Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 15:24:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524660.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_SRR10524660 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524660.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 15:24:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524660.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,728,753
Mapped reads	2,521,954 / 92.42%
Unmapped reads	206,799 / 7.58%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,203 / 0.41%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	135,922 / 4.98%
Duplication rate	3.94%
Clipped reads	2,527,706 / 92.63%

2.2. ACGT Content

Number/percentage of A's	37,946,473 / 25.33%
Number/percentage of C's	27,095,456 / 18.09%
Number/percentage of T's	46,460,834 / 31.01%
Number/percentage of G's	38,278,741 / 25.55%
Number/percentage of N's	20,319 / 0.01%
GC Percentage	43.64%

2.3. Coverage

Mean	0.0484

Standard Deviation	0.4365

2.4. Mapping Quality

Mean Mapping Quality	46.01

2.5. Mismatches and indels

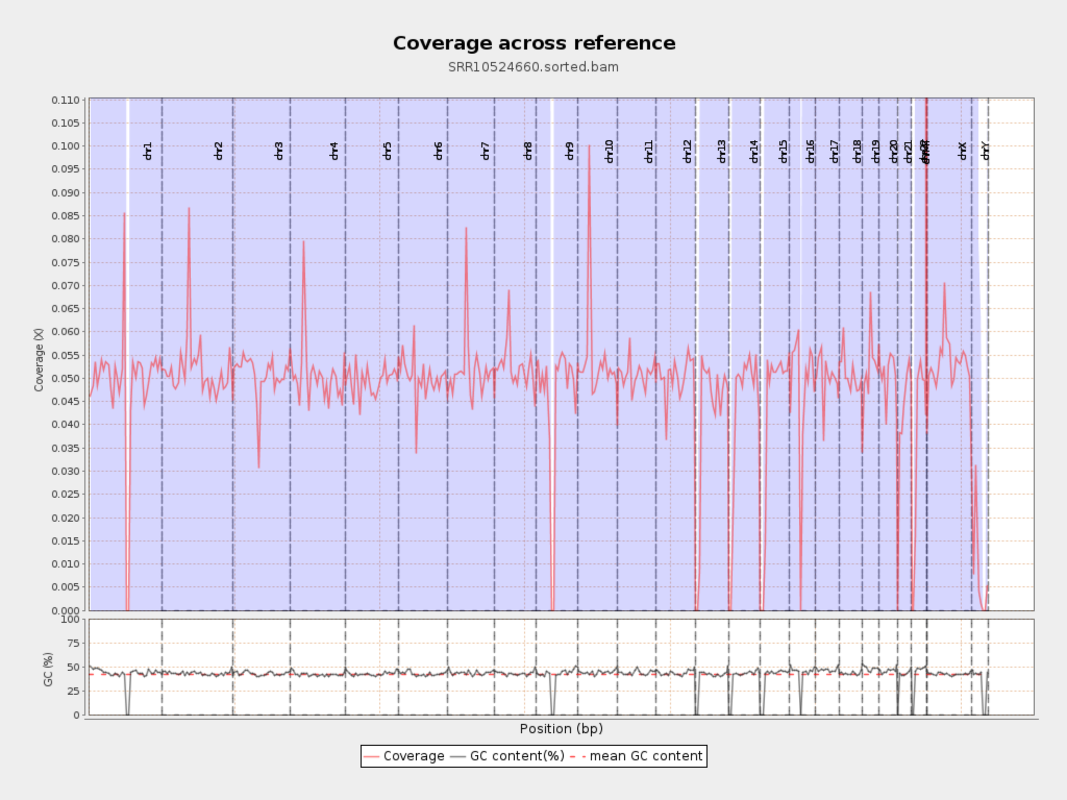
General error rate	0.51%
Mismatches	746,748
Insertions	10,515
Mapped reads with at least one insertion	0.41%
Deletions	27,985
Mapped reads with at least one deletion	1.1%
Homopolymer indels	42.56%

2.6. Chromosome stats

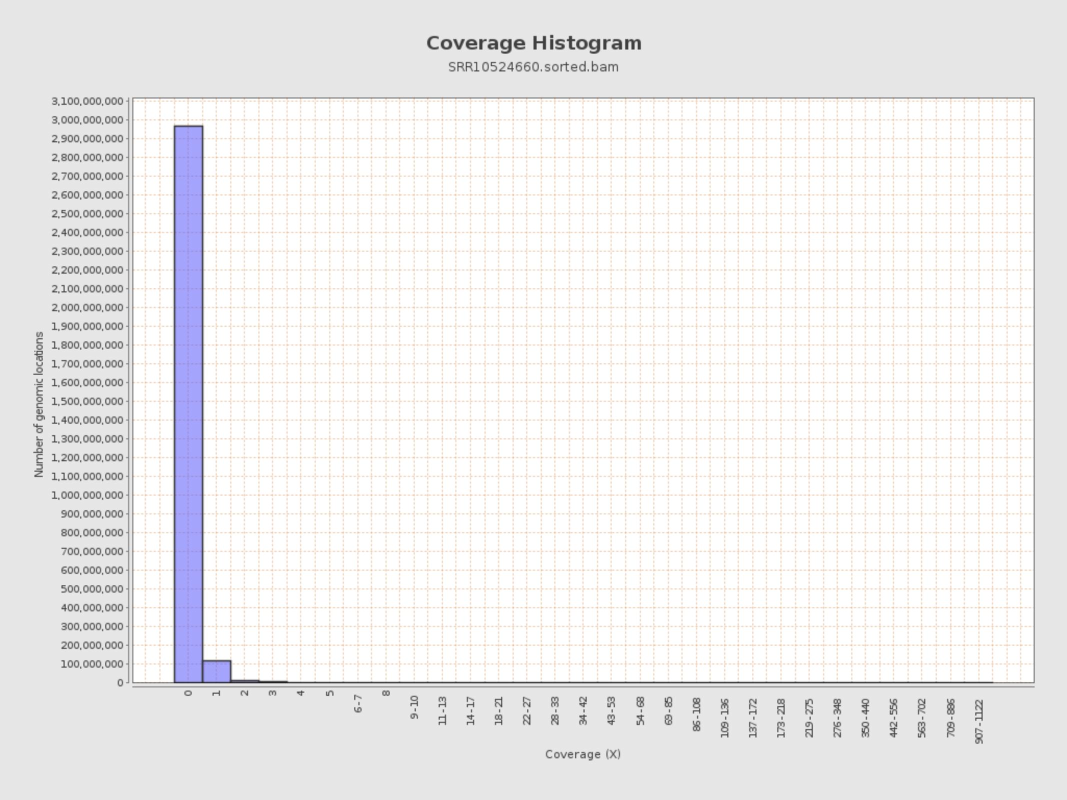
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12081750	0.0485	0.851
chr2	243199373	12678177	0.0521	0.5806
chr3	198022430	10025683	0.0506	0.2531
chr4	191154276	9653508	0.0505	0.3016
chr5	180915260	8953764	0.0495	0.2529
chr6	171115067	8590293	0.0502	0.2991
chr7	159138663	8257131	0.0519	0.5406

chr8	146364022	7685373	0.0525	0.4739
chr9	141213431	6314433	0.0447	0.3475
chr10	135534747	7319728	0.054	0.4545
chr11	135006516	6854107	0.0508	0.3508
chr12	133851895	6740117	0.0504	0.2575
chr13	115169878	4672551	0.0406	0.2265
chr14	107349540	4537812	0.0423	0.2459
chr15	102531392	4287907	0.0418	0.23
chr16	90354753	4311147	0.0477	0.2798
chr17	81195210	4055018	0.0499	0.2764
chr18	78077248	3986426	0.0511	0.6958
chr19	59128983	3118752	0.0527	0.606
chr20	63025520	3185062	0.0505	0.262
chr21	48129895	1993201	0.0414	0.2868
chr22	51304566	1777219	0.0346	0.2096
chrMT	16571	28559	1.7234	1.6599
chrX	155270560	8254068	0.0532	0.2972
chrY	59373566	484929	0.0082	0.2977

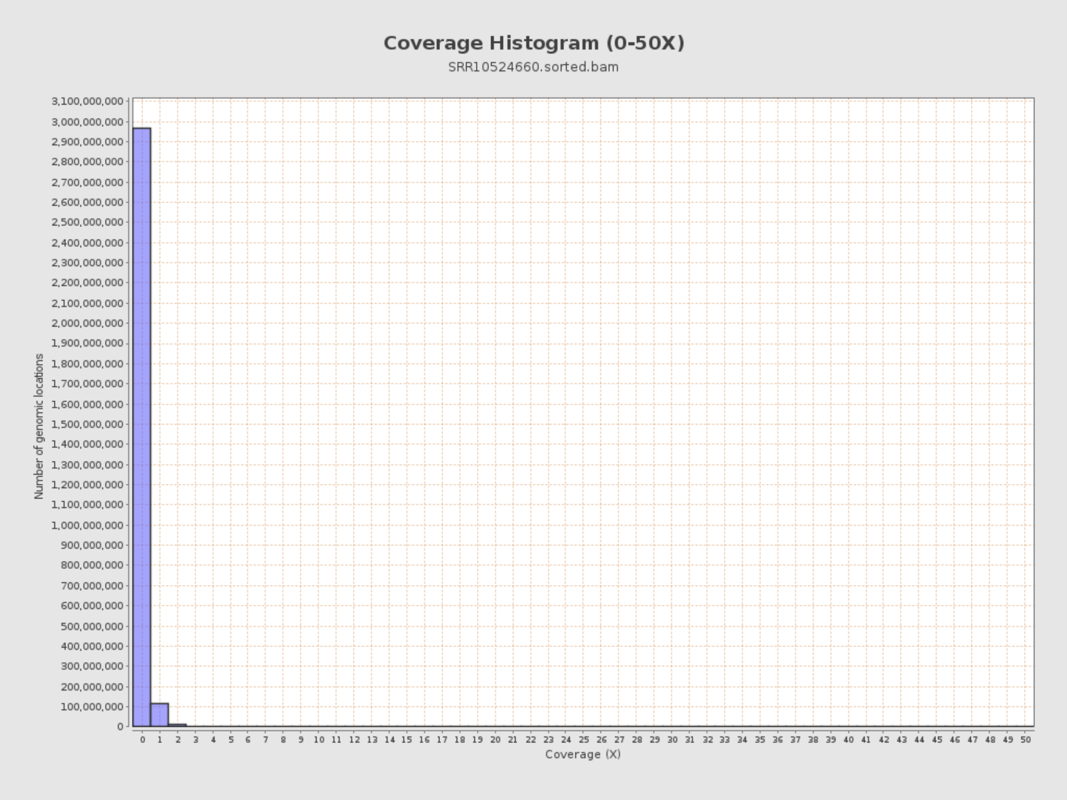
3. Results : Coverage across reference



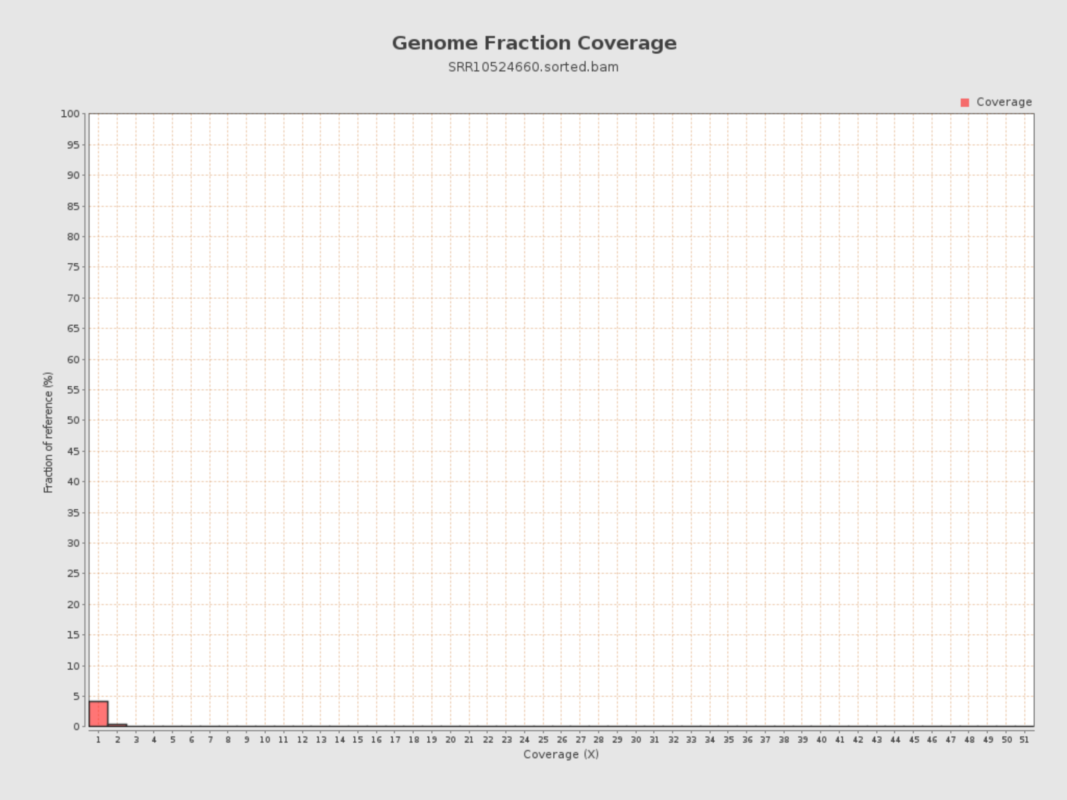
4. Results : Coverage Histogram



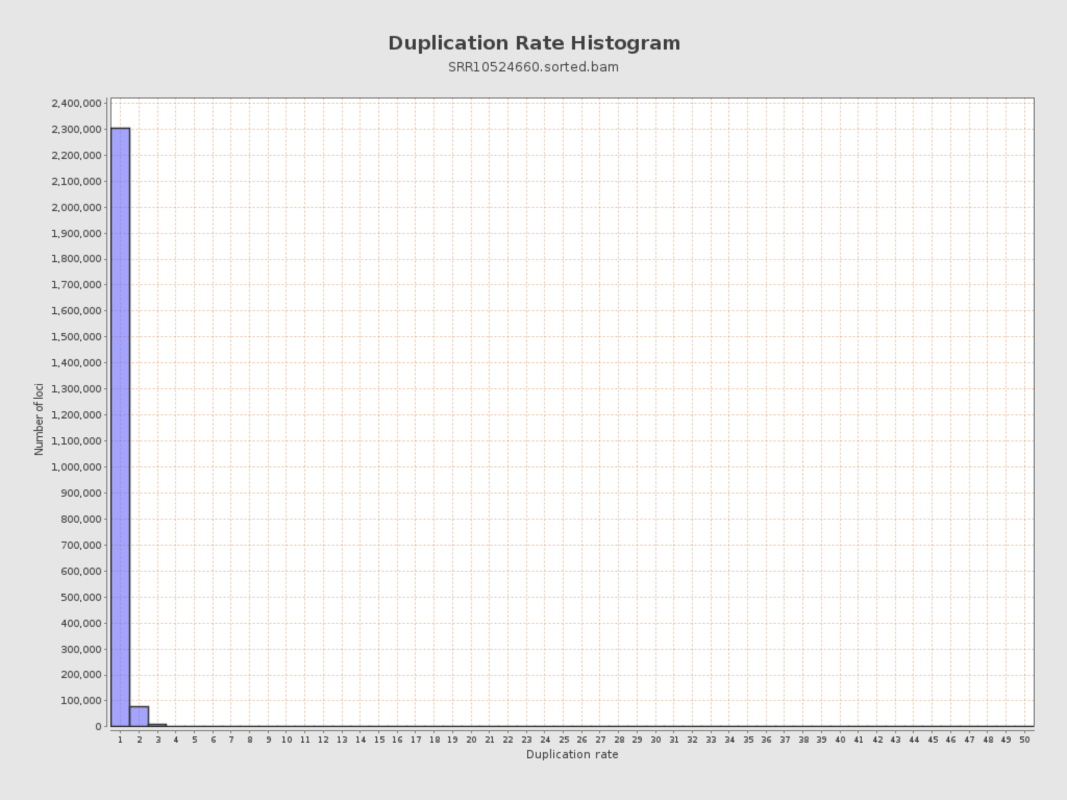
5. Results : Coverage Histogram (0-50X)



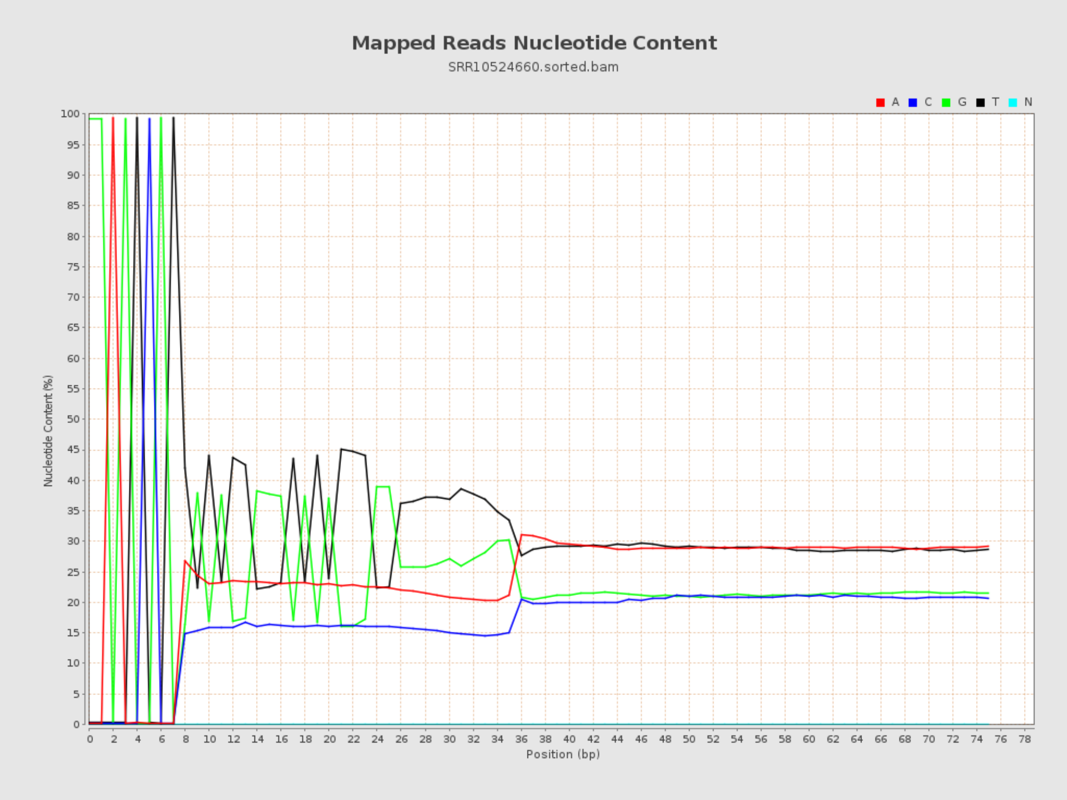
6. Results : Genome Fraction Coverage



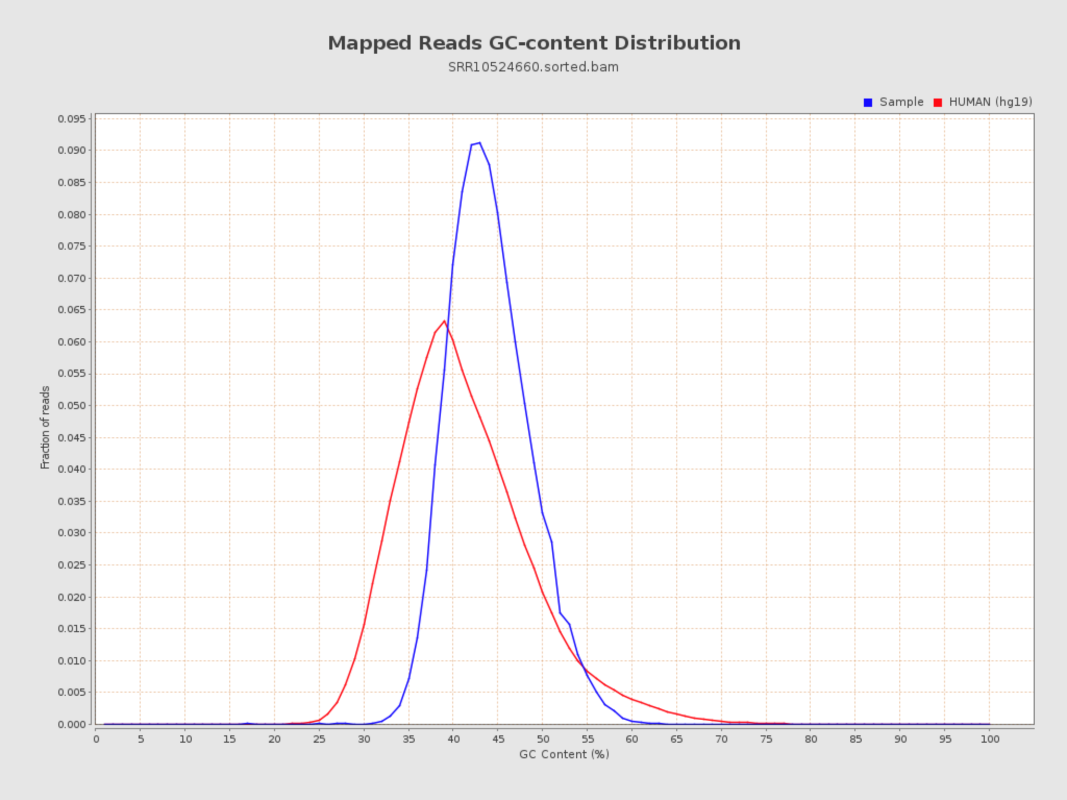
7. Results : Duplication Rate Histogram



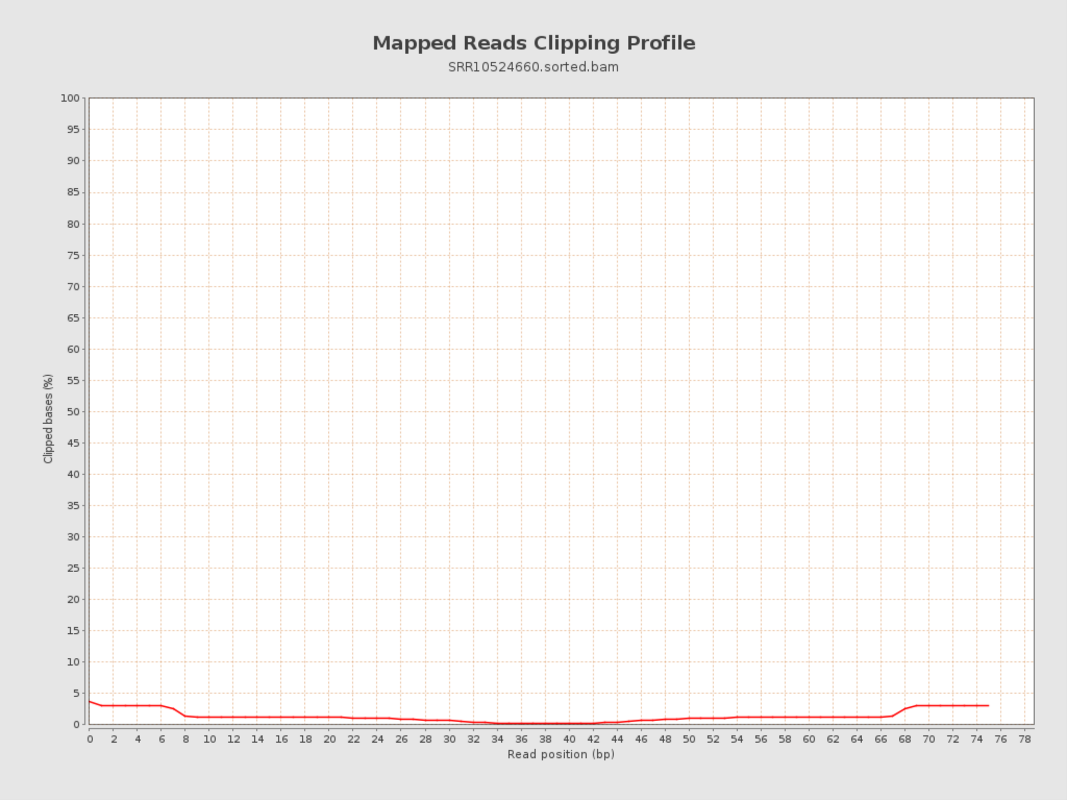
8. Results : Mapped Reads Nucleotide Content



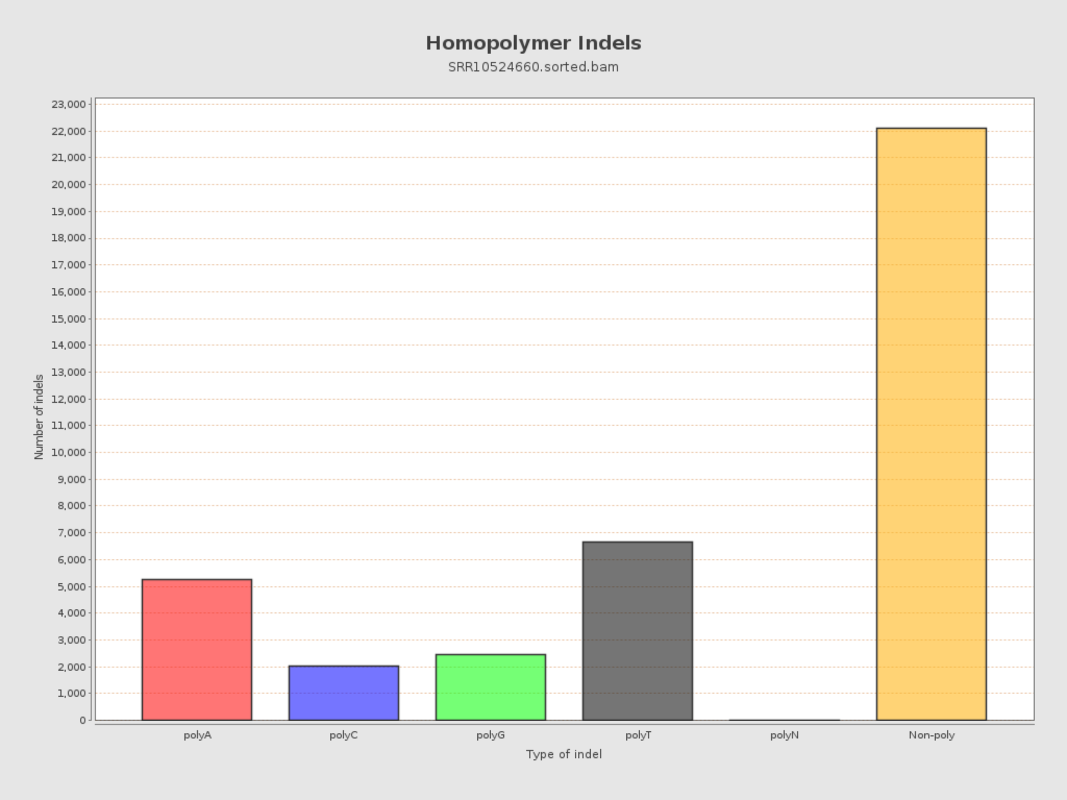
9. Results : Mapped Reads GC-content Distribution



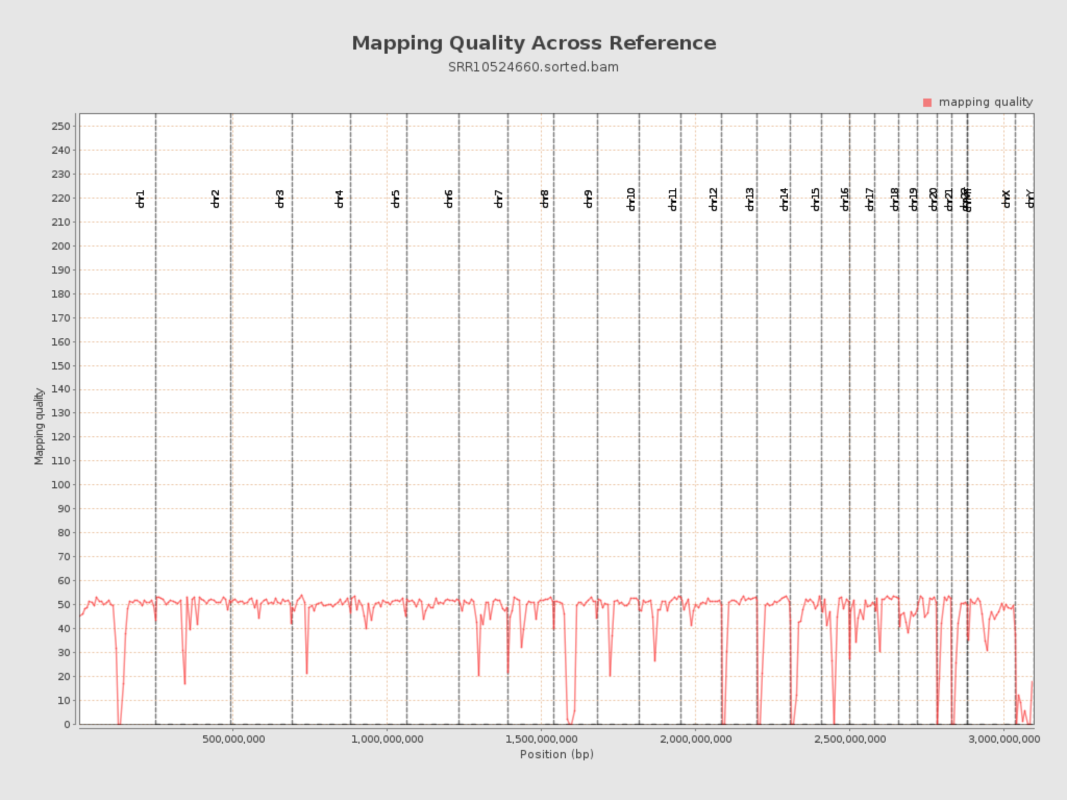
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram