Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 16:50:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525081.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_SRR10525081 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525081.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 16:50:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525081.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,908,284
Mapped reads	1,502,869 / 78.75%
Unmapped reads	405,415 / 21.25%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,622 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	72,699 / 3.81%
Duplication rate	3.9%
Clipped reads	1,505,068 / 78.87%

2.2. ACGT Content

Number/percentage of A's	23,514,256 / 26.4%
Number/percentage of C's	16,783,273 / 18.84%
Number/percentage of T's	28,077,883 / 31.52%
Number/percentage of G's	20,681,748 / 23.22%
Number/percentage of N's	9,568 / 0.01%
GC Percentage	42.06%

2.3. Coverage

Mean	0.0288

Standard Deviation	0.2636

2.4. Mapping Quality

Mean Mapping Quality	45.92

2.5. Mismatches and indels

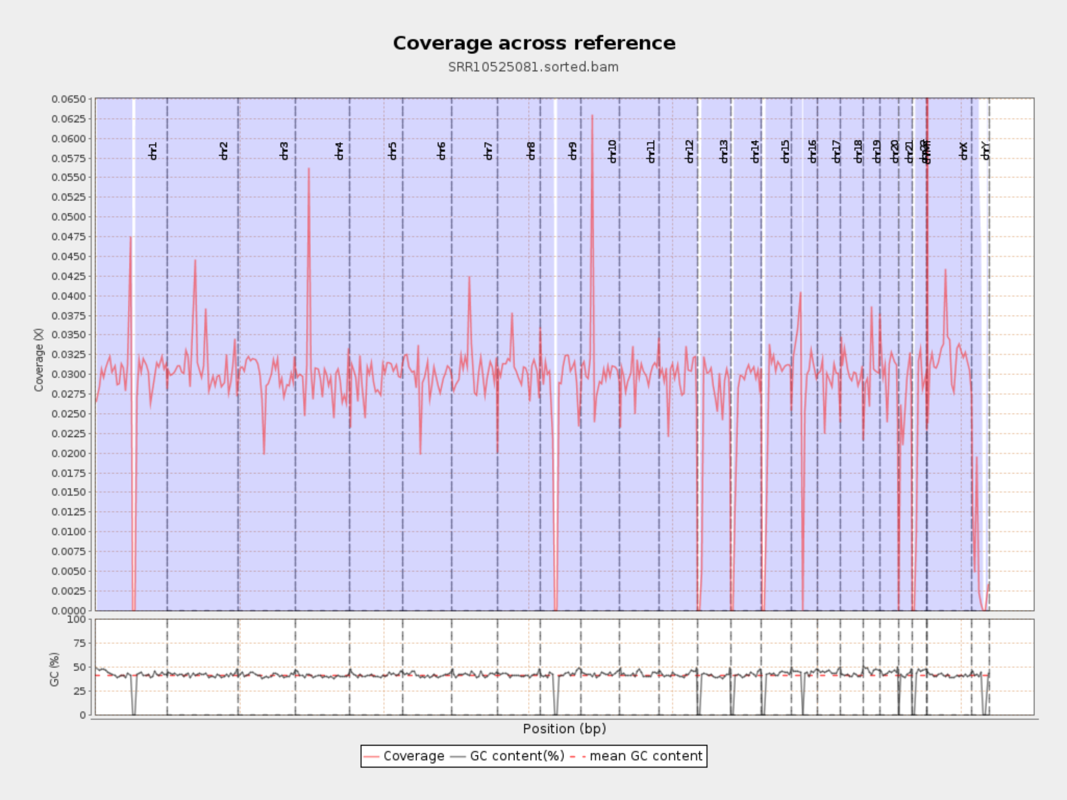
General error rate	0.49%
Mismatches	422,832
Insertions	6,640
Mapped reads with at least one insertion	0.44%
Deletions	17,665
Mapped reads with at least one deletion	1.17%
Homopolymer indels	40.77%

2.6. Chromosome stats

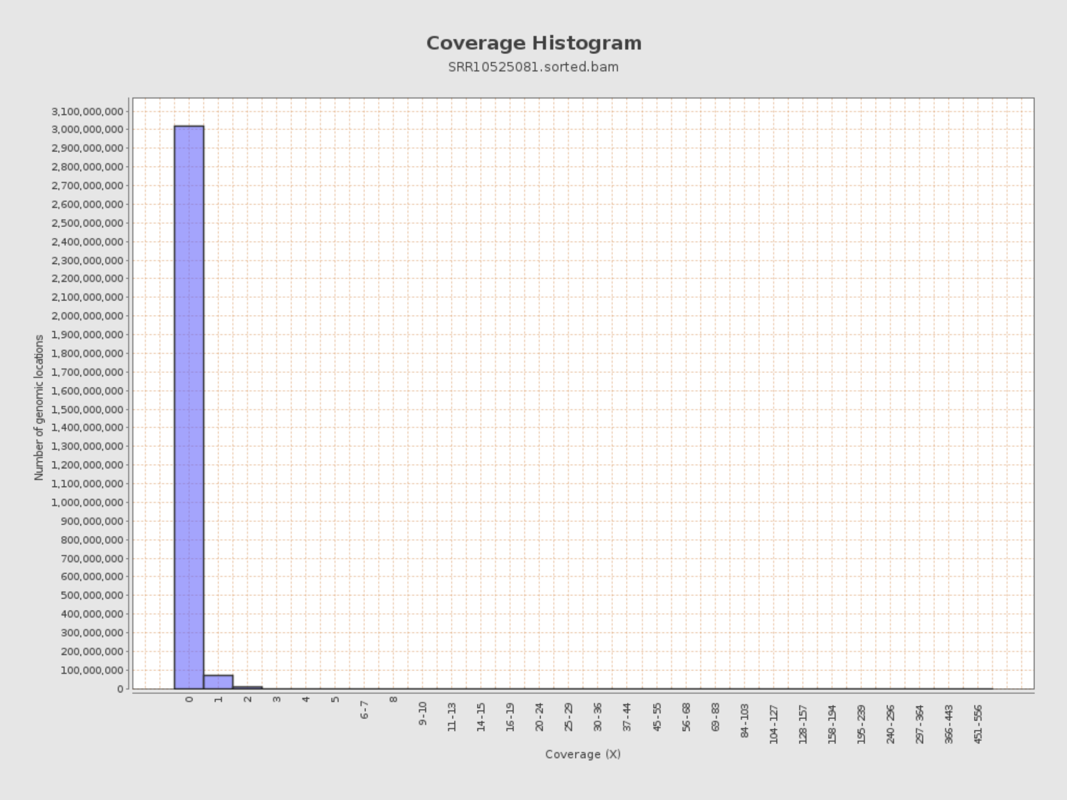
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7178771	0.0288	0.4583
chr2	243199373	7573670	0.0311	0.3264
chr3	198022430	5893779	0.0298	0.1924
chr4	191154276	5770237	0.0302	0.2221
chr5	180915260	5387732	0.0298	0.1915
chr6	171115067	5086469	0.0297	0.2071
chr7	159138663	4895495	0.0308	0.304

chr8	146364022	4495366	0.0307	0.2871
chr9	141213431	3731125	0.0264	0.2211
chr10	135534747	4289468	0.0316	0.3073
chr11	135006516	4047695	0.03	0.224
chr12	133851895	3988873	0.0298	0.1949
chr13	115169878	2783254	0.0242	0.1719
chr14	107349540	2673155	0.0249	0.1784
chr15	102531392	2619162	0.0255	0.1782
chr16	90354753	2630405	0.0291	0.2048
chr17	81195210	2369584	0.0292	0.1985
chr18	78077248	2382957	0.0305	0.3474
chr19	59128983	1798744	0.0304	0.3322
chr20	63025520	1907904	0.0303	0.1994
chr21	48129895	1182707	0.0246	0.2011
chr22	51304566	1075897	0.021	0.1611
chrMT	16571	15844	0.9561	1.0703
chrX	155270560	5010111	0.0323	0.2147
chrY	59373566	307172	0.0052	0.1725

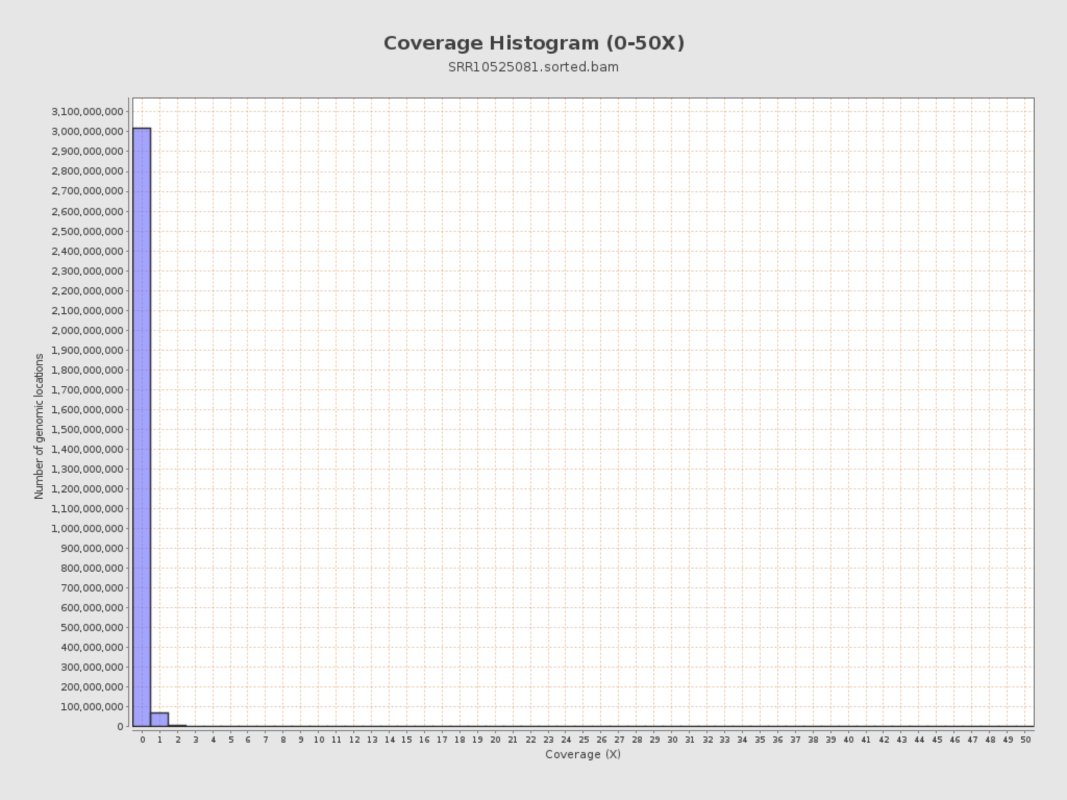
3. Results : Coverage across reference



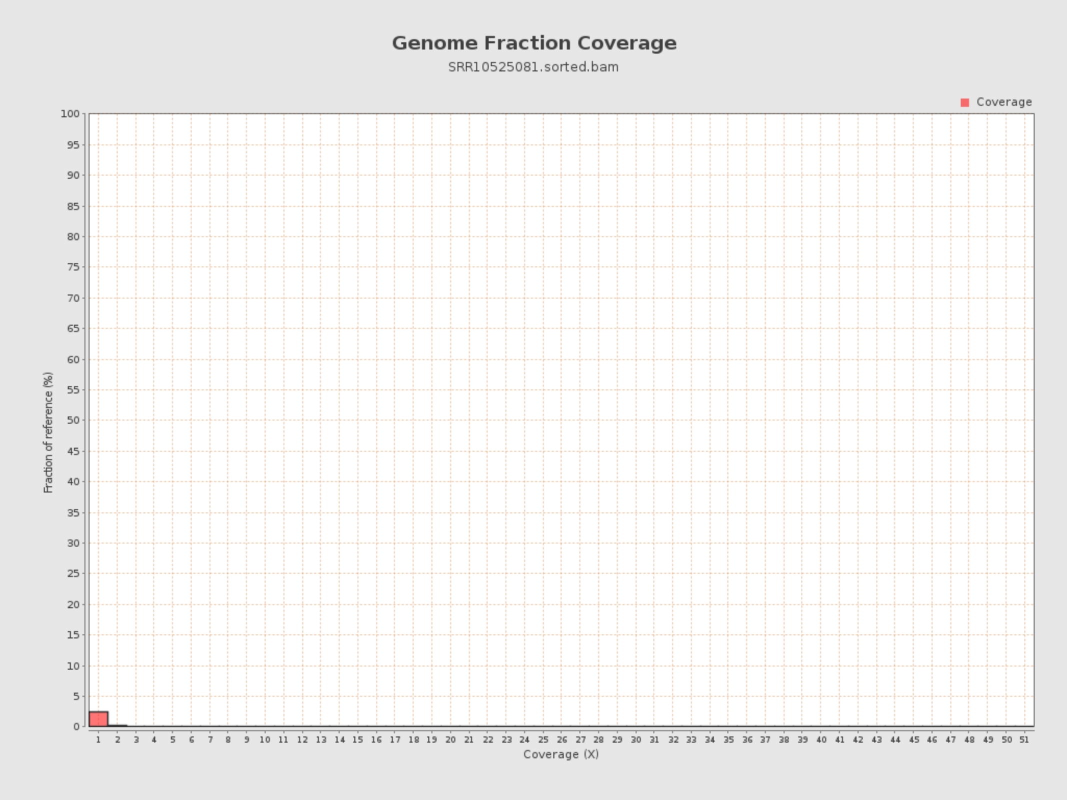
4. Results : Coverage Histogram



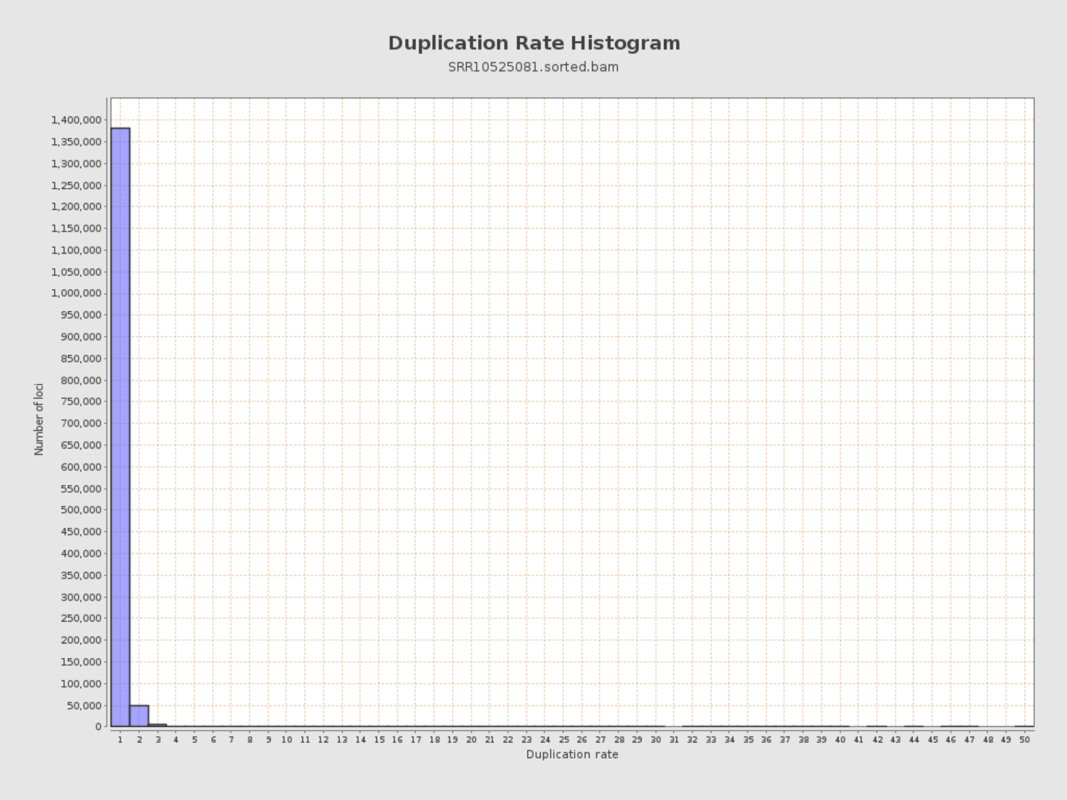
5. Results : Coverage Histogram (0-50X)



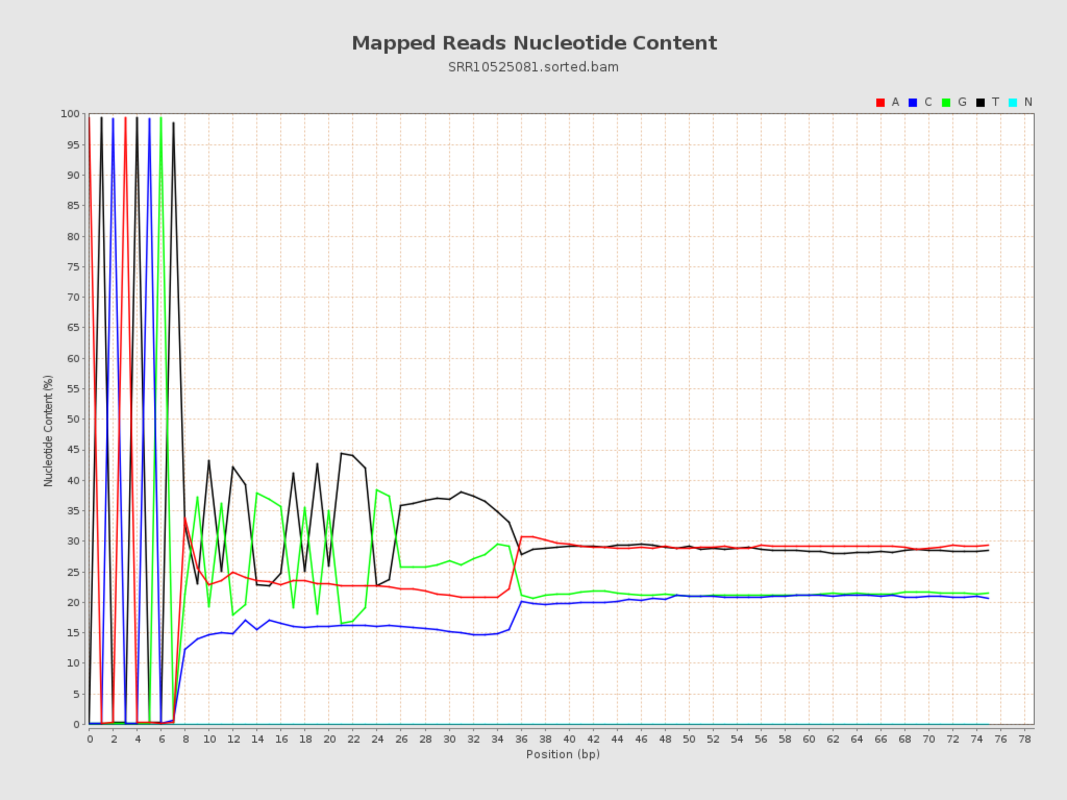
6. Results : Genome Fraction Coverage



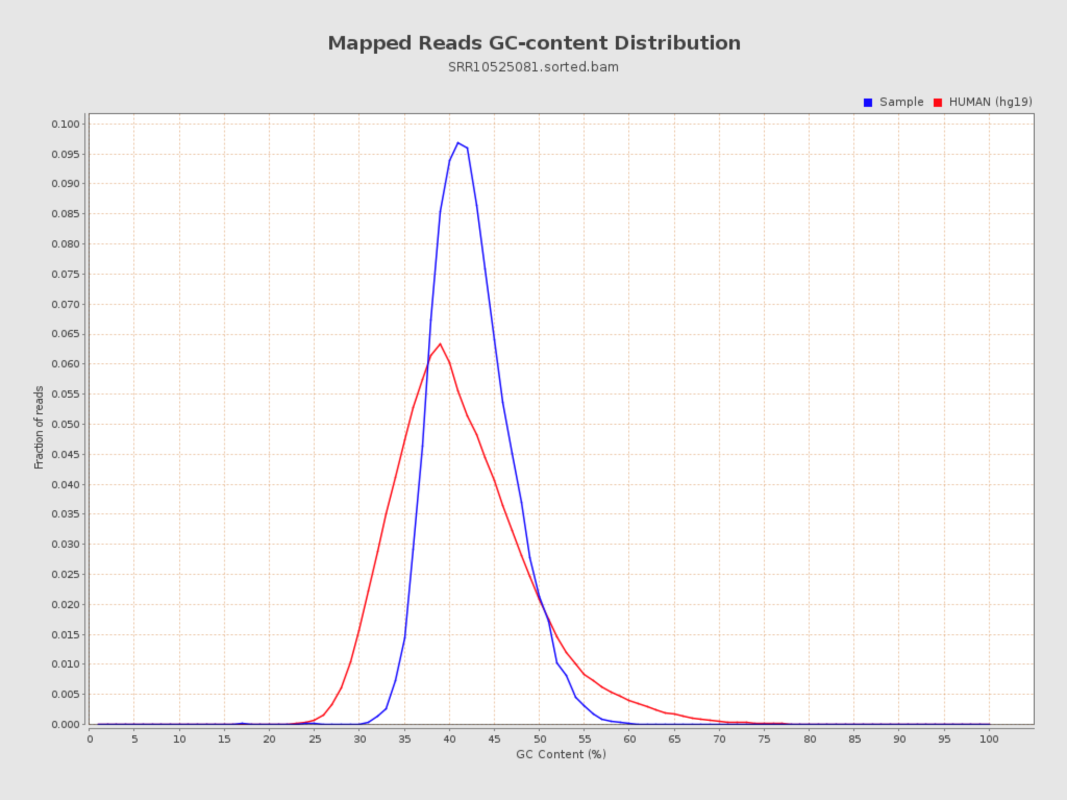
7. Results : Duplication Rate Histogram



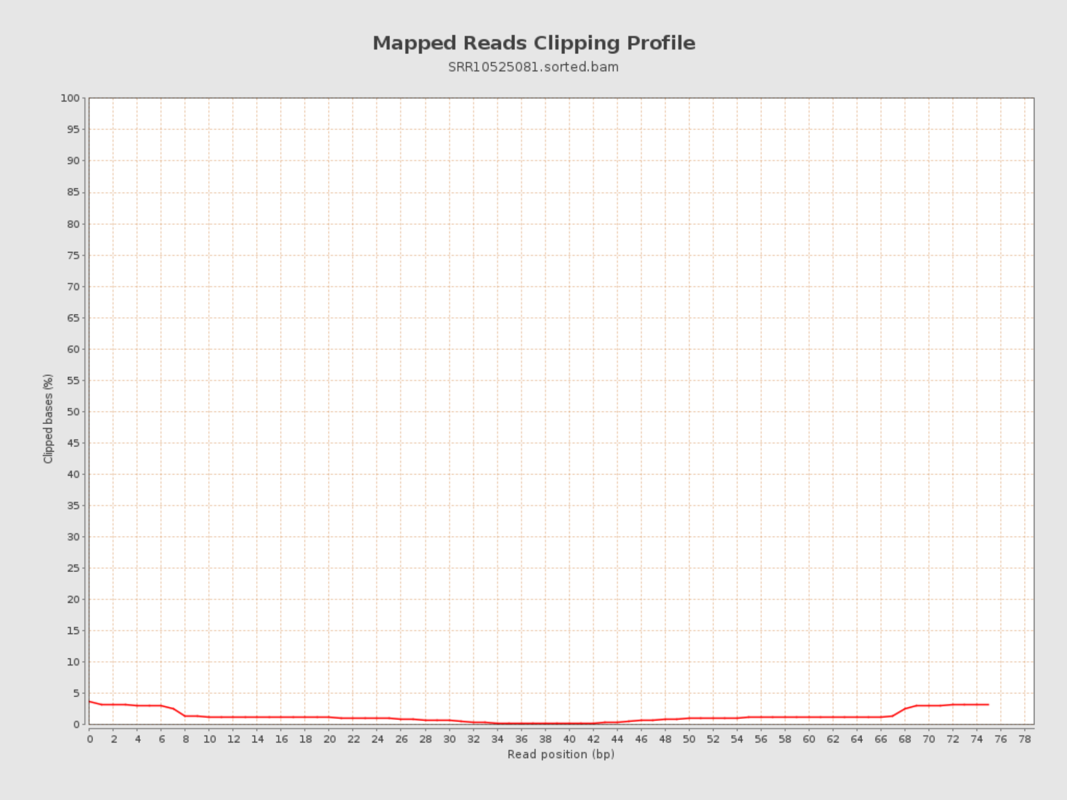
8. Results : Mapped Reads Nucleotide Content



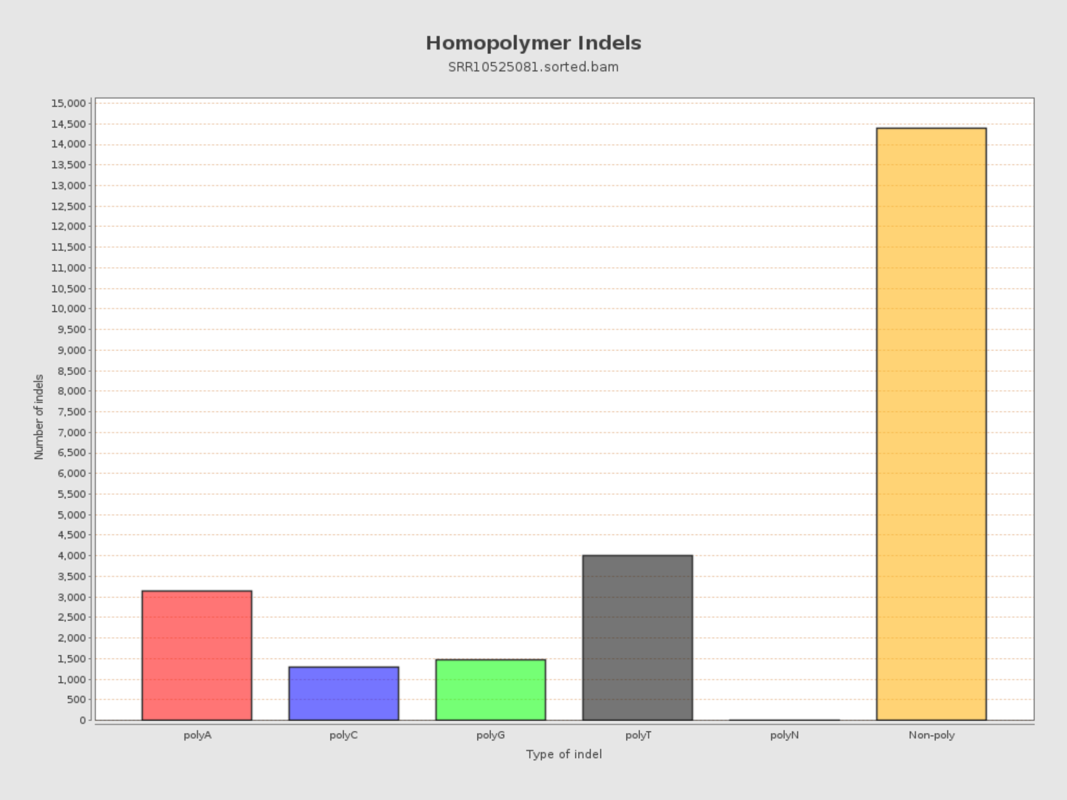
9. Results : Mapped Reads GC-content Distribution



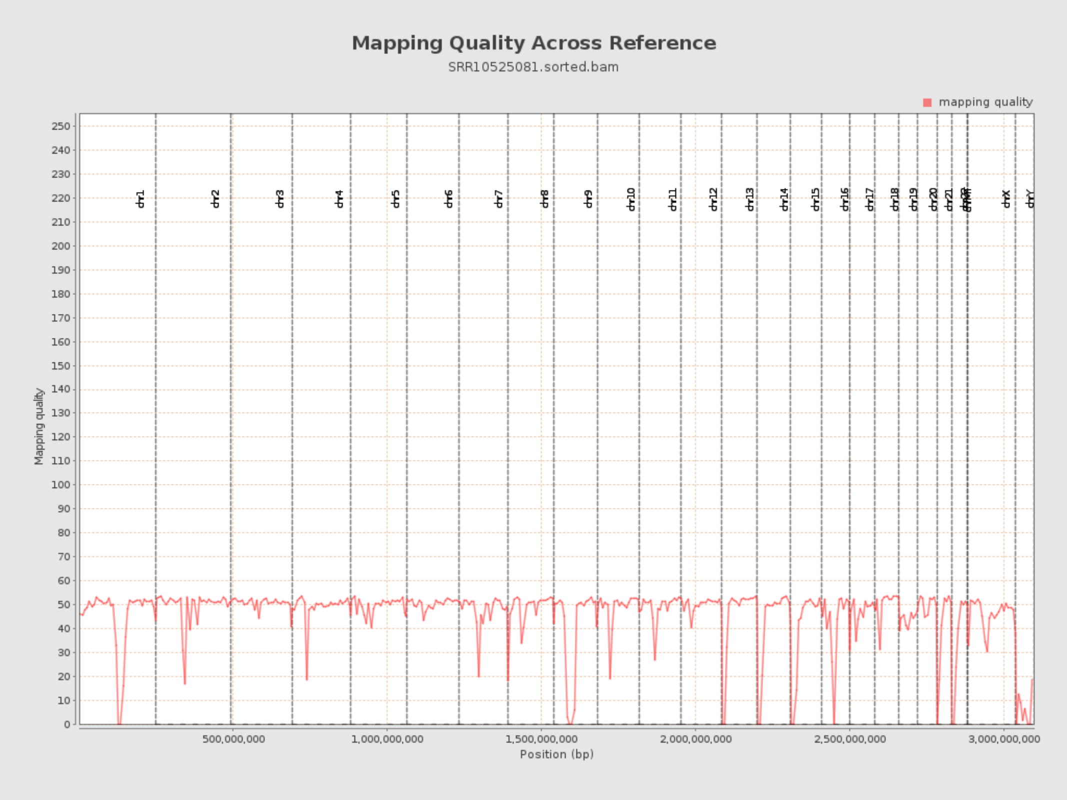
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram