Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 17:05:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234116.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_SRR6234116 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234116.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 17:05:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234116.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	845,579
Mapped reads	597,610 / 70.67%
Unmapped reads	247,969 / 29.33%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,561 / 0.3%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	13,278 / 1.57%
Duplication rate	1.63%
Clipped reads	268,898 / 31.8%

2.2. ACGT Content

Number/percentage of A's	11,152,243 / 28.34%
Number/percentage of C's	6,766,003 / 17.19%
Number/percentage of T's	12,619,313 / 32.07%
Number/percentage of G's	8,809,919 / 22.39%
Number/percentage of N's	7,124 / 0.02%
GC Percentage	39.58%

2.3. Coverage

Mean	0.0127

Standard Deviation	0.1602

2.4. Mapping Quality

Mean Mapping Quality	44.44

2.5. Mismatches and indels

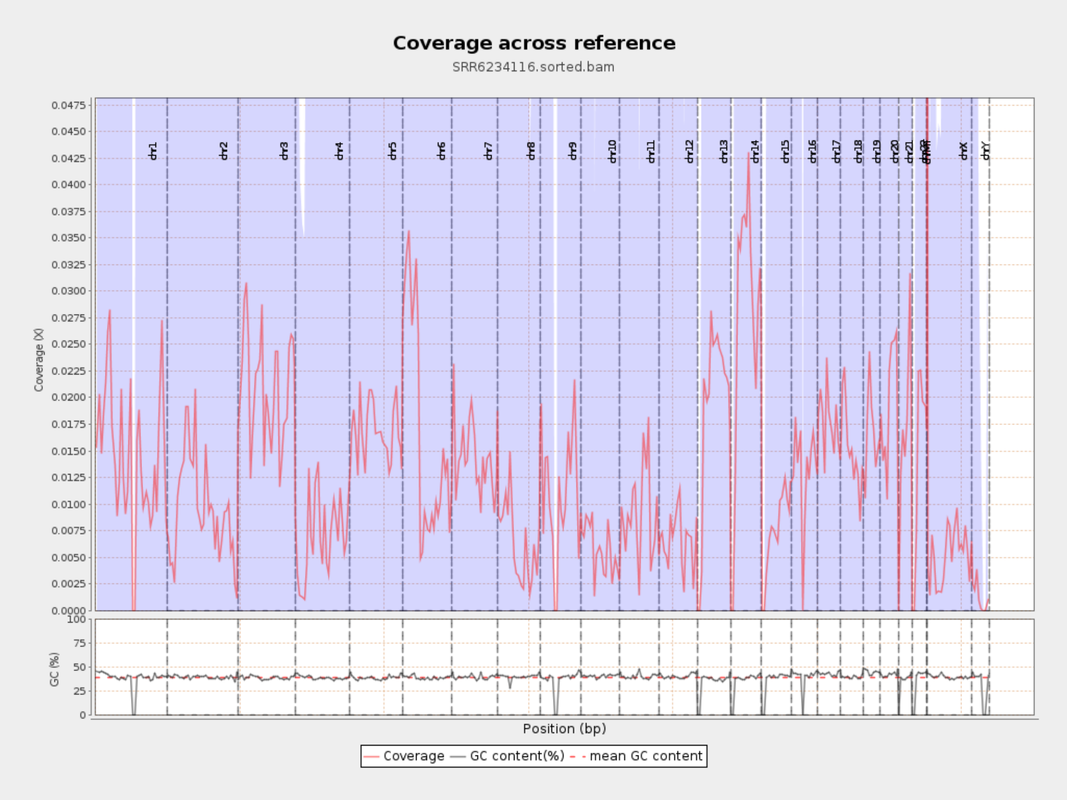
General error rate	0.96%
Mismatches	371,154
Insertions	3,460
Mapped reads with at least one insertion	0.57%
Deletions	11,955
Mapped reads with at least one deletion	1.97%
Homopolymer indels	46.1%

2.6. Chromosome stats

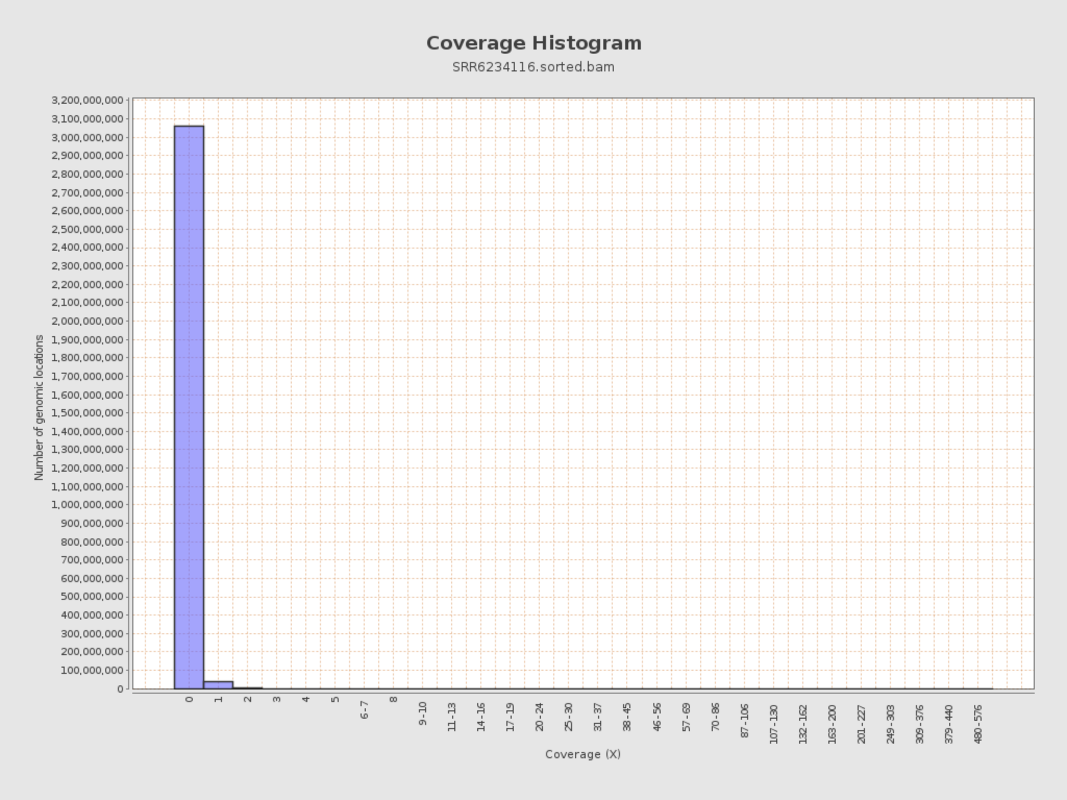
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3577196	0.0144	0.2184
chr2	243199373	2338274	0.0096	0.1534
chr3	198022430	4172321	0.0211	0.1521
chr4	191154276	1343048	0.007	0.0892
chr5	180915260	3061549	0.0169	0.1356
chr6	171115067	2864566	0.0167	0.1434
chr7	159138663	2280752	0.0143	0.1484

chr8	146364022	928969	0.0063	0.3595
chr9	141213431	1557963	0.011	0.1335
chr10	135534747	781229	0.0058	0.0943
chr11	135006516	1224692	0.0091	0.1188
chr12	133851895	873698	0.0065	0.085
chr13	115169878	2227303	0.0193	0.1453
chr14	107349540	2923563	0.0272	0.1759
chr15	102531392	749876	0.0073	0.0896
chr16	90354753	1167950	0.0129	0.128
chr17	81195210	1445954	0.0178	0.1436
chr18	78077248	1183658	0.0152	0.2317
chr19	59128983	988866	0.0167	0.164
chr20	63025520	1230315	0.0195	0.1485
chr21	48129895	821802	0.0171	0.1394
chr22	51304566	738807	0.0144	0.126
chrMT	16571	5809	0.3506	0.6514
chrX	155270560	811842	0.0052	0.0809
chrY	59373566	75846	0.0013	0.0435

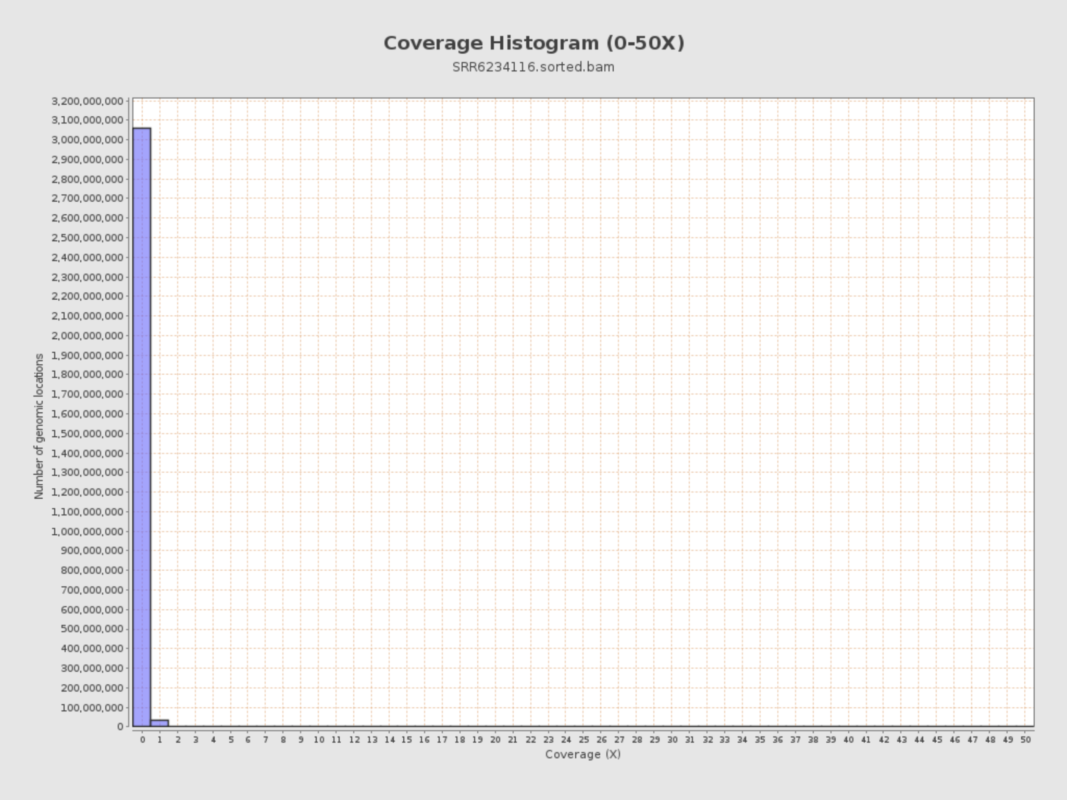
3. Results : Coverage across reference



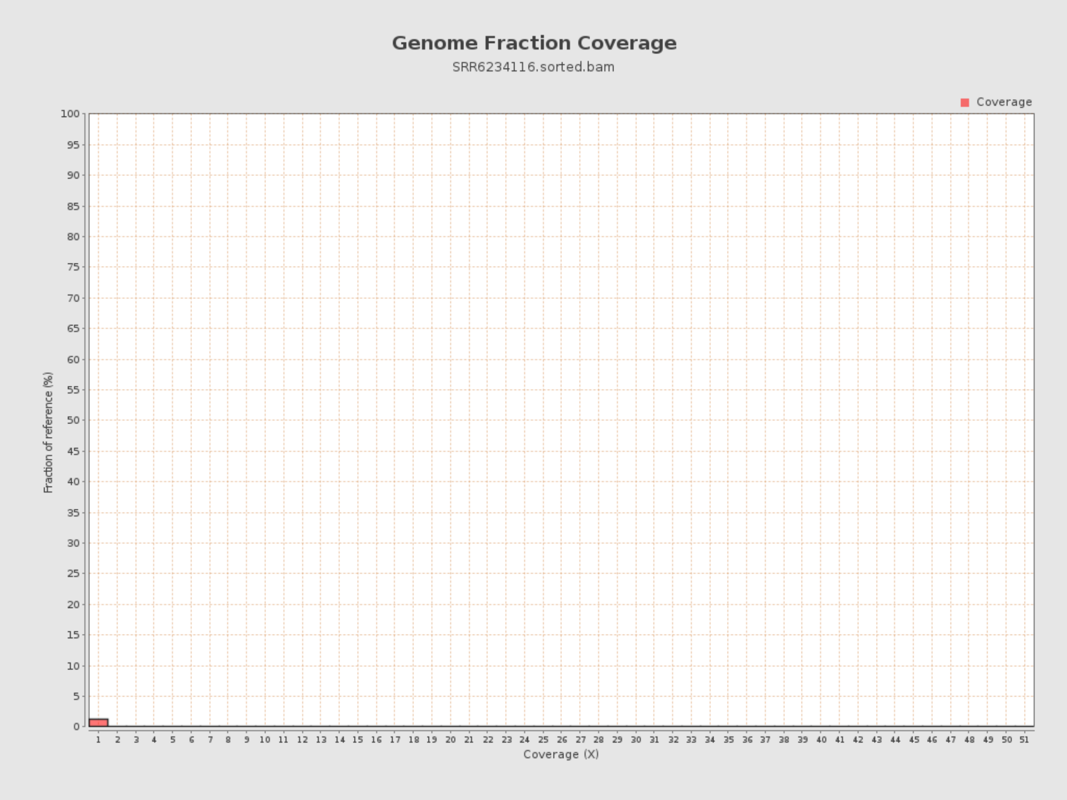
4. Results : Coverage Histogram



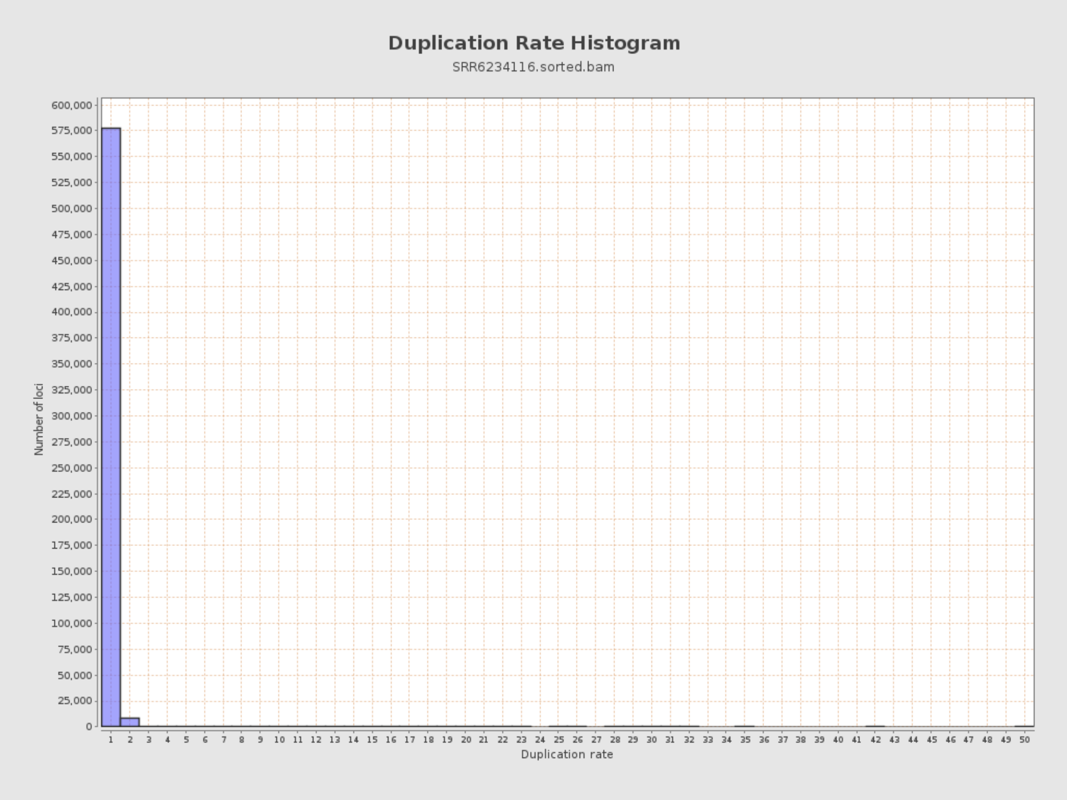
5. Results : Coverage Histogram (0-50X)



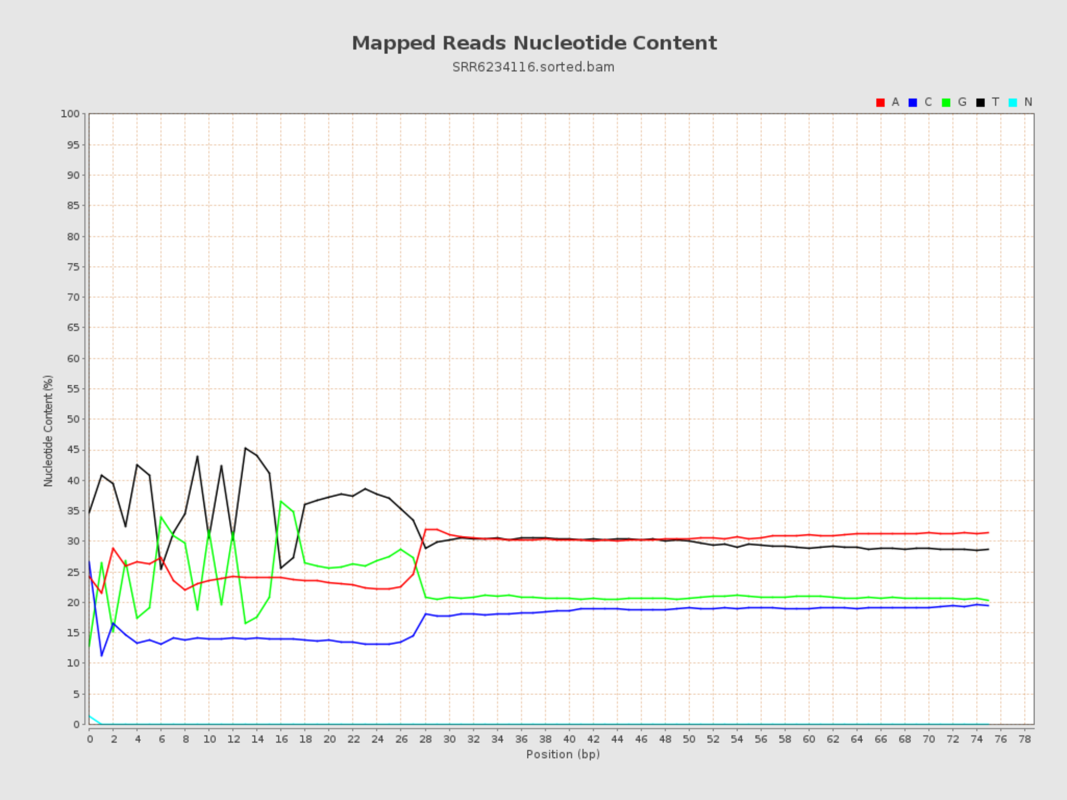
6. Results : Genome Fraction Coverage



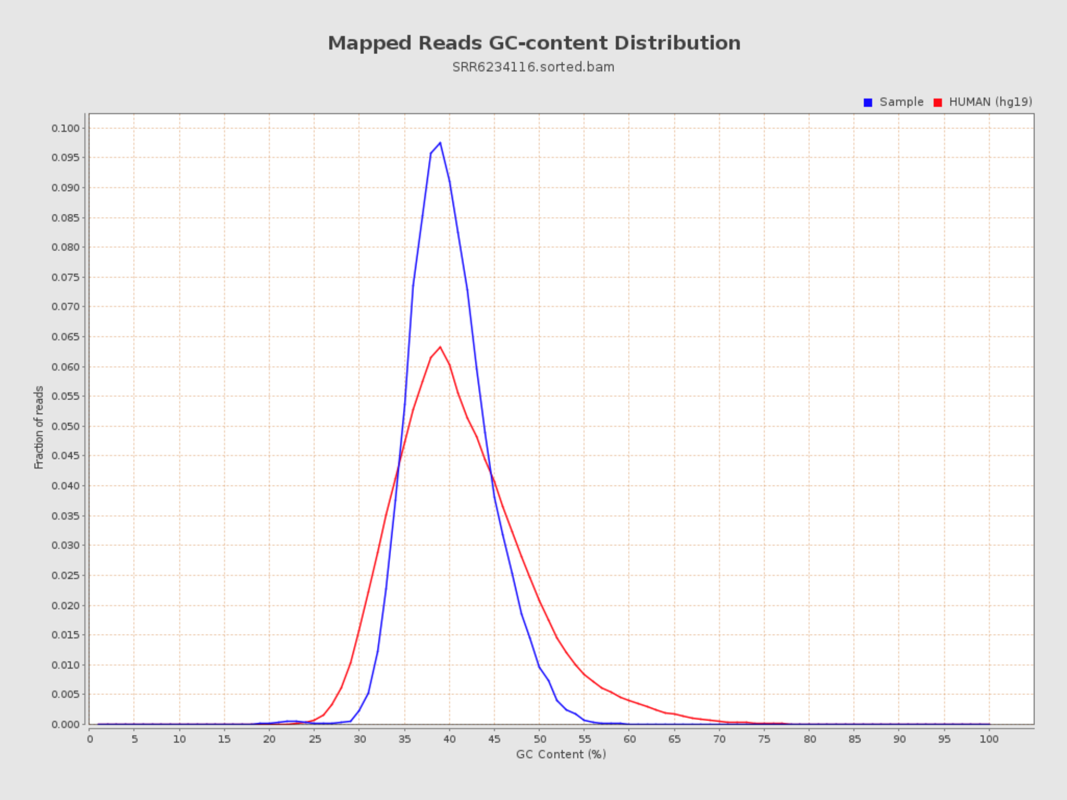
7. Results : Duplication Rate Histogram



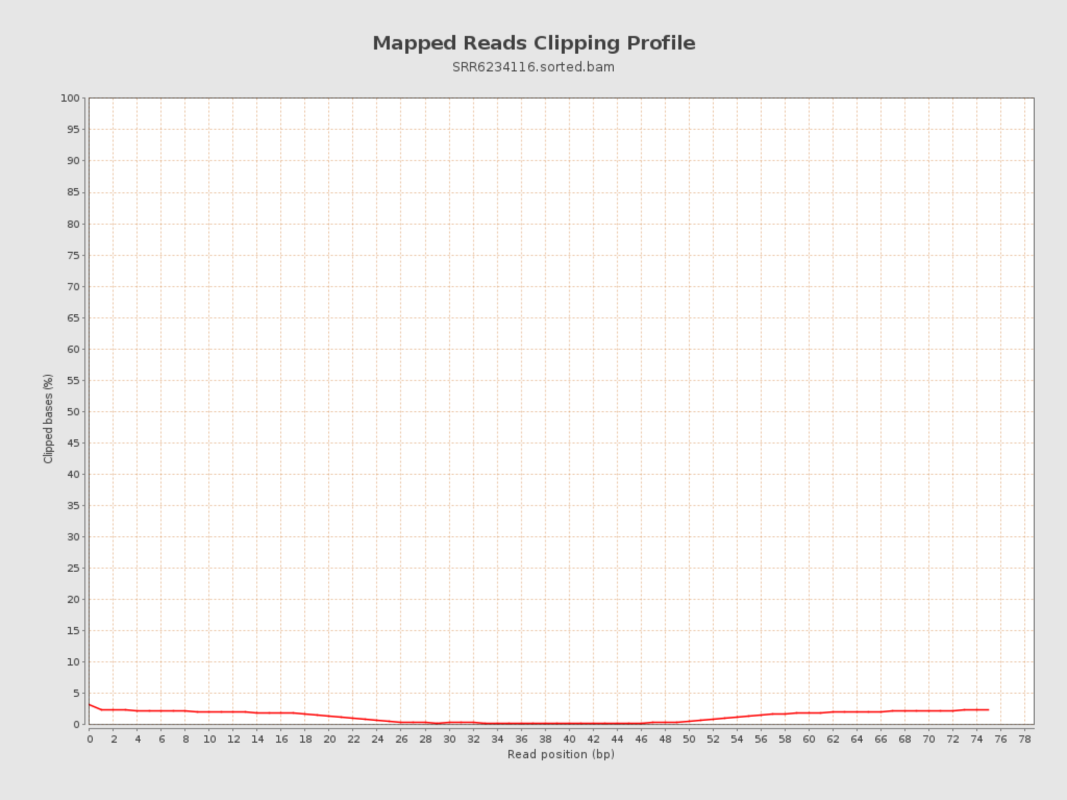
8. Results : Mapped Reads Nucleotide Content



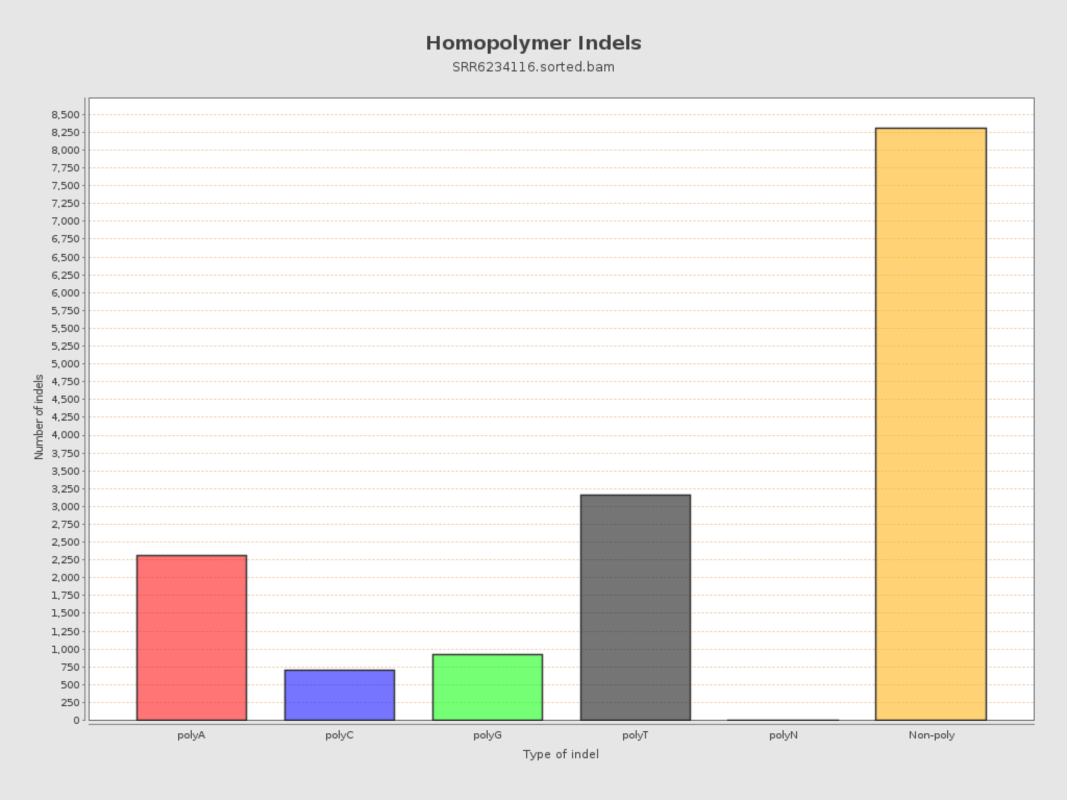
9. Results : Mapped Reads GC-content Distribution



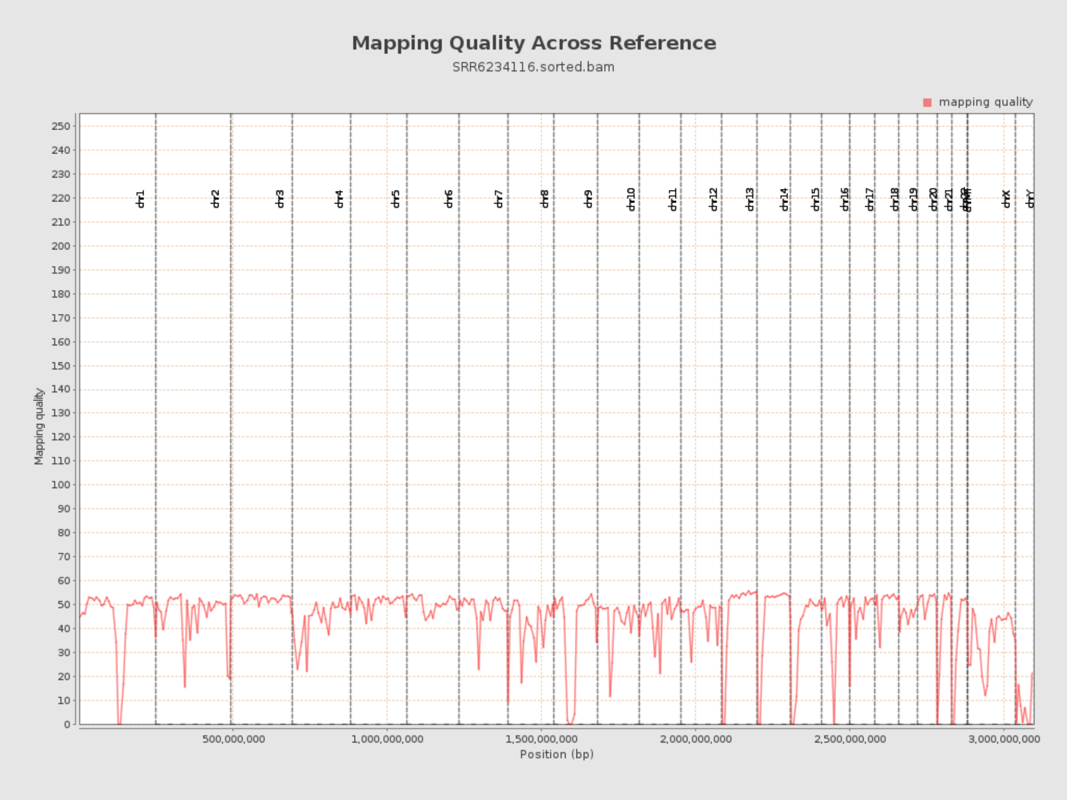
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram