Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 13:08:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525011.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_SRR10525011 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525011.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 13:08:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525011.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,808,542
Mapped reads	1,557,010 / 86.09%
Unmapped reads	251,532 / 13.91%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,598 / 0.53%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	209,085 / 11.56%
Duplication rate	10.42%
Clipped reads	1,563,078 / 86.43%

2.2. ACGT Content

Number/percentage of A's	20,811,344 / 24.27%
Number/percentage of C's	17,099,493 / 19.94%
Number/percentage of T's	27,822,862 / 32.44%
Number/percentage of G's	20,027,986 / 23.35%
Number/percentage of N's	2,286 / 0%
GC Percentage	43.29%

2.3. Coverage

Mean	0.0277

Standard Deviation	0.2991

2.4. Mapping Quality

Mean Mapping Quality	44.86

2.5. Mismatches and indels

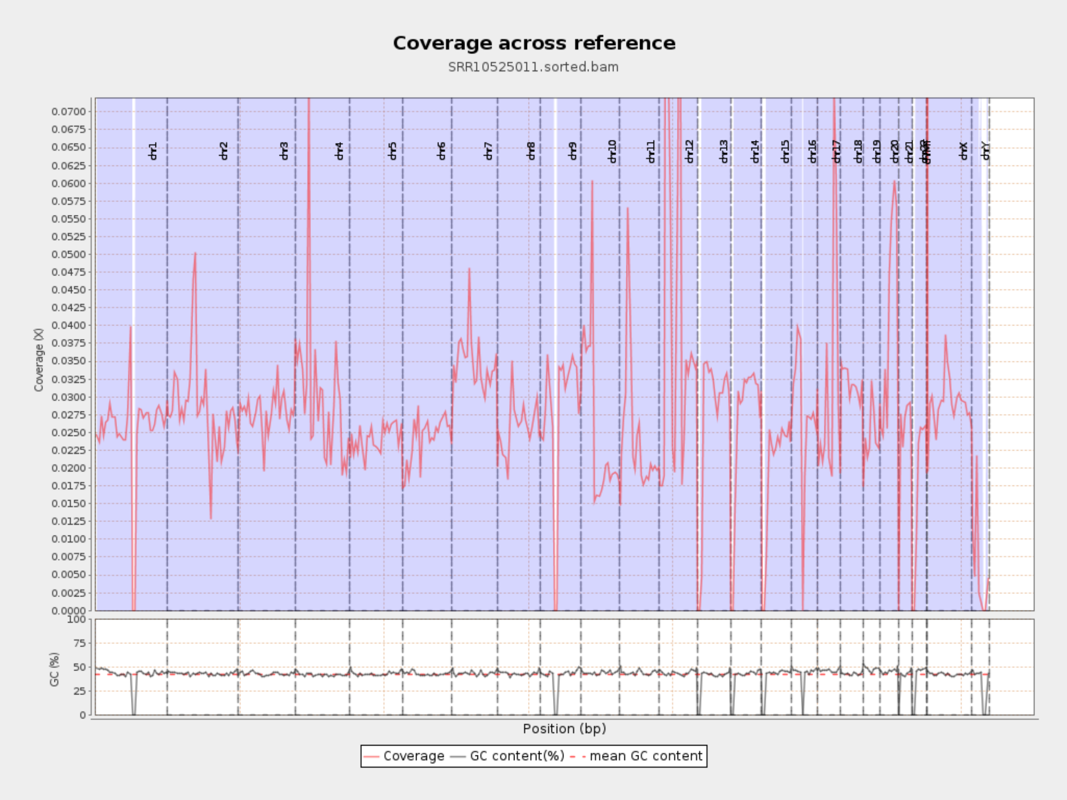
General error rate	0.59%
Mismatches	497,150
Insertions	5,256
Mapped reads with at least one insertion	0.34%
Deletions	20,480
Mapped reads with at least one deletion	1.3%
Homopolymer indels	41.02%

2.6. Chromosome stats

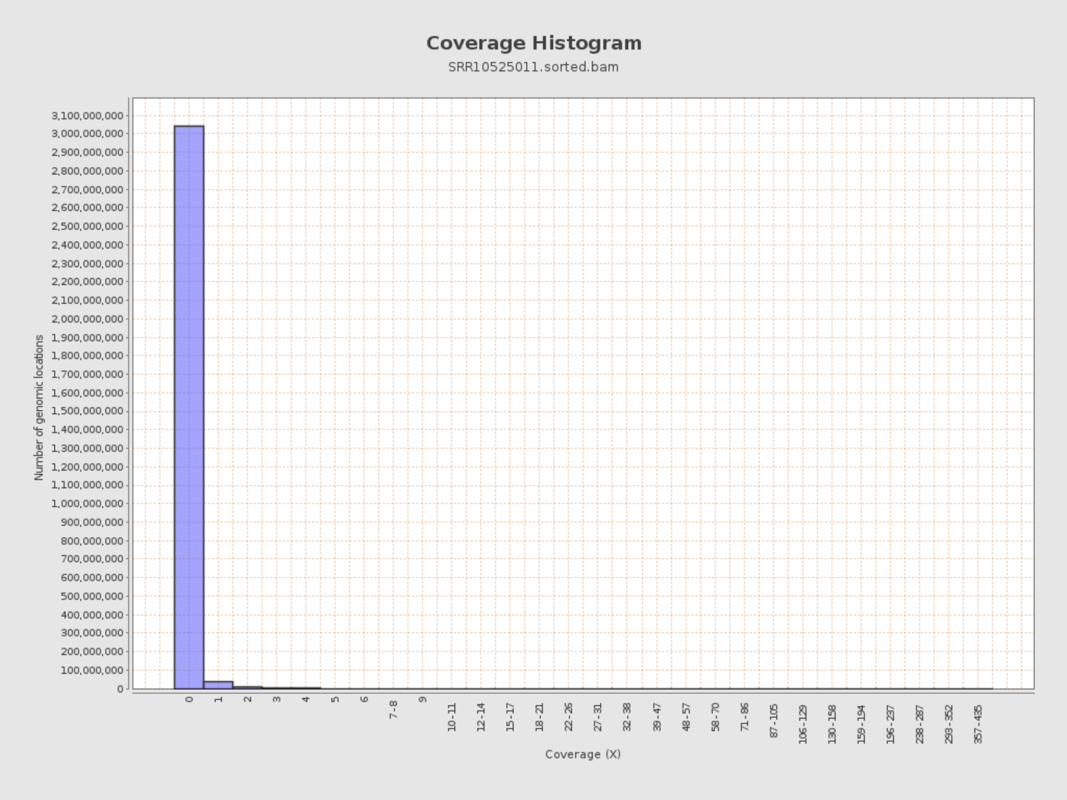
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6271616	0.0252	0.3863
chr2	243199373	6886342	0.0283	0.3382
chr3	198022430	5513967	0.0278	0.2369
chr4	191154276	5768318	0.0302	0.3039
chr5	180915260	4395239	0.0243	0.2214
chr6	171115067	4131273	0.0241	0.2319
chr7	159138663	5552891	0.0349	0.355

chr8	146364022	3795279	0.0259	0.3208
chr9	141213431	3952199	0.028	0.2891
chr10	135534747	3519450	0.026	0.355
chr11	135006516	3308916	0.0245	0.2502
chr12	133851895	5979109	0.0447	0.3216
chr13	115169878	3065216	0.0266	0.2328
chr14	107349540	2800356	0.0261	0.2386
chr15	102531392	2000471	0.0195	0.1977
chr16	90354753	2439016	0.027	0.2458
chr17	81195210	2612569	0.0322	0.2661
chr18	78077248	2491502	0.0319	0.4192
chr19	59128983	1471150	0.0249	0.3215
chr20	63025520	2615536	0.0415	0.3079
chr21	48129895	1169525	0.0243	0.2512
chr22	51304566	894240	0.0174	0.1871
chrMT	16571	296320	17.8818	12.0152
chrX	155270560	4538012	0.0292	0.2617
chrY	59373566	329788	0.0056	0.1918

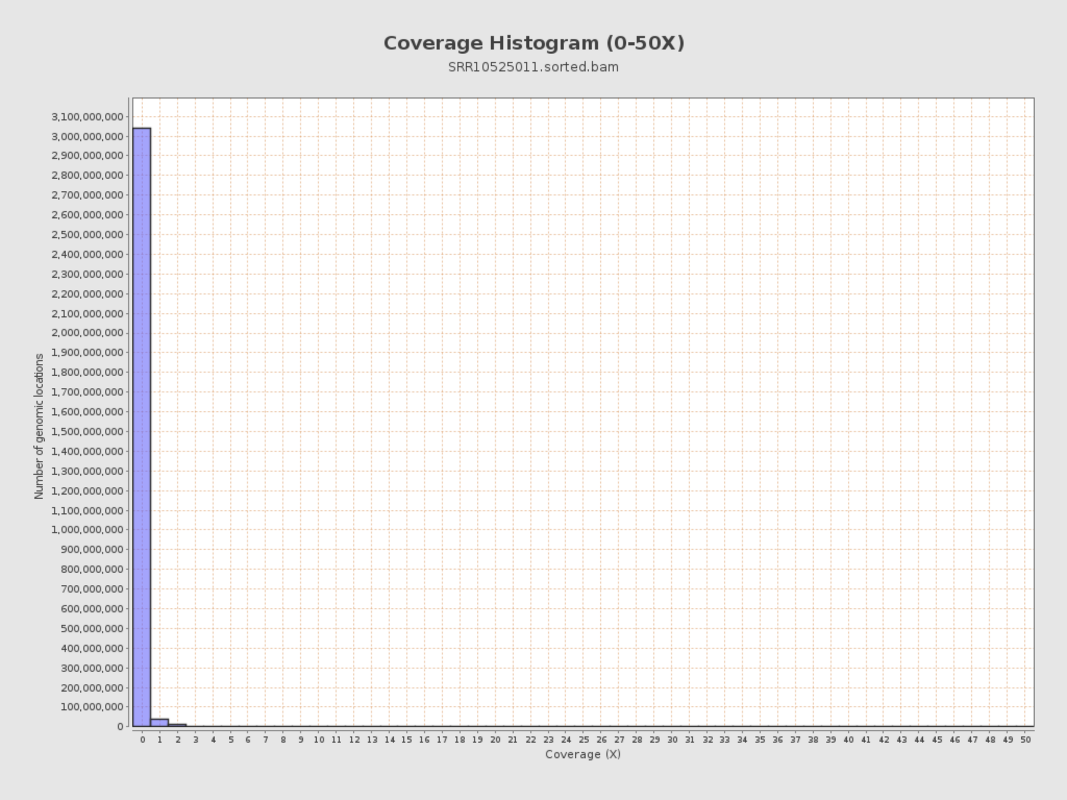
3. Results : Coverage across reference



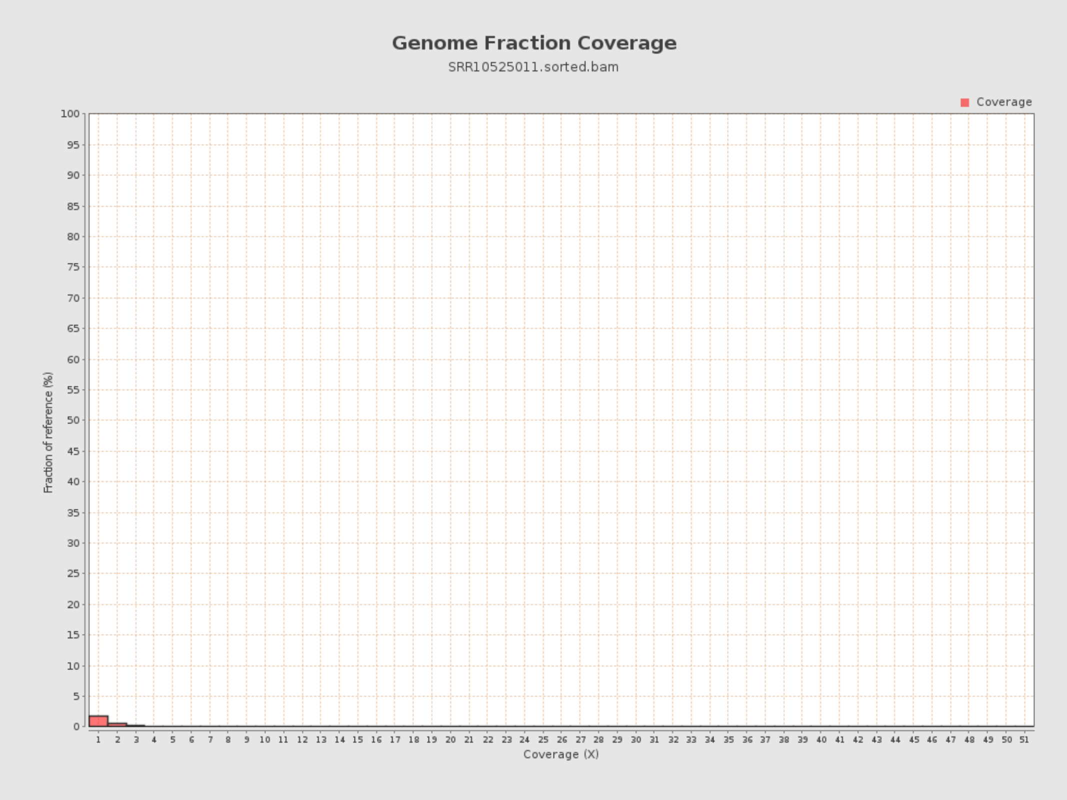
4. Results : Coverage Histogram



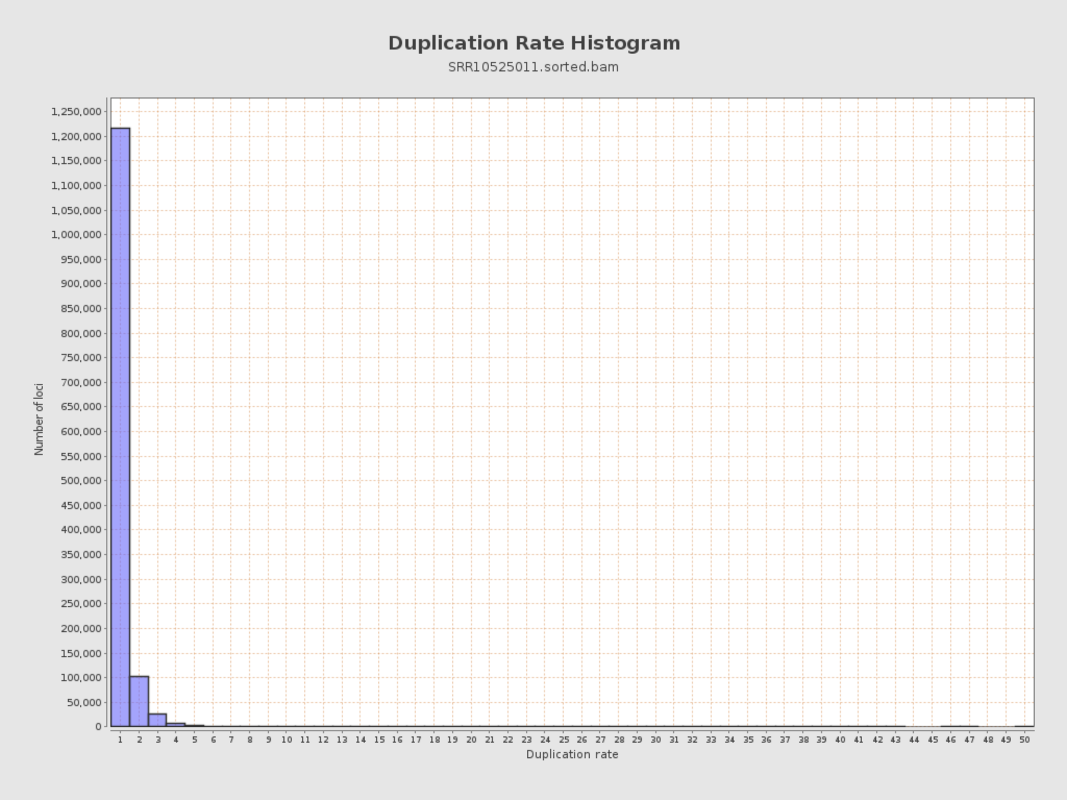
5. Results : Coverage Histogram (0-50X)



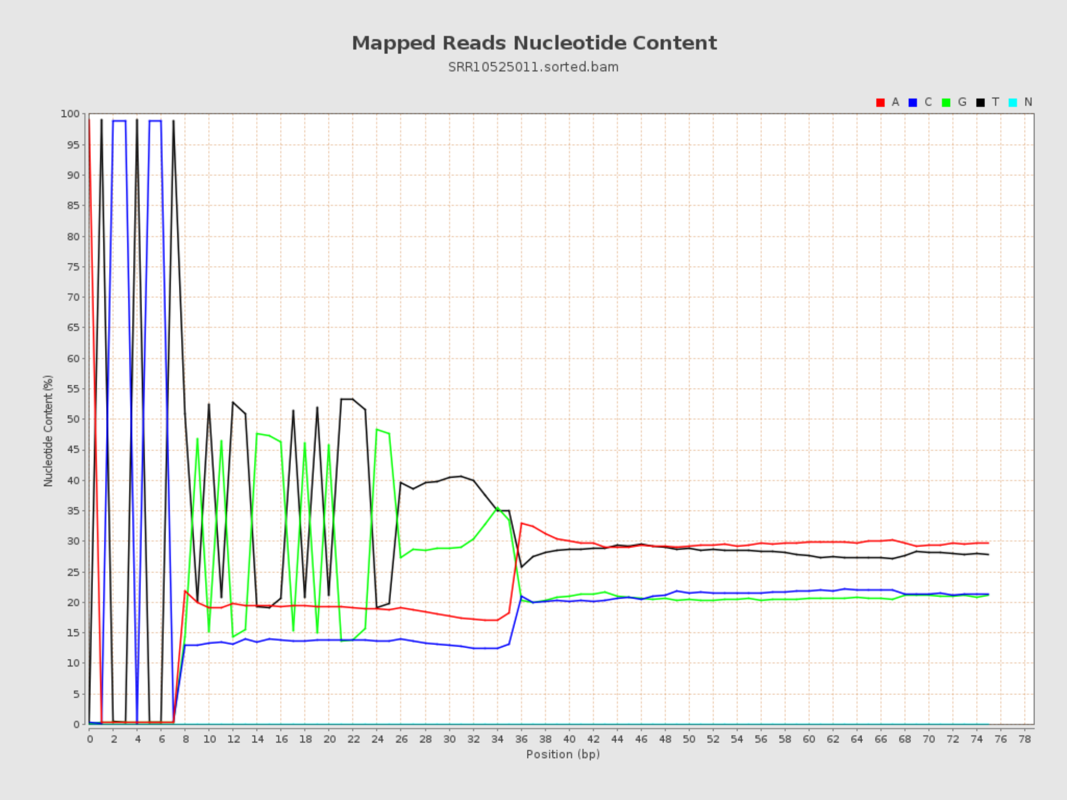
6. Results : Genome Fraction Coverage



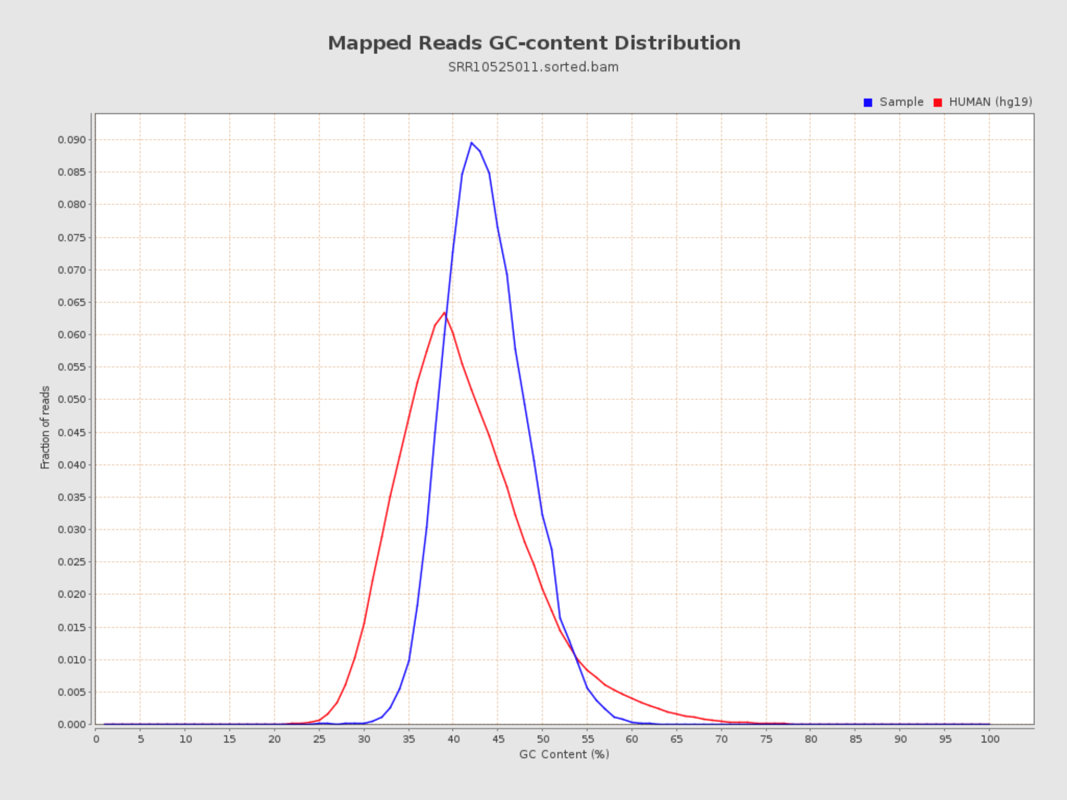
7. Results : Duplication Rate Histogram



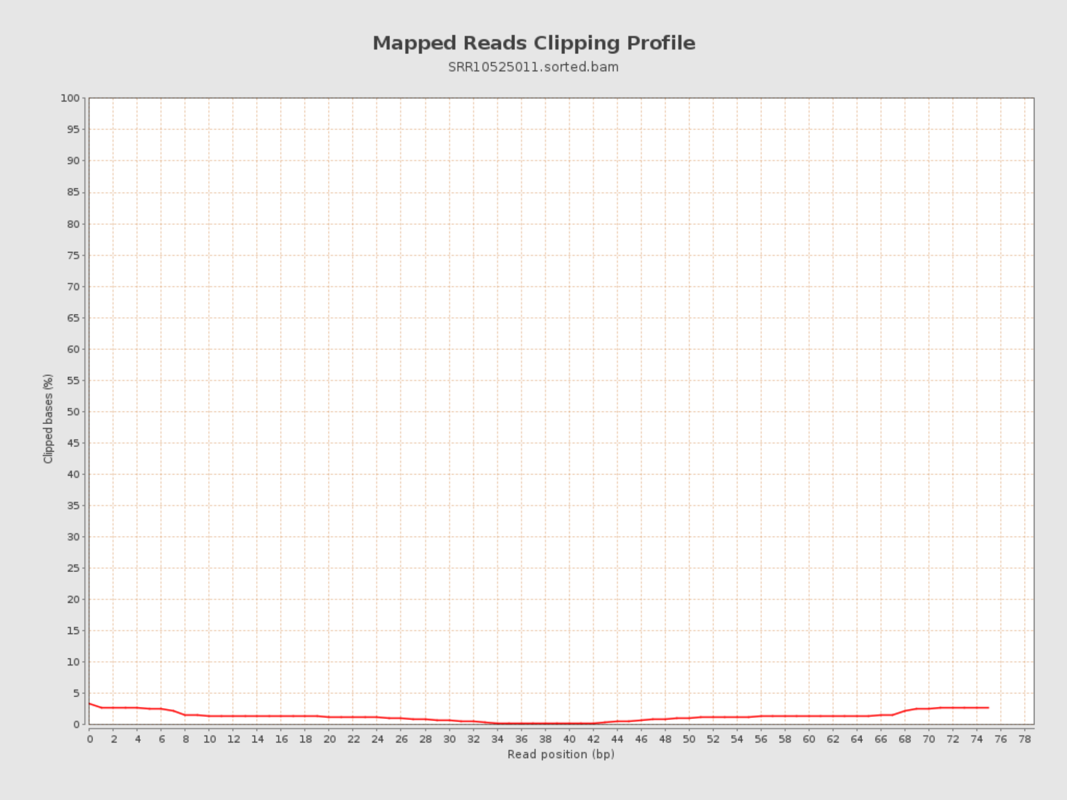
8. Results : Mapped Reads Nucleotide Content



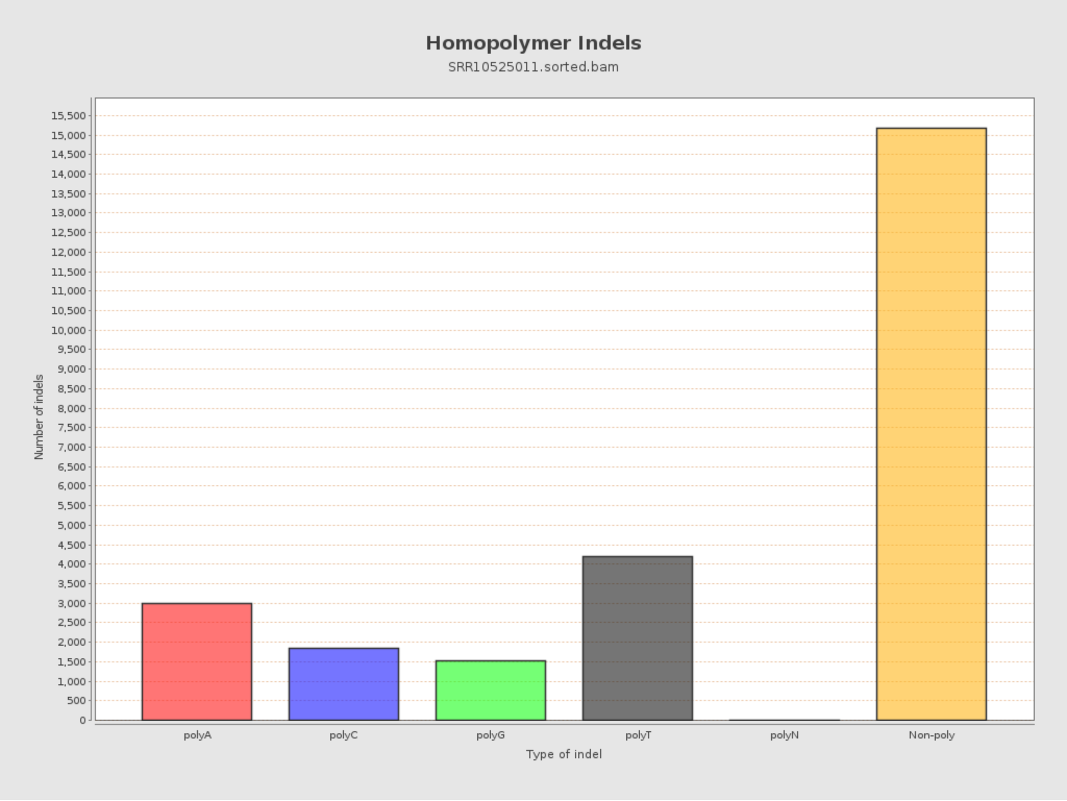
9. Results : Mapped Reads GC-content Distribution



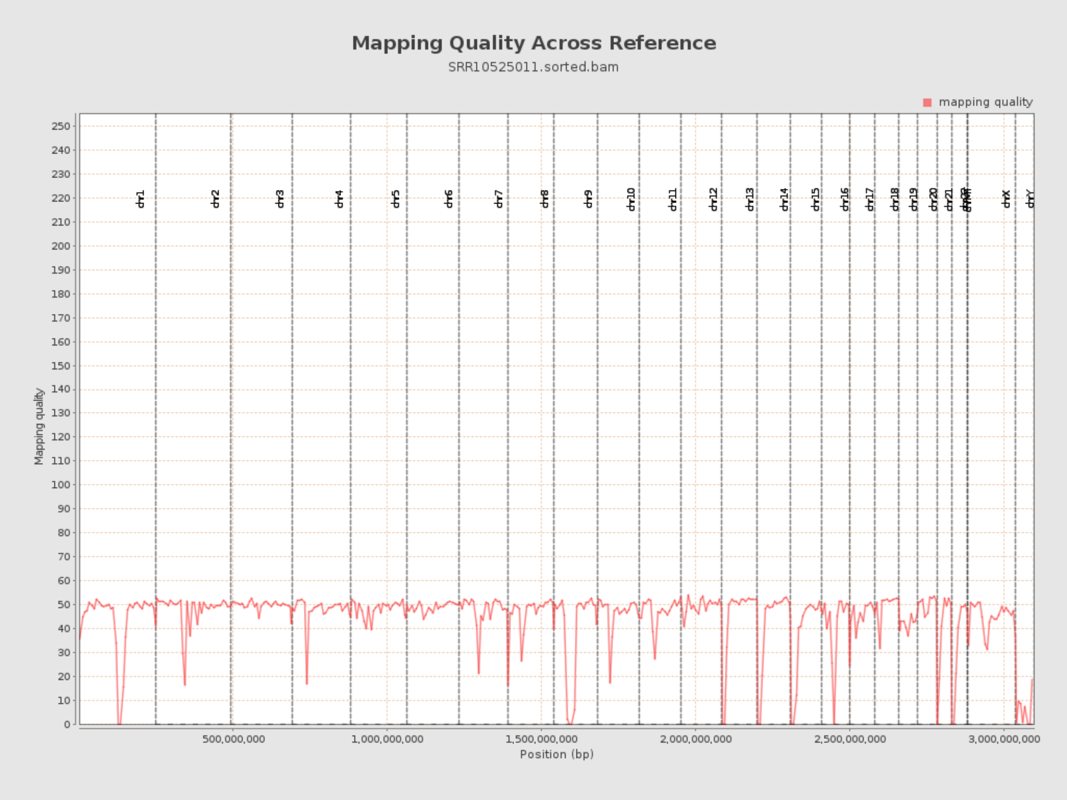
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram