Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 18:12:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525106.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_SRR10525106 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525106.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 18:12:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525106.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,107,941
Mapped reads	990,087 / 89.36%
Unmapped reads	117,854 / 10.64%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	23,692 / 2.14%
Read min/max/mean length	30 / 101 / 101.78
Duplicated reads (estimated)	25,001 / 2.26%
Duplication rate	1.51%
Clipped reads	1,012,109 / 91.35%

2.2. ACGT Content

Number/percentage of A's	20,438,583 / 26.8%
Number/percentage of C's	14,837,081 / 19.46%
Number/percentage of T's	23,578,164 / 30.92%
Number/percentage of G's	17,400,746 / 22.82%
Number/percentage of N's	2,884 / 0%
GC Percentage	42.27%

2.3. Coverage

Mean	0.0246

Standard Deviation	0.268

2.4. Mapping Quality

Mean Mapping Quality	46.72

2.5. Mismatches and indels

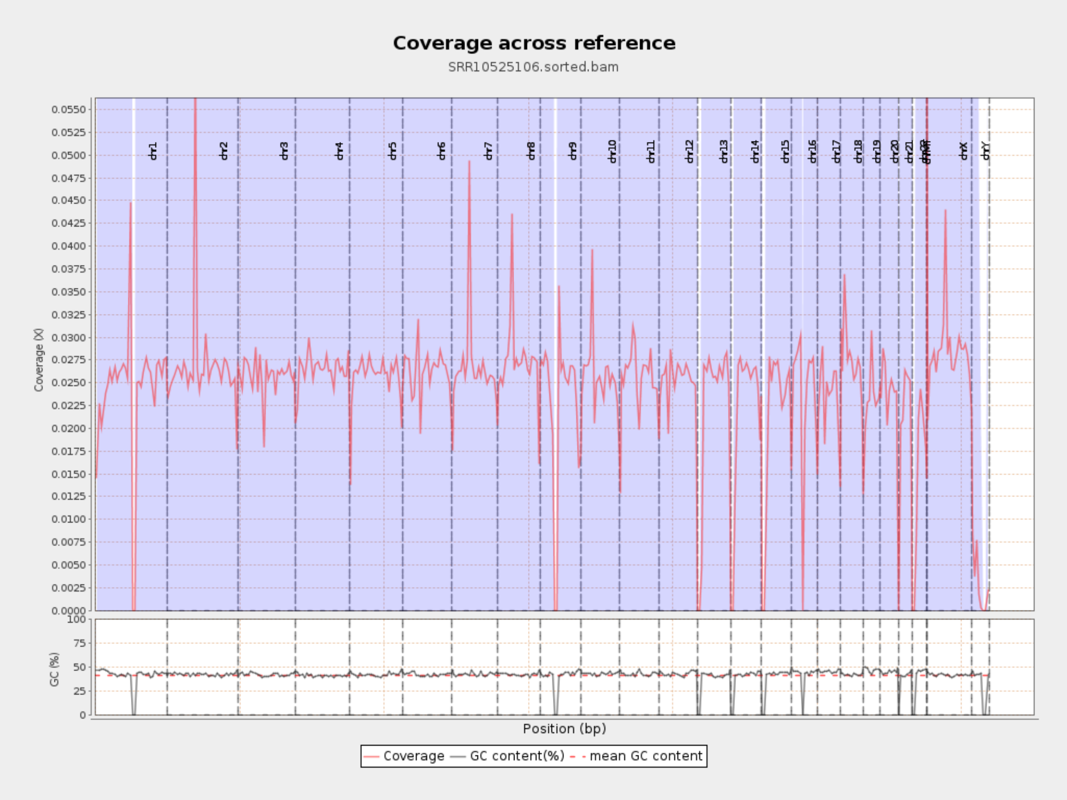
General error rate	0.76%
Mismatches	568,265
Insertions	6,420
Mapped reads with at least one insertion	0.64%
Deletions	17,584
Mapped reads with at least one deletion	1.75%
Homopolymer indels	44.45%

2.6. Chromosome stats

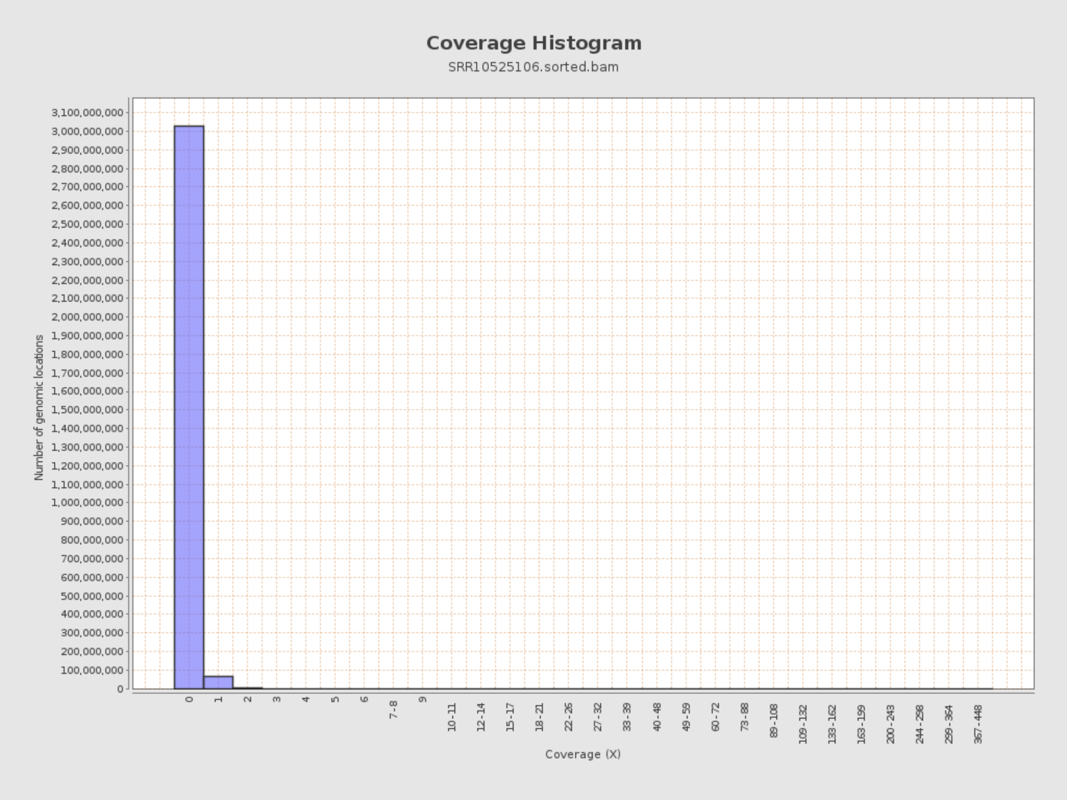
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6015480	0.0241	0.3965
chr2	243199373	6570369	0.027	0.3862
chr3	198022430	5109836	0.0258	0.1699
chr4	191154276	5053502	0.0264	0.178
chr5	180915260	4711147	0.026	0.1741
chr6	171115067	4499924	0.0263	0.1924
chr7	159138663	4274502	0.0269	0.4048

chr8	146364022	4026200	0.0275	0.3442
chr9	141213431	3228972	0.0229	0.2706
chr10	135534747	3494207	0.0258	0.2472
chr11	135006516	3484074	0.0258	0.2596
chr12	133851895	3399250	0.0254	0.1712
chr13	115169878	2522697	0.0219	0.1564
chr14	107349540	2314042	0.0216	0.1779
chr15	102531392	2143470	0.0209	0.1535
chr16	90354753	2093198	0.0232	0.1738
chr17	81195210	1913397	0.0236	0.1964
chr18	78077248	2167048	0.0278	0.4541
chr19	59128983	1376024	0.0233	0.3011
chr20	63025520	1515541	0.024	0.169
chr21	48129895	1004370	0.0209	0.1605
chr22	51304566	754092	0.0147	0.1278
chrMT	16571	1204	0.0727	0.4562
chrX	155270560	4446454	0.0286	0.227
chrY	59373566	168165	0.0028	0.0699

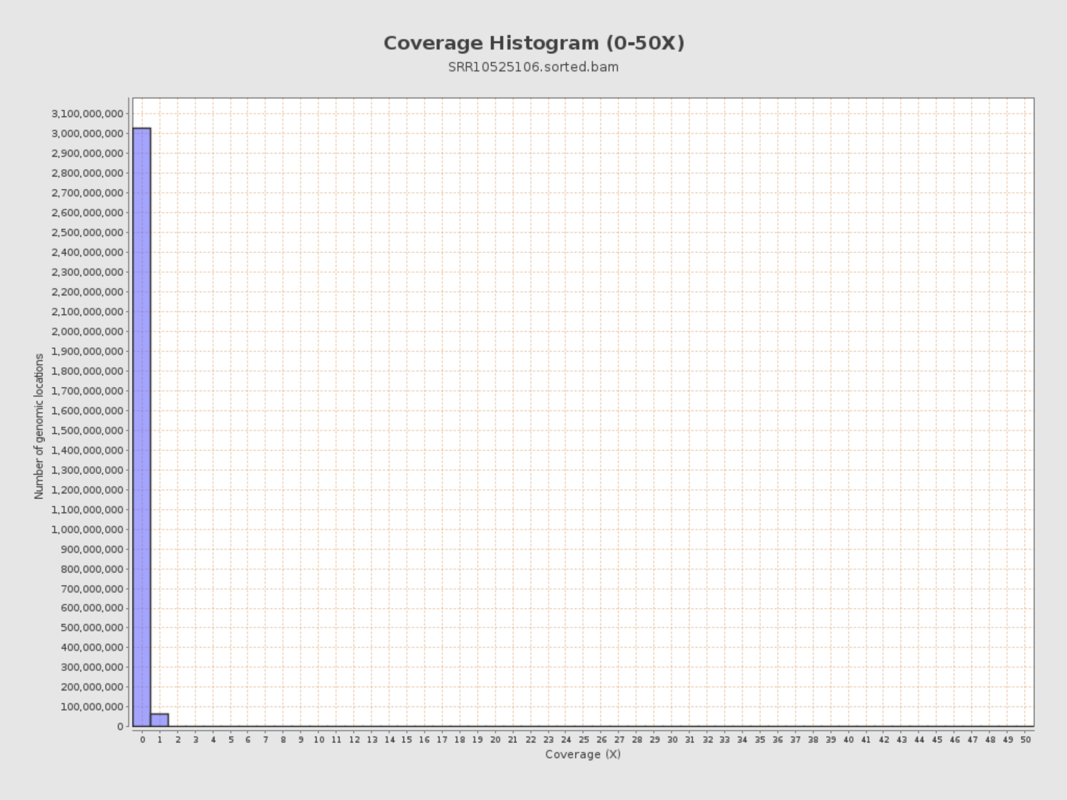
3. Results : Coverage across reference



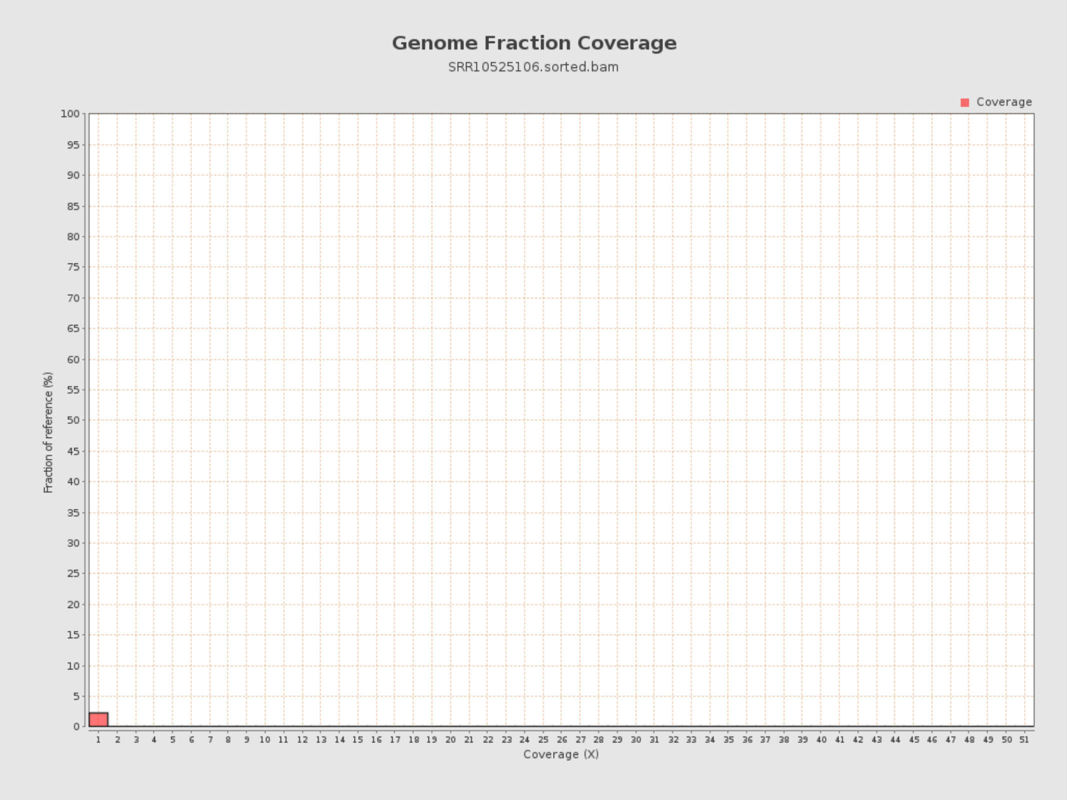
4. Results : Coverage Histogram



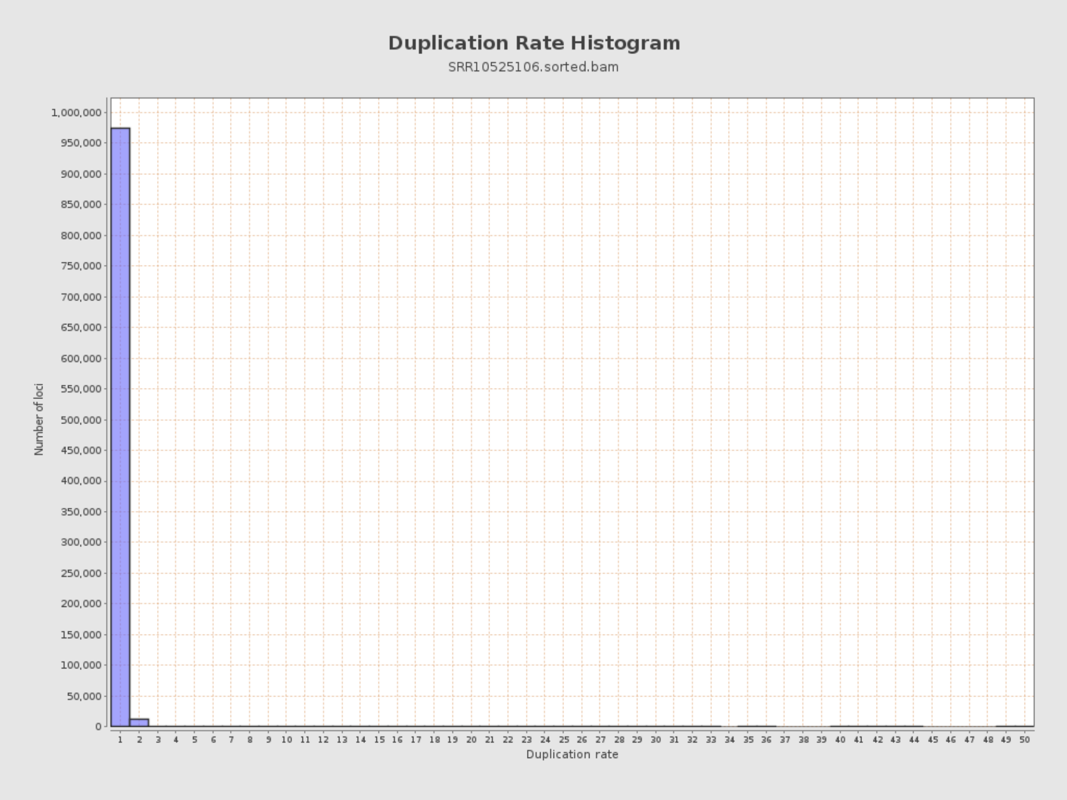
5. Results : Coverage Histogram (0-50X)



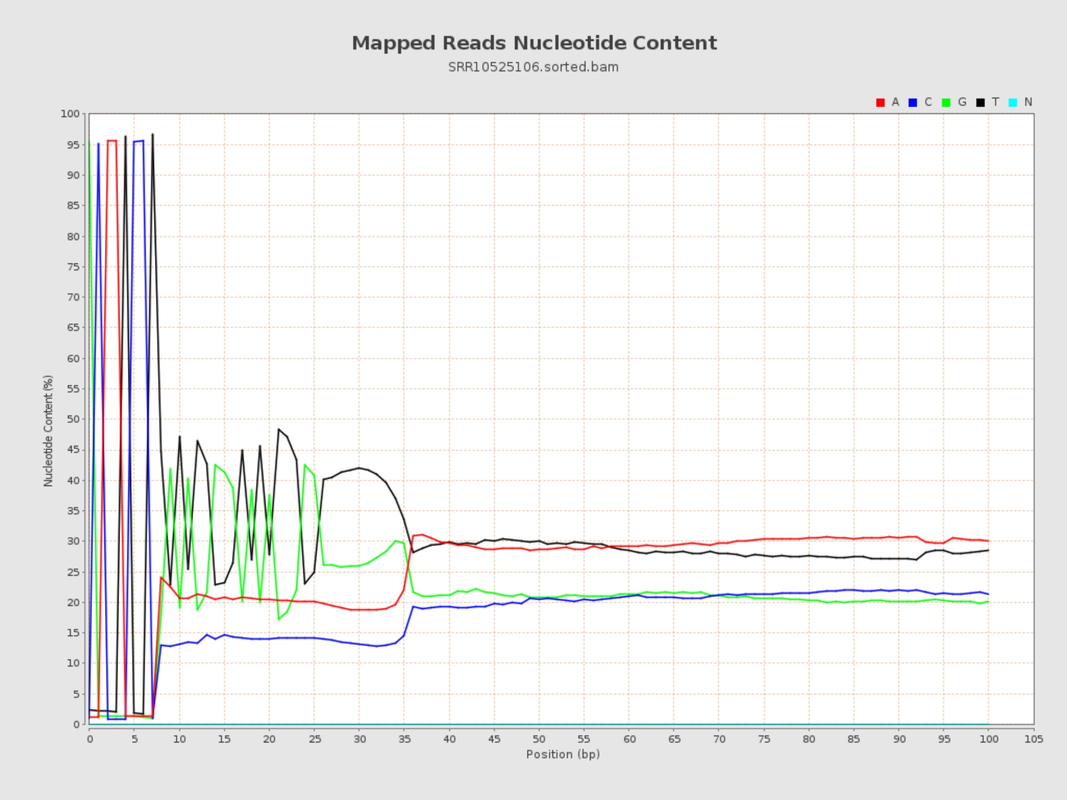
6. Results : Genome Fraction Coverage



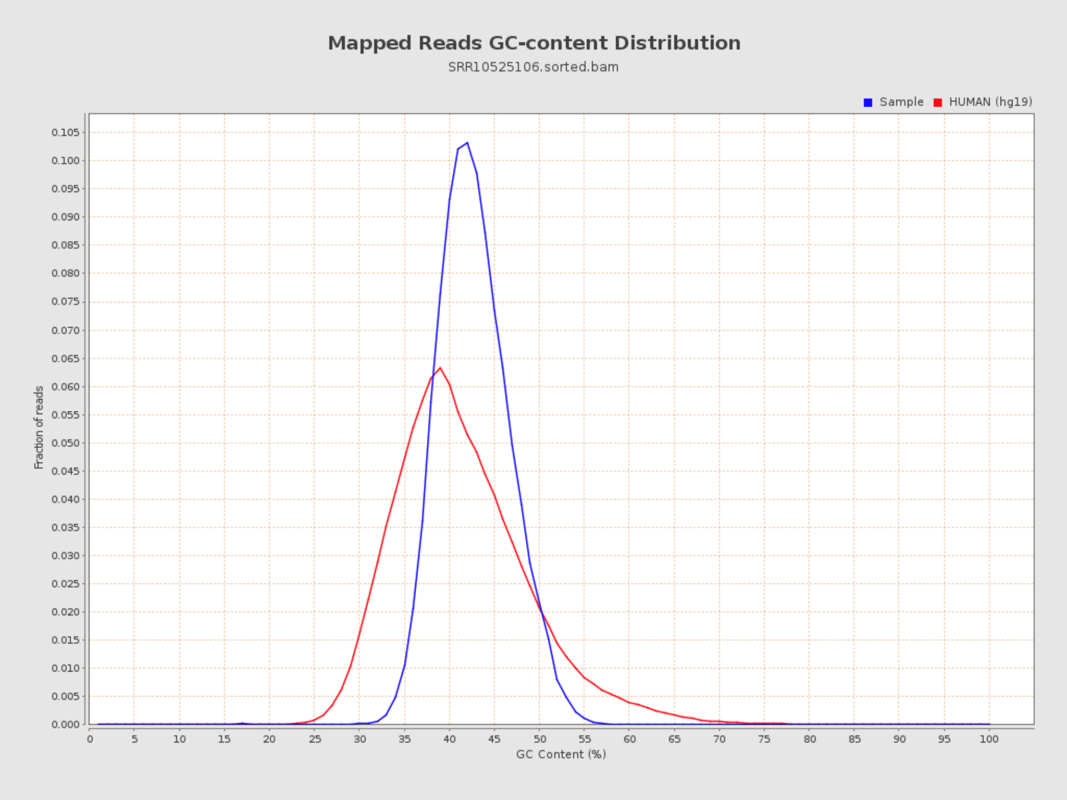
7. Results : Duplication Rate Histogram



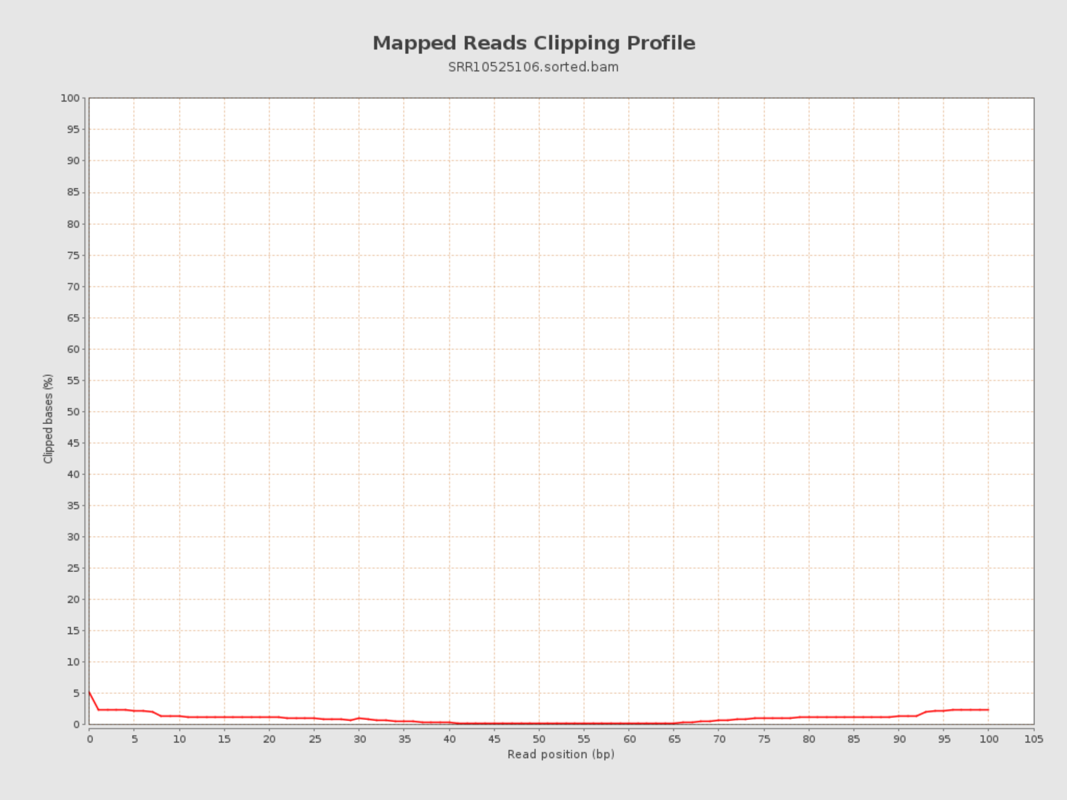
8. Results : Mapped Reads Nucleotide Content



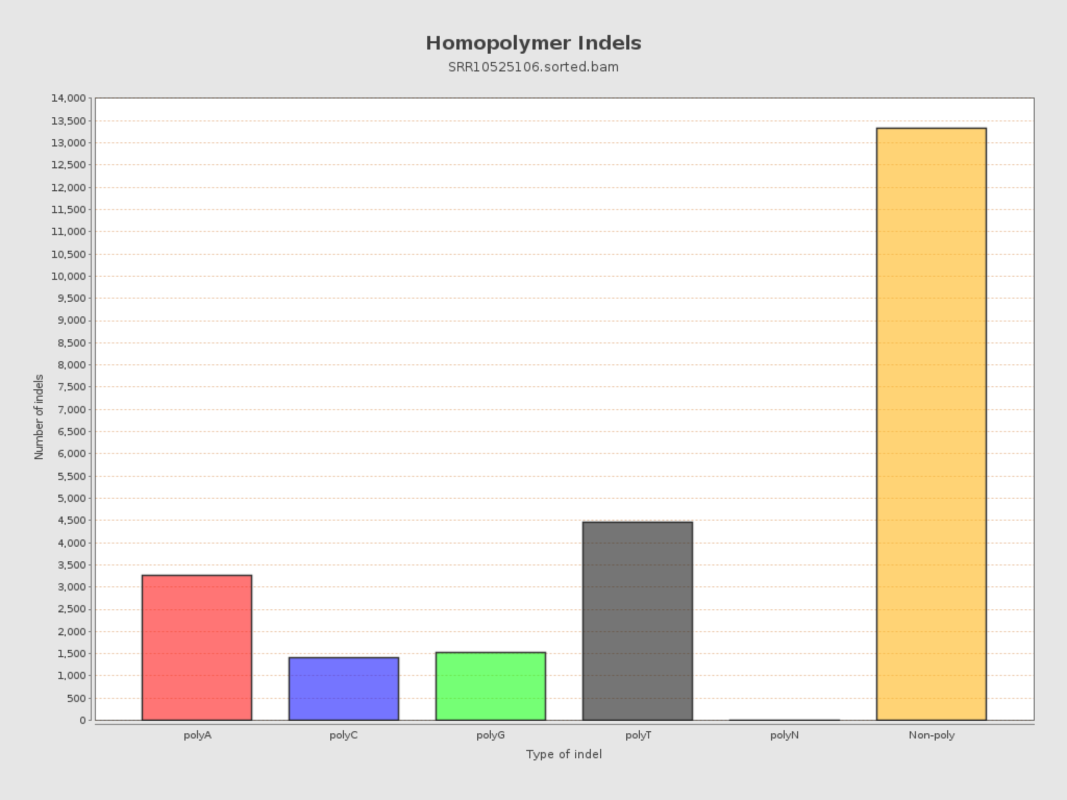
9. Results : Mapped Reads GC-content Distribution



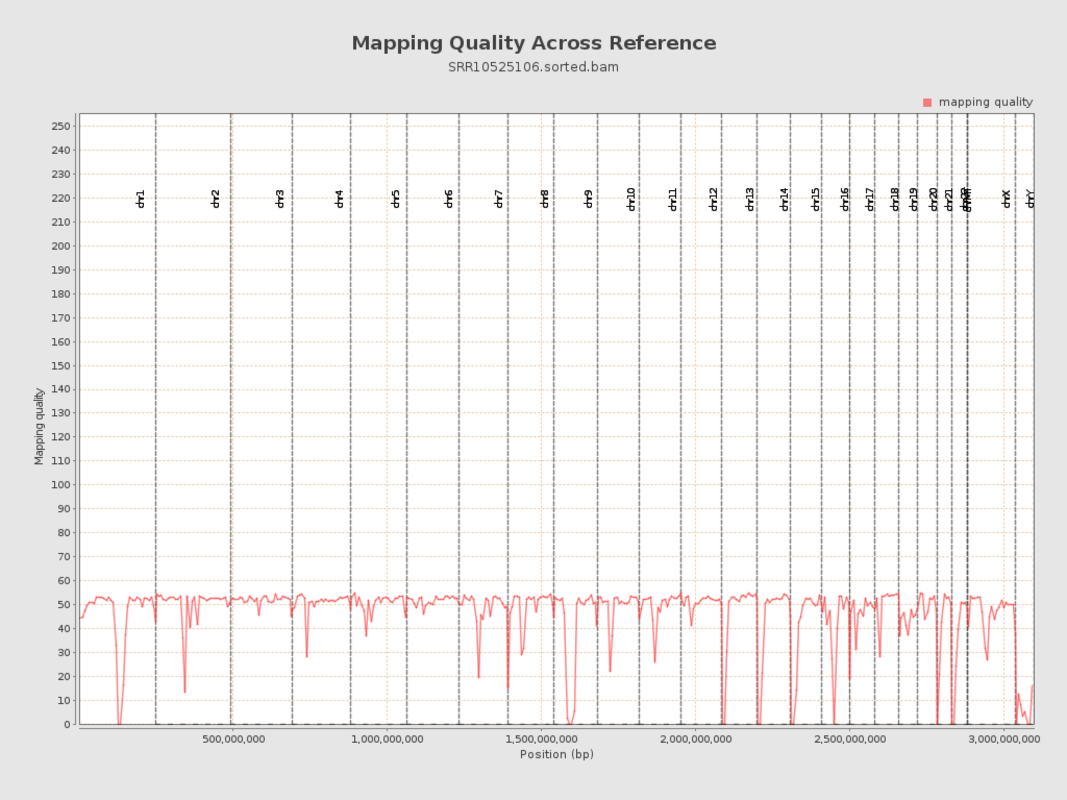
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram