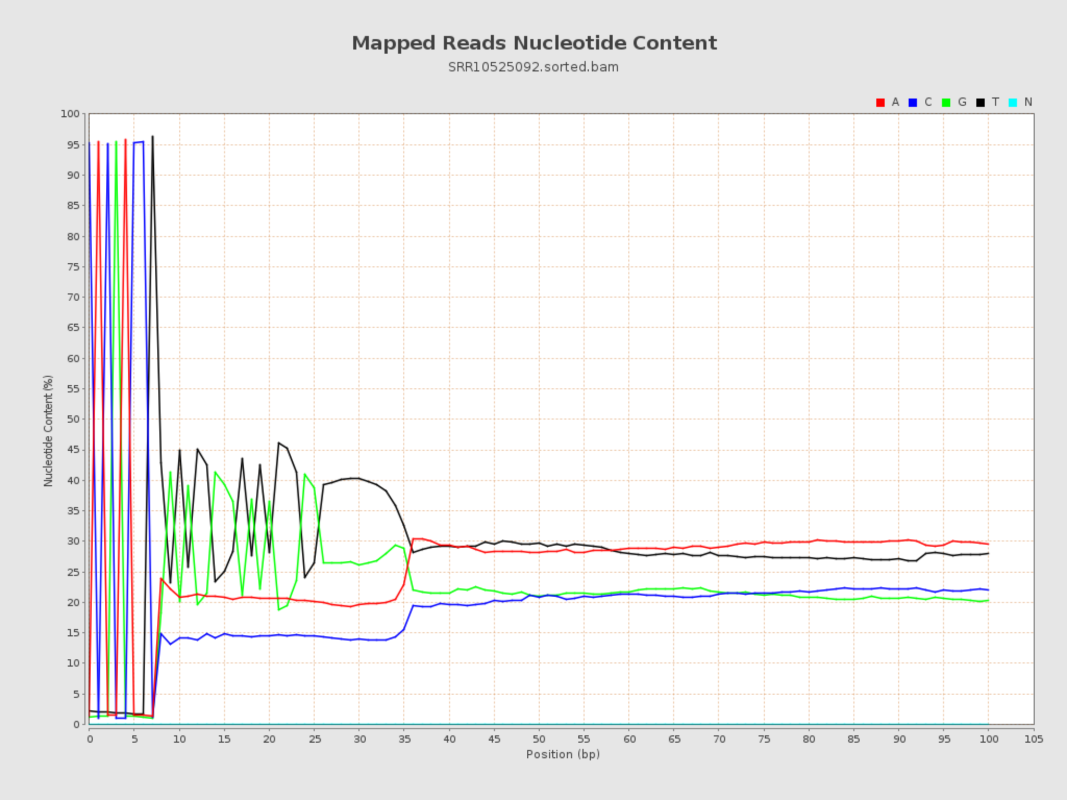
6. Results : Genome Fraction Coverage



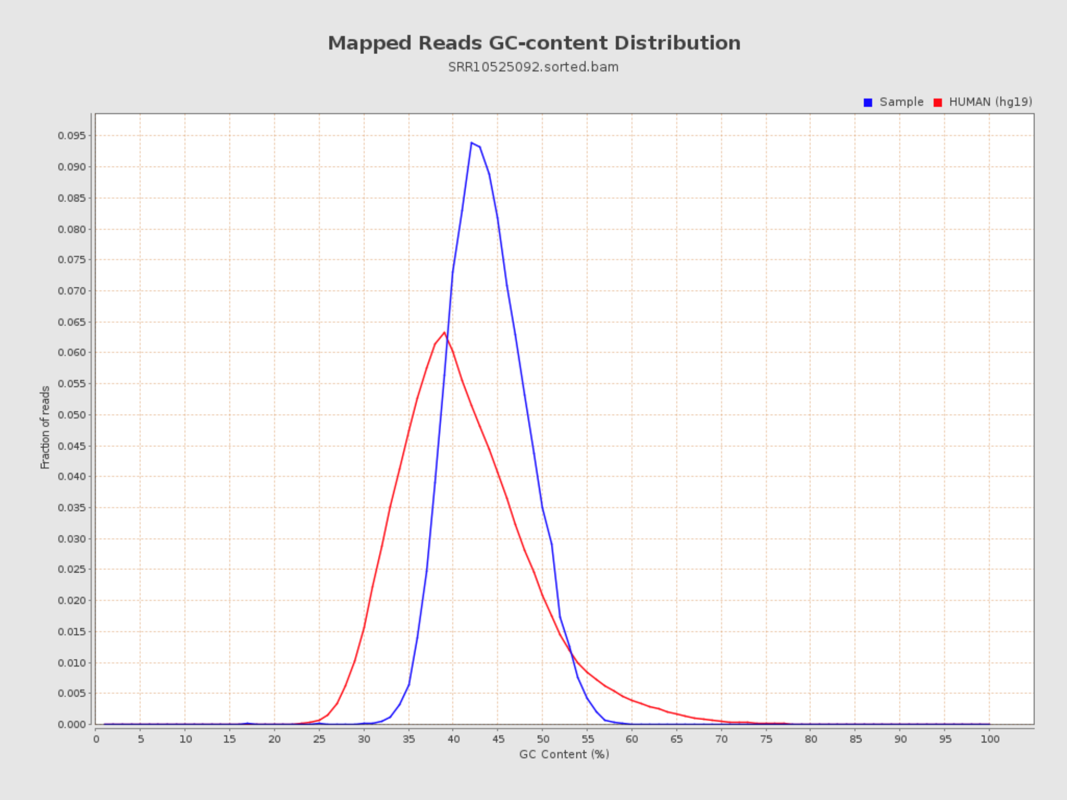
7. Results : Duplication Rate Histogram



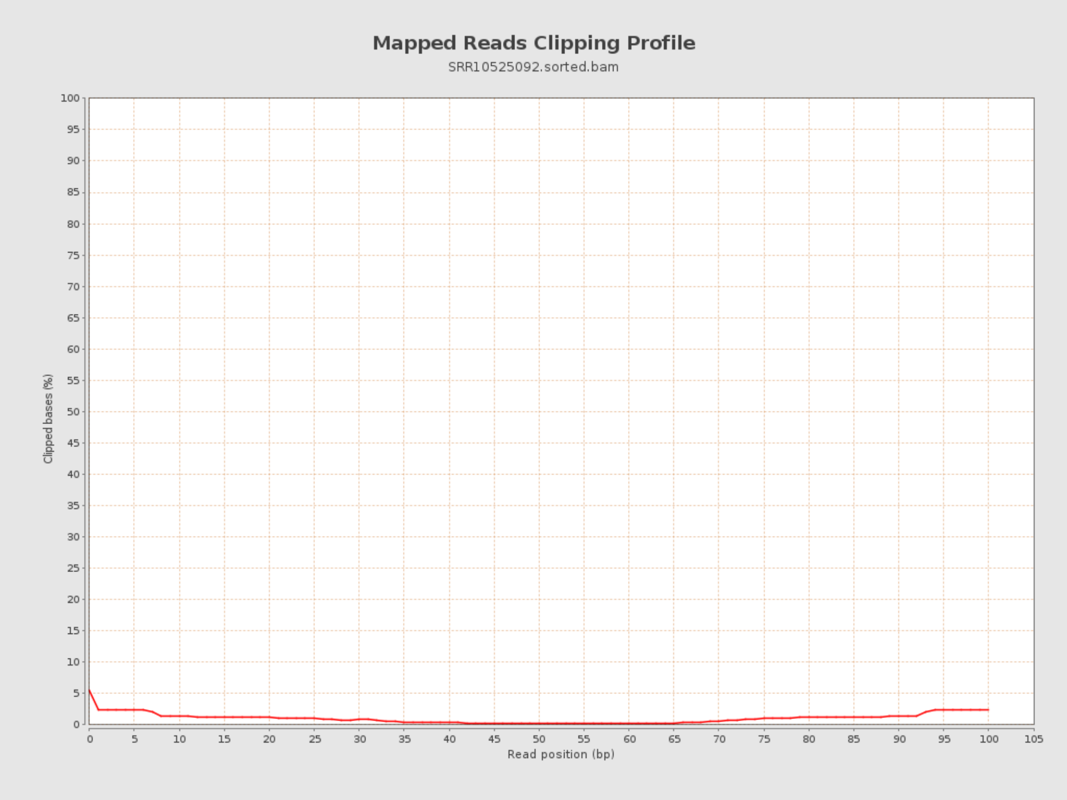
8. Results : Mapped Reads Nucleotide Content



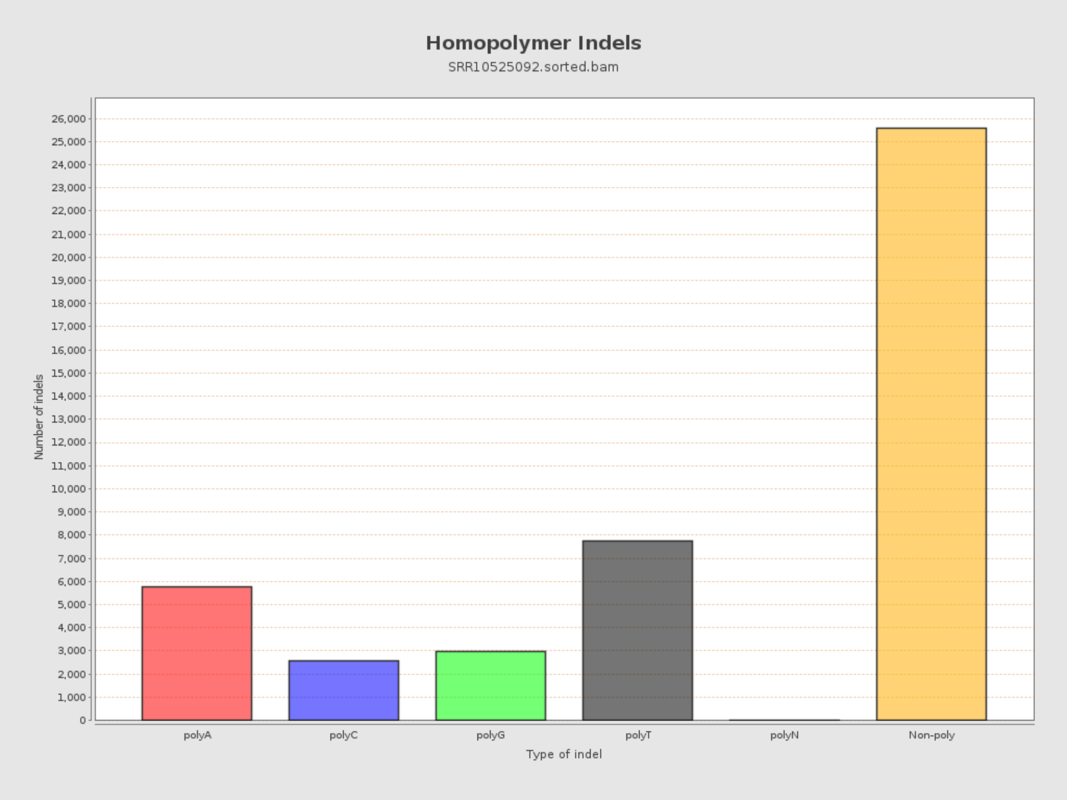
9. Results : Mapped Reads GC-content Distribution



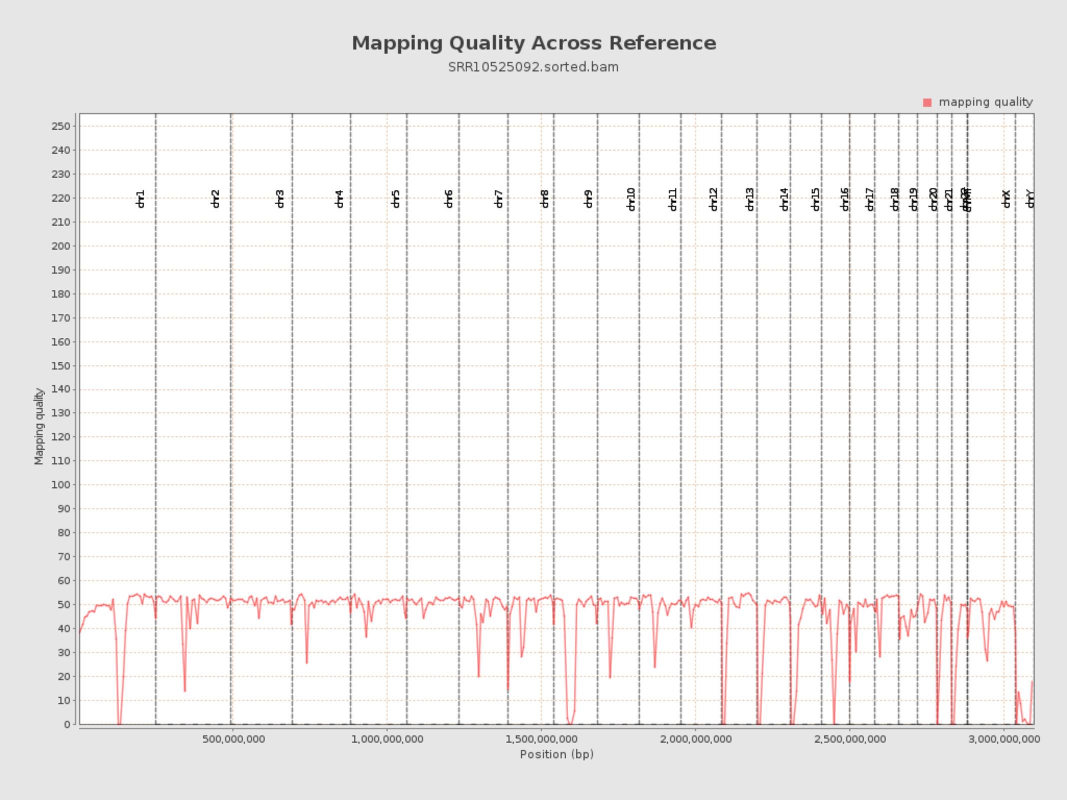
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram