Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 17:57:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234130.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_SRR6234130 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234130.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 17:57:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234130.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,394,099
Mapped reads	2,929,547 / 86.31%
Unmapped reads	464,552 / 13.69%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	29,612 / 0.87%
Read min/max/mean length	30 / 76 / 76.31
Duplicated reads (estimated)	762,535 / 22.47%
Duplication rate	10.34%
Clipped reads	1,058,330 / 31.18%

2.2. ACGT Content

Number/percentage of A's	48,326,323 / 24.04%
Number/percentage of C's	33,537,674 / 16.68%
Number/percentage of T's	51,721,052 / 25.72%
Number/percentage of G's	67,440,981 / 33.54%
Number/percentage of N's	39,829 / 0.02%
GC Percentage	50.22%

2.3. Coverage

Mean	0.065

Standard Deviation	60.5378

2.4. Mapping Quality

Mean Mapping Quality	40.08

2.5. Mismatches and indels

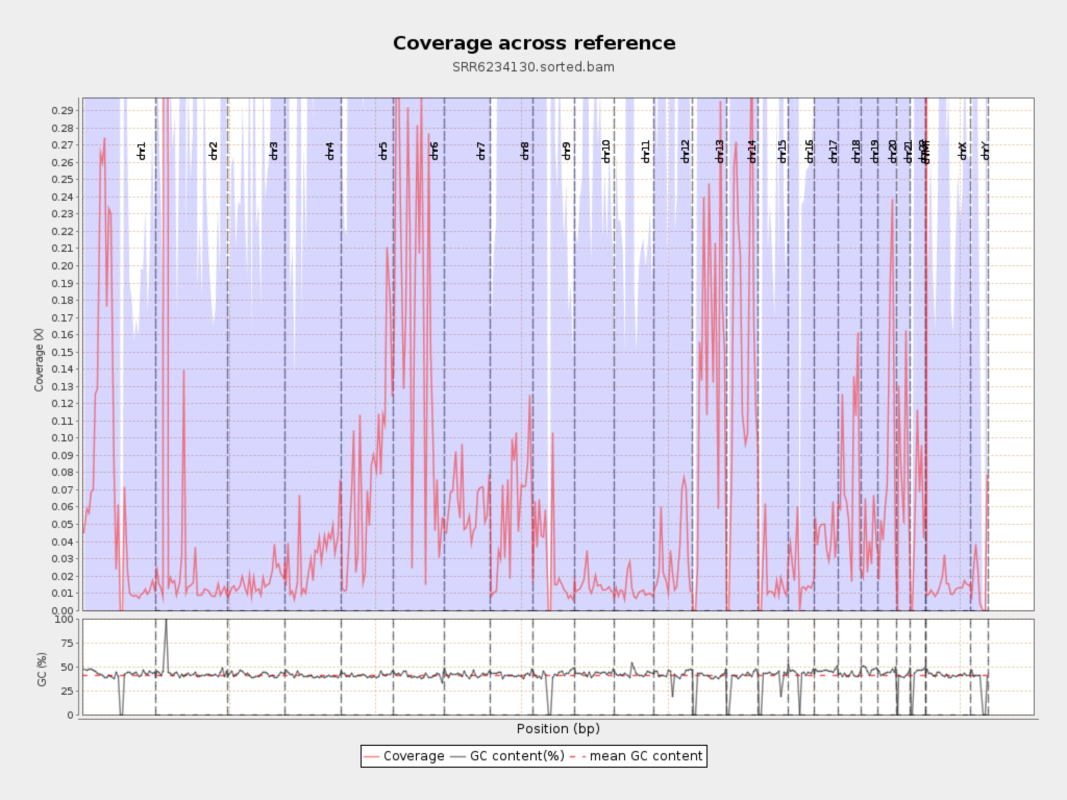
General error rate	0.67%
Mismatches	1,321,402
Insertions	13,825
Mapped reads with at least one insertion	0.47%
Deletions	39,549
Mapped reads with at least one deletion	1.34%
Homopolymer indels	45.45%

2.6. Chromosome stats

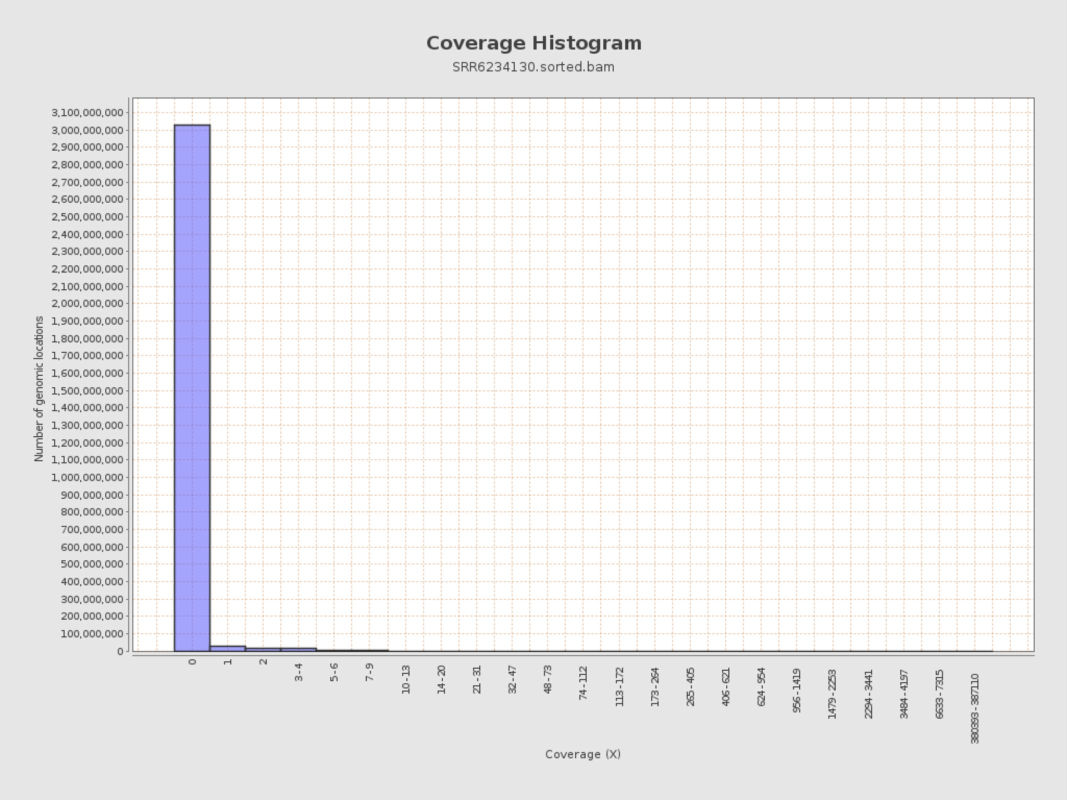
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	18450977	0.074	0.6647
chr2	243199373	34328087	0.1412	215.9699
chr3	198022430	3294016	0.0166	0.2691
chr4	191154276	5889980	0.0308	0.3717
chr5	180915260	14020197	0.0775	0.5975
chr6	171115067	28797371	0.1683	1.3922
chr7	159138663	9705309	0.061	0.788

chr8	146364022	8634312	0.059	0.7636
chr9	141213431	4056345	0.0287	0.6597
chr10	135534747	1989302	0.0147	0.27
chr11	135006516	1595439	0.0118	0.4576
chr12	133851895	4178974	0.0312	0.9674
chr13	115169878	16617399	0.1443	0.8311
chr14	107349540	17206269	0.1603	0.9535
chr15	102531392	1582338	0.0154	0.9975
chr16	90354753	1890689	0.0209	0.4359
chr17	81195210	3539658	0.0436	0.4169
chr18	78077248	6476527	0.083	1.7983
chr19	59128983	2281073	0.0386	0.4883
chr20	63025520	6051507	0.096	0.7266
chr21	48129895	4021066	0.0835	0.6687
chr22	51304566	2939306	0.0573	0.5382
chrMT	16571	101536	6.1273	6.5479
chrX	155270560	2131922	0.0137	0.3282
chrY	59373566	1351823	0.0228	0.4118

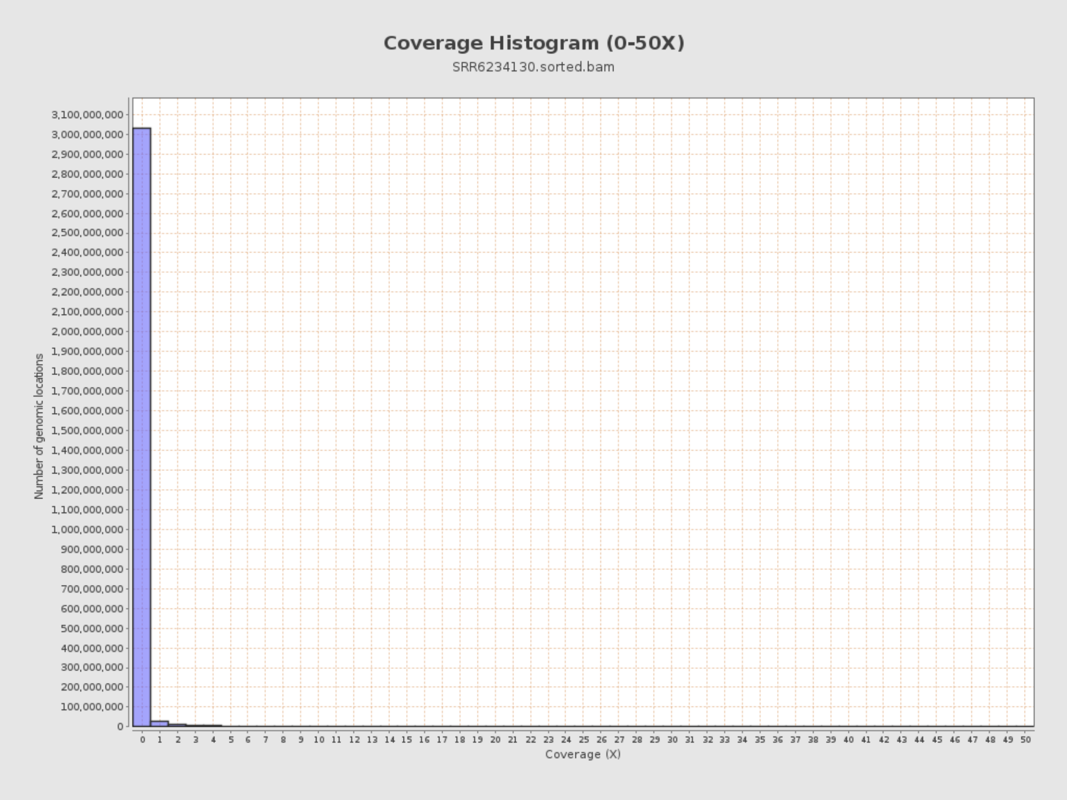
3. Results : Coverage across reference



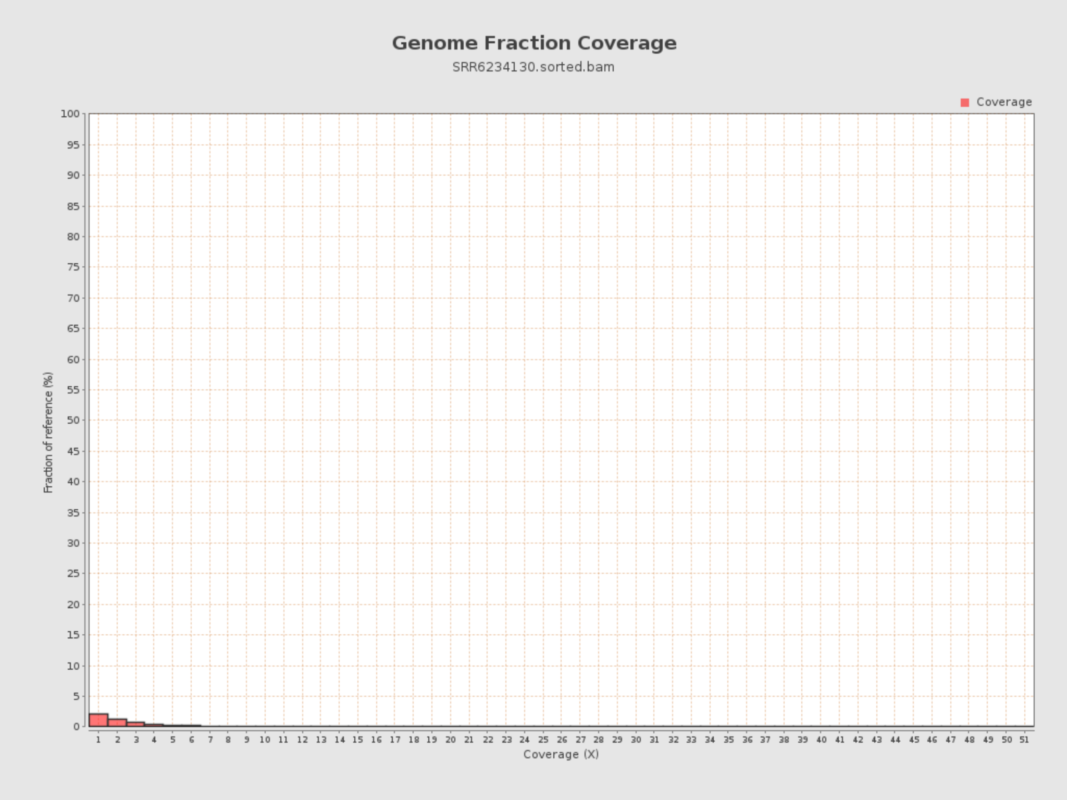
4. Results : Coverage Histogram



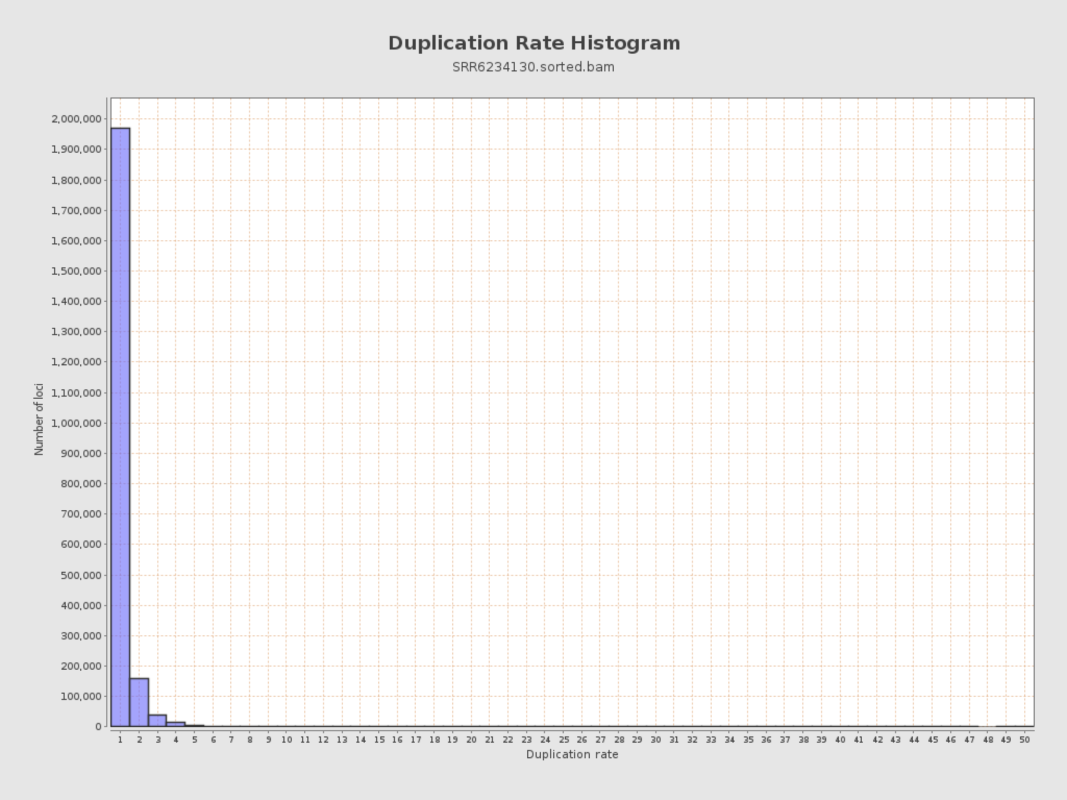
5. Results : Coverage Histogram (0-50X)



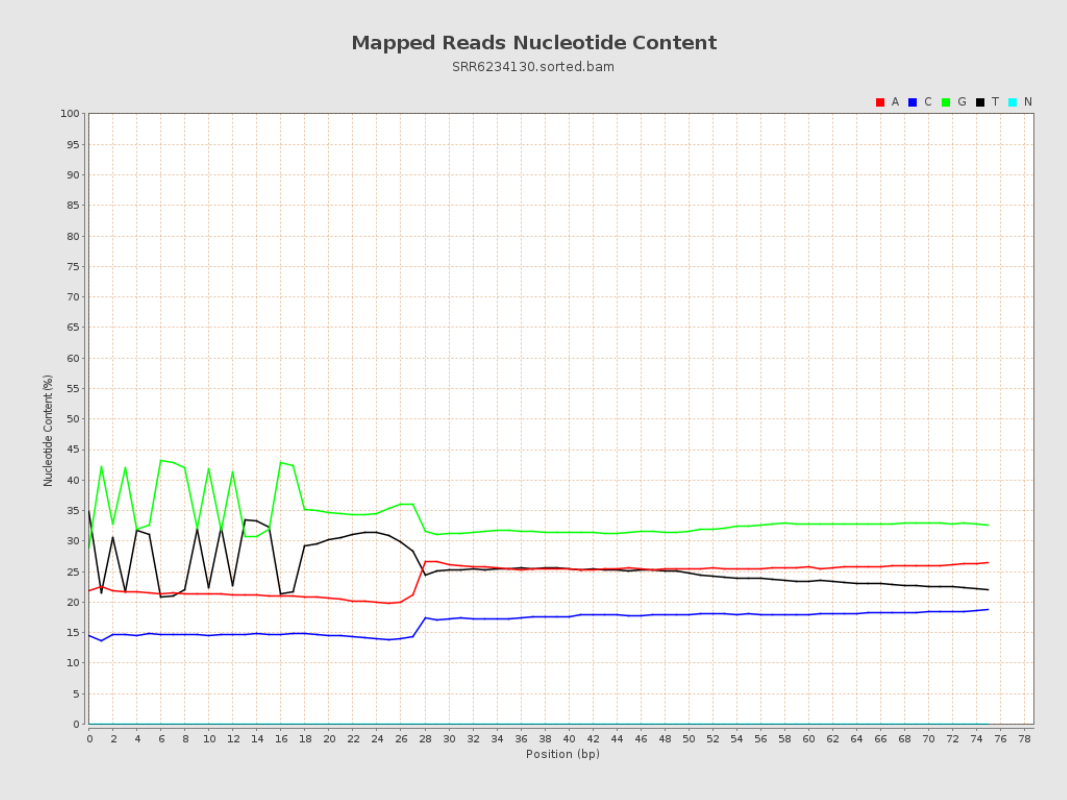
6. Results : Genome Fraction Coverage



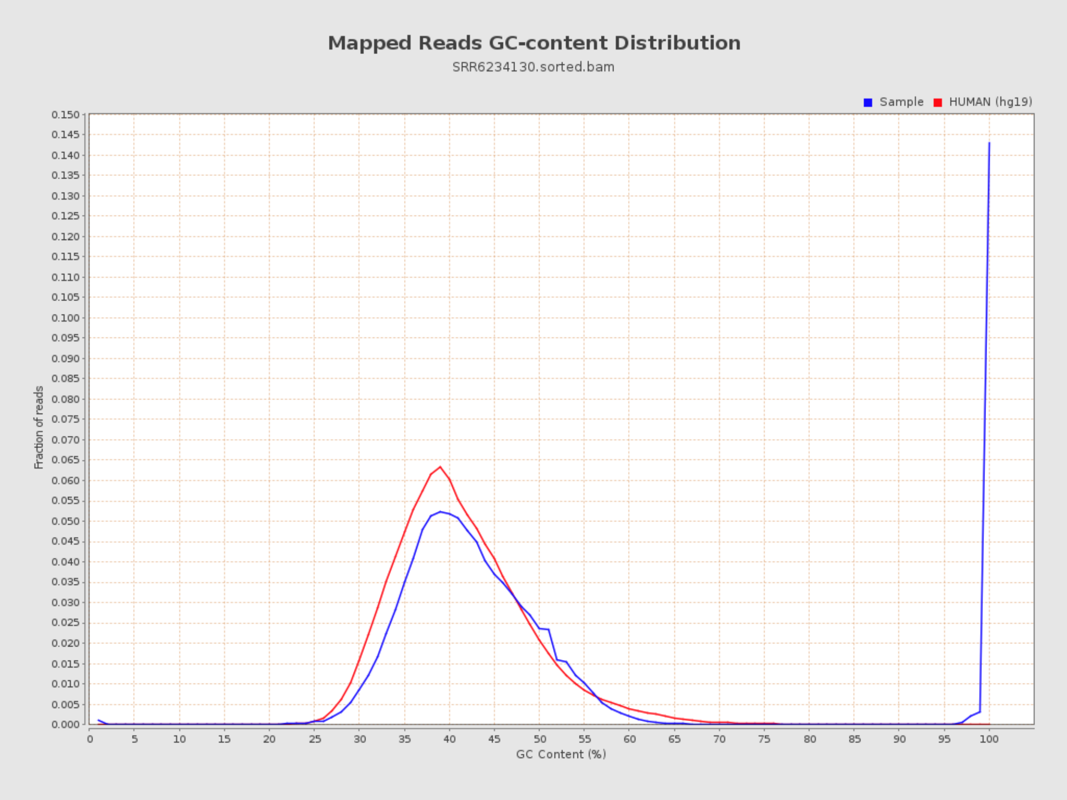
7. Results : Duplication Rate Histogram



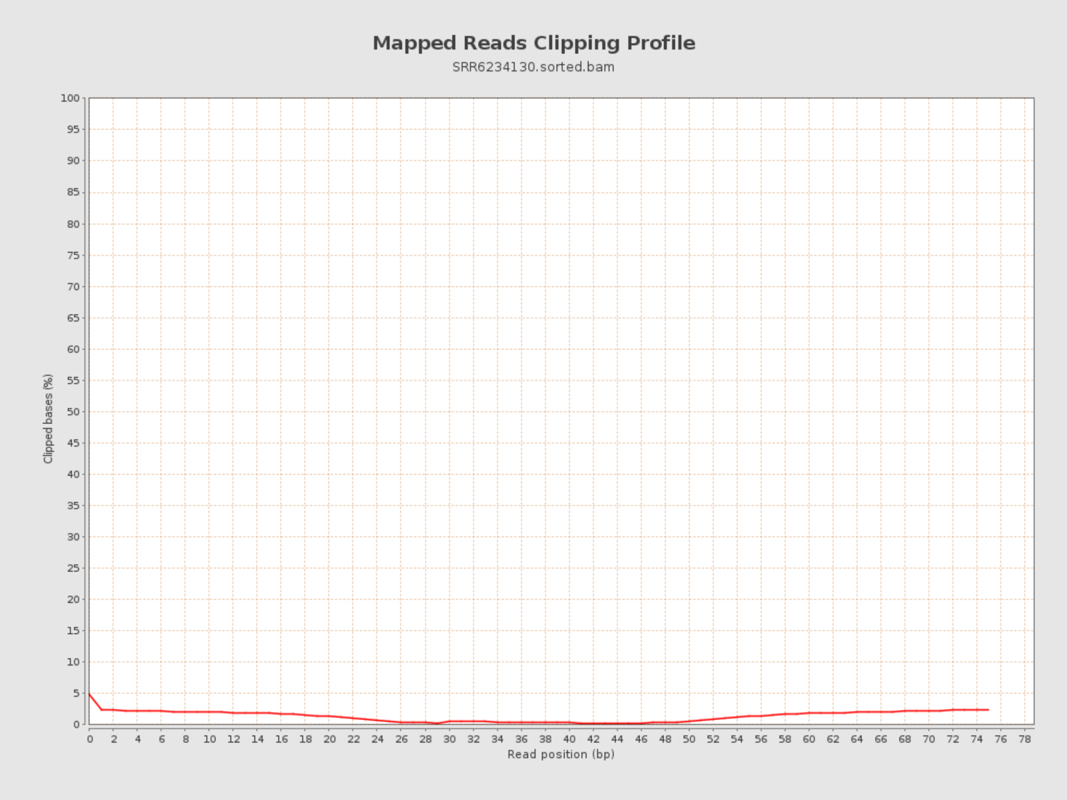
8. Results : Mapped Reads Nucleotide Content



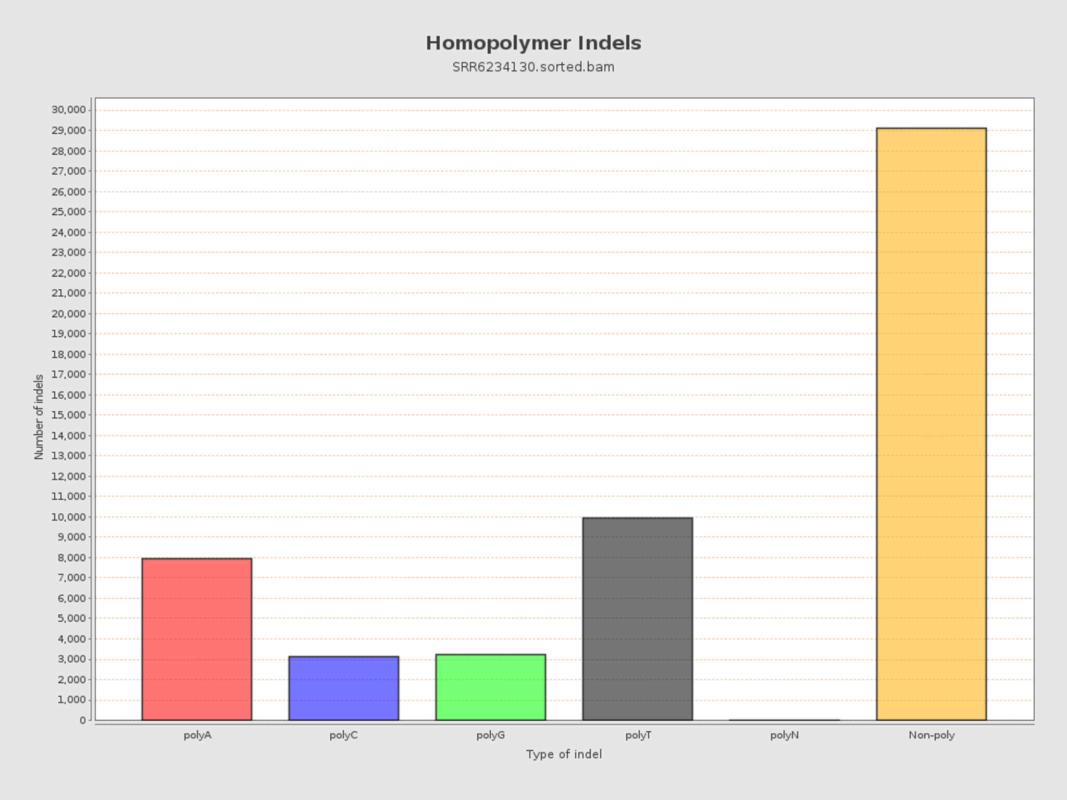
9. Results : Mapped Reads GC-content Distribution



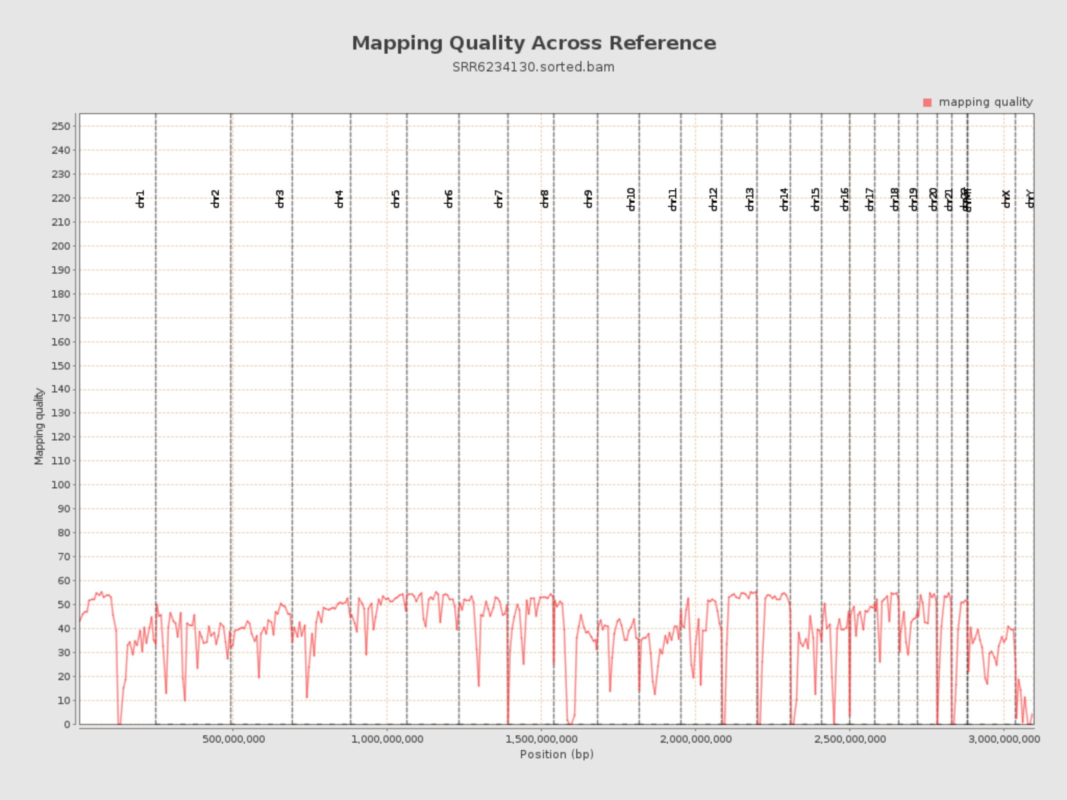
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram