Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 11:03:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234026.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_SRR6234026 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234026.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 11:03:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234026.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,702,655
Mapped reads	2,865,308 / 60.93%
Unmapped reads	1,837,347 / 39.07%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	24,070 / 0.51%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	361,730 / 7.69%
Duplication rate	9.13%
Clipped reads	1,255,586 / 26.7%

2.2. ACGT Content

Number/percentage of A's	54,062,594 / 28.36%
Number/percentage of C's	34,909,094 / 18.31%
Number/percentage of T's	61,200,061 / 32.1%
Number/percentage of G's	40,426,793 / 21.2%
Number/percentage of N's	55,997 / 0.03%
GC Percentage	39.51%

2.3. Coverage

Mean	0.0616

Standard Deviation	0.822

2.4. Mapping Quality

Mean Mapping Quality	39.13

2.5. Mismatches and indels

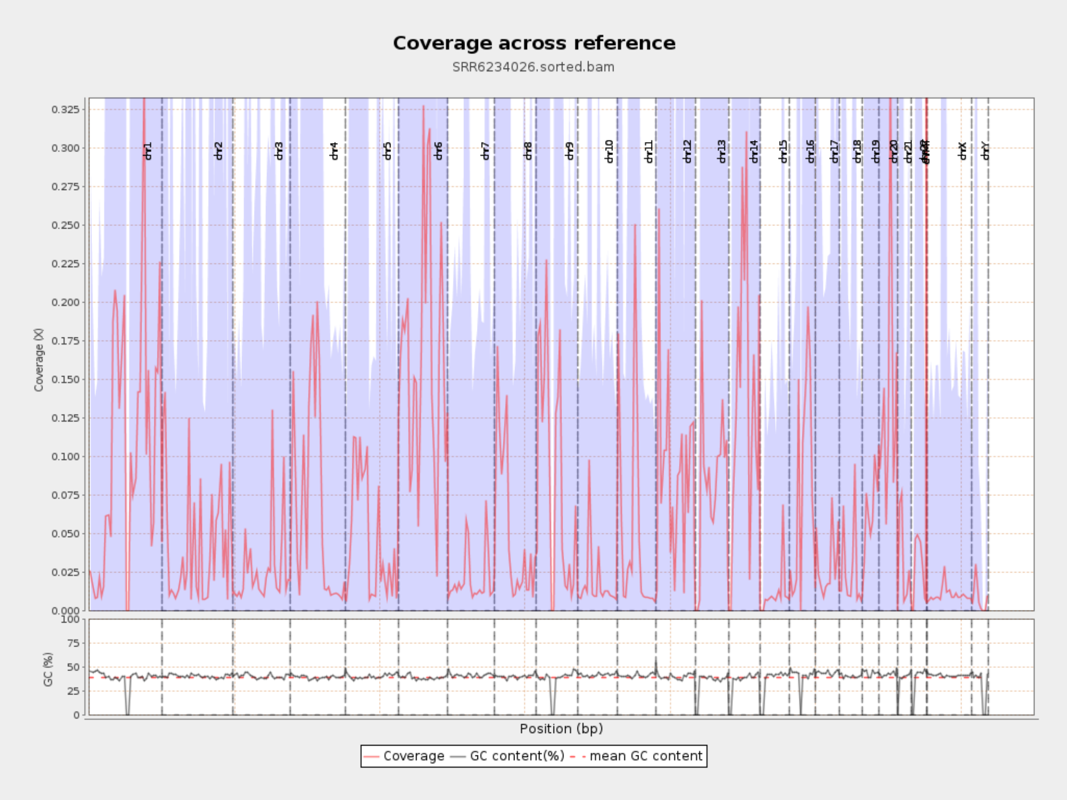
General error rate	0.84%
Mismatches	1,574,621
Insertions	16,556
Mapped reads with at least one insertion	0.57%
Deletions	50,061
Mapped reads with at least one deletion	1.73%
Homopolymer indels	45.13%

2.6. Chromosome stats

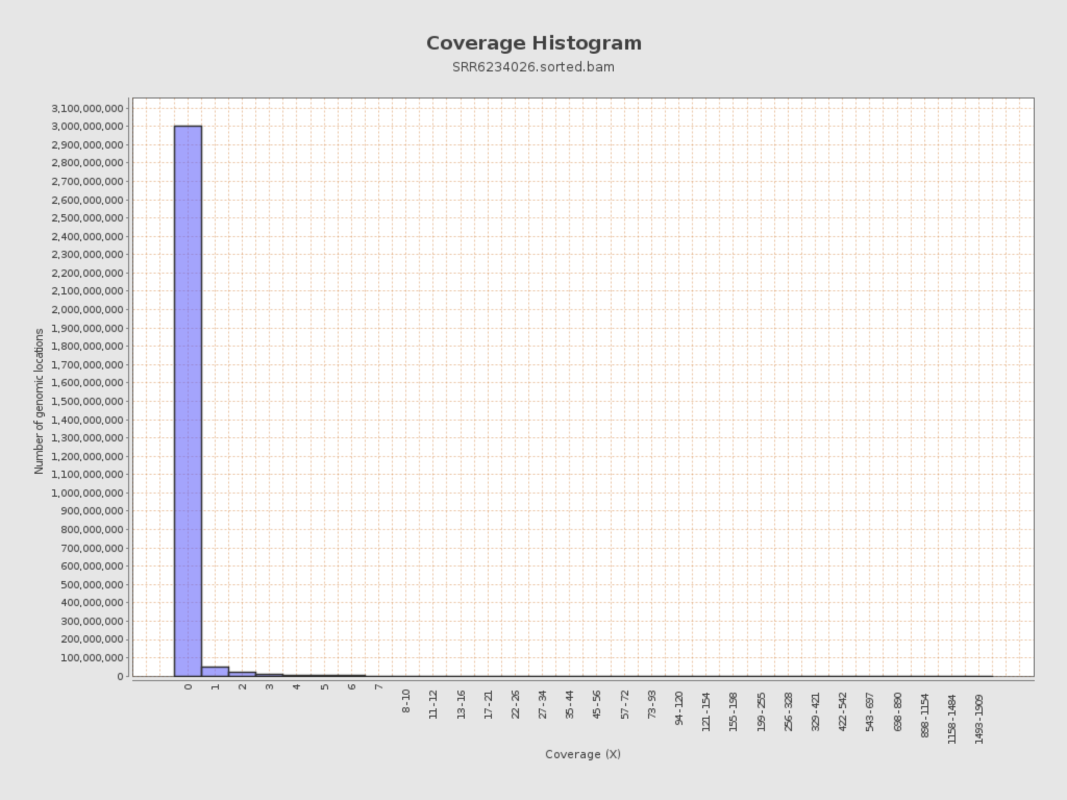
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	26439427	0.1061	1.7175
chr2	243199373	10294525	0.0423	0.7094
chr3	198022430	5541103	0.028	0.3042
chr4	191154276	13047078	0.0683	0.5066
chr5	180915260	8323318	0.046	0.3975
chr6	171115067	28448155	0.1663	1.0493
chr7	159138663	3403315	0.0214	0.4557

chr8	146364022	7518463	0.0514	1.1646
chr9	141213431	12428786	0.088	0.904
chr10	135534747	2351158	0.0173	0.6596
chr11	135006516	6658583	0.0493	0.5157
chr12	133851895	12142173	0.0907	0.5666
chr13	115169878	9415441	0.0818	0.5225
chr14	107349540	14326589	0.1335	0.7337
chr15	102531392	1197365	0.0117	0.1812
chr16	90354753	7276341	0.0805	0.5949
chr17	81195210	2408826	0.0297	0.304
chr18	78077248	2147003	0.0275	1.6378
chr19	59128983	3762666	0.0636	0.9957
chr20	63025520	8655010	0.1373	0.6896
chr21	48129895	1491807	0.031	0.4206
chr22	51304566	1386307	0.027	0.2768
chrMT	16571	25047	1.5115	2.0235
chrX	155270560	1588390	0.0102	0.3021
chrY	59373566	466948	0.0079	0.2085

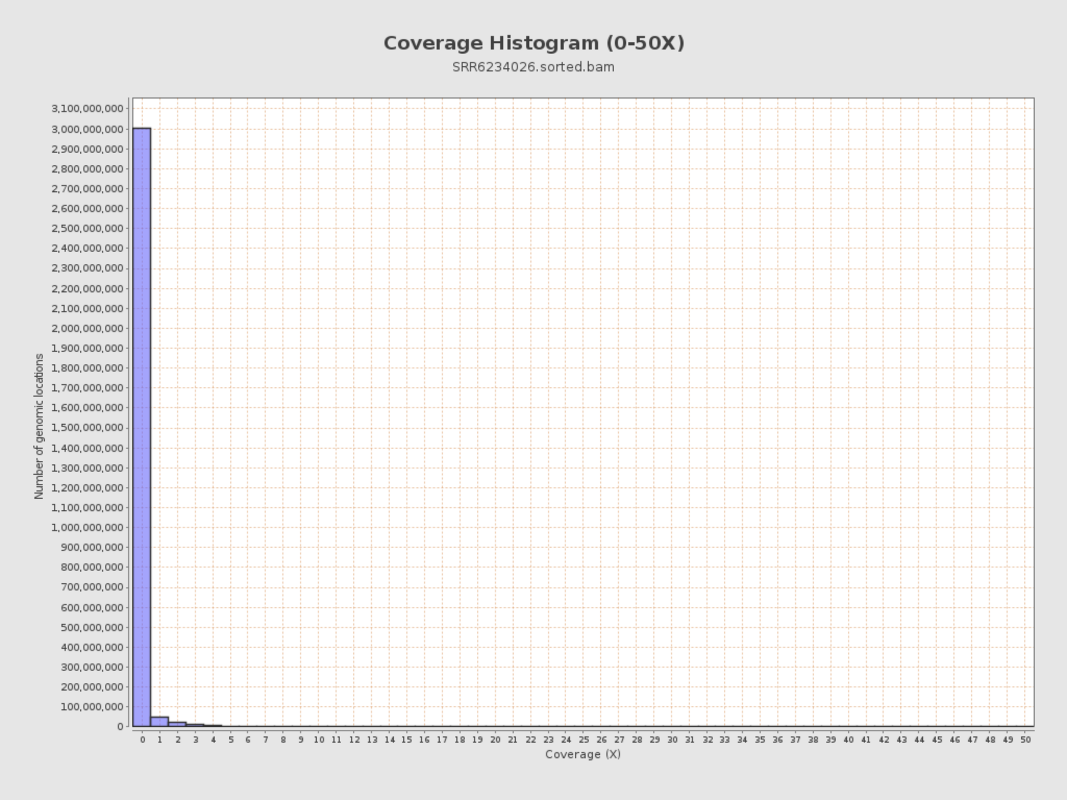
3. Results : Coverage across reference



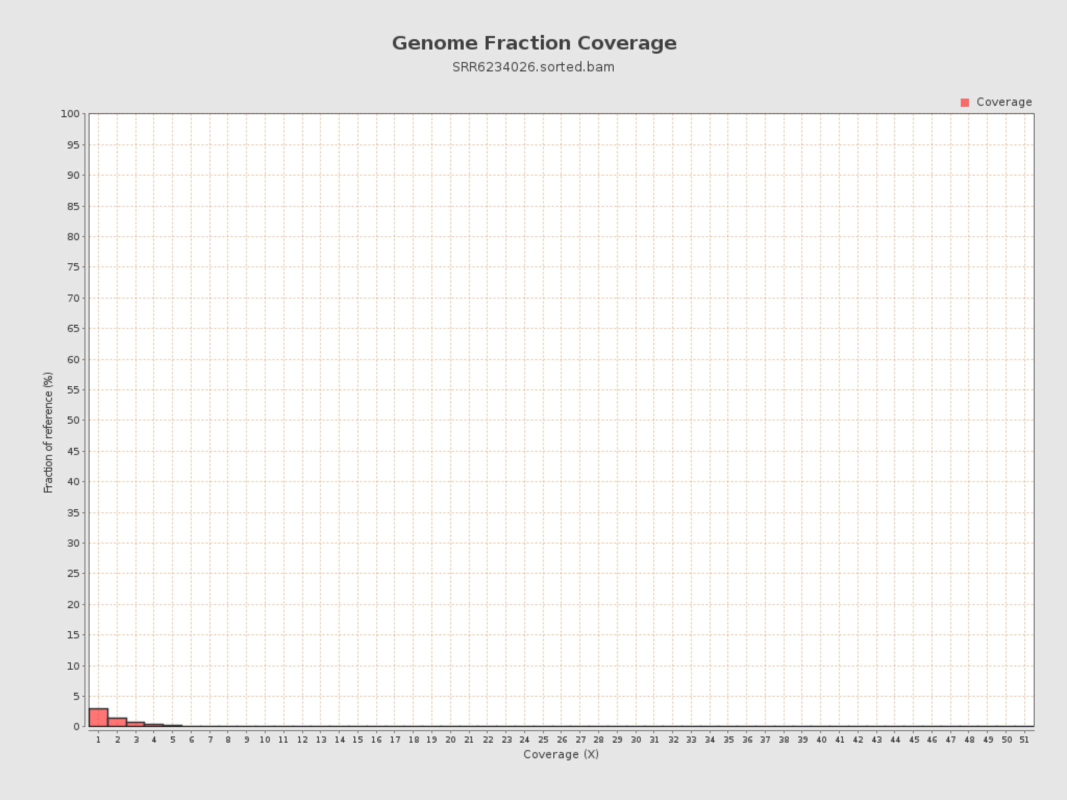
4. Results : Coverage Histogram



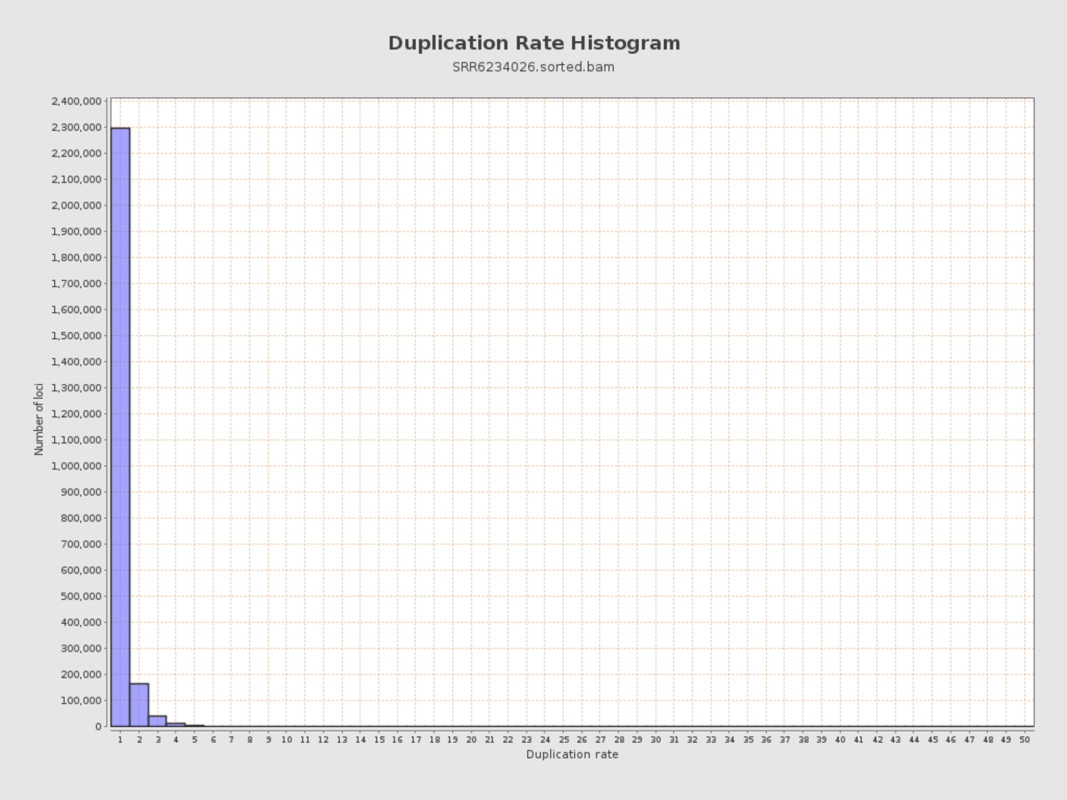
5. Results : Coverage Histogram (0-50X)



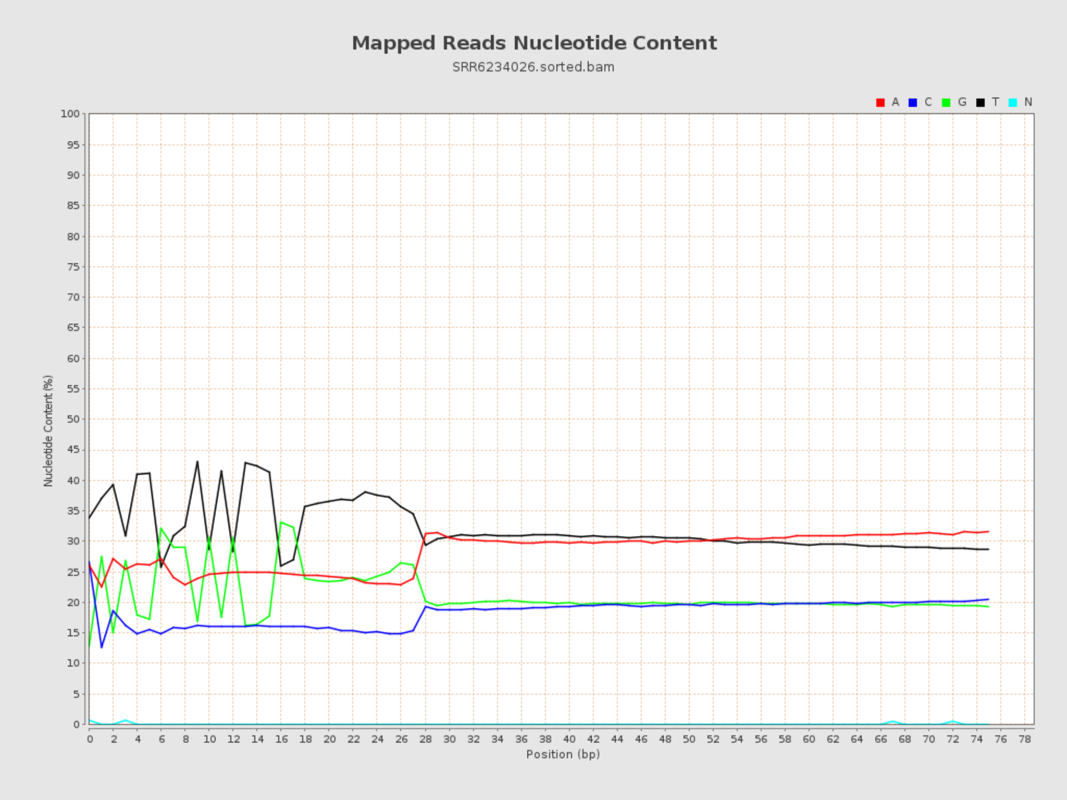
6. Results : Genome Fraction Coverage



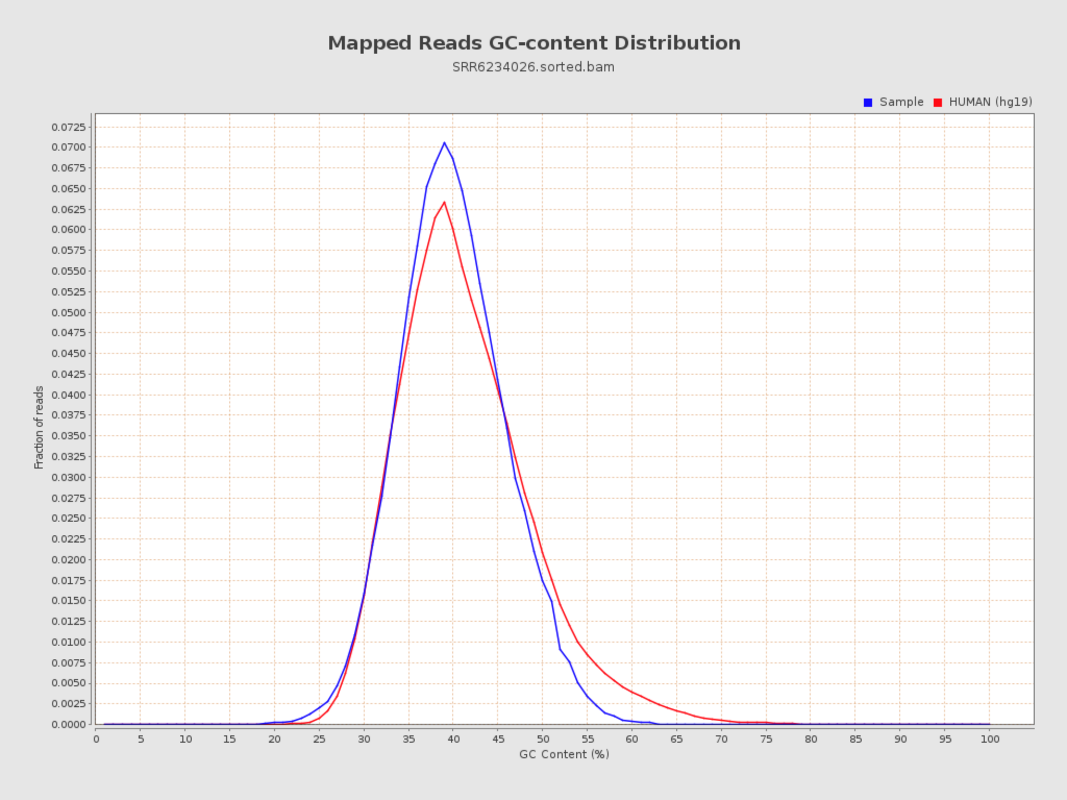
7. Results : Duplication Rate Histogram



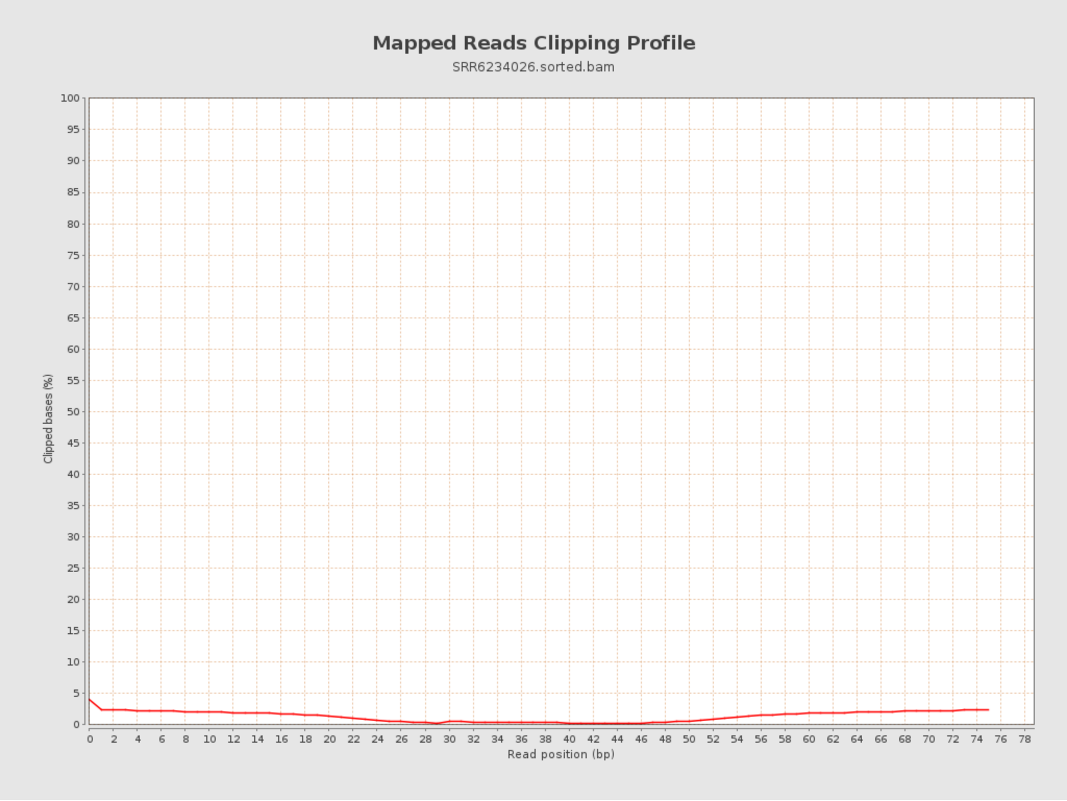
8. Results : Mapped Reads Nucleotide Content



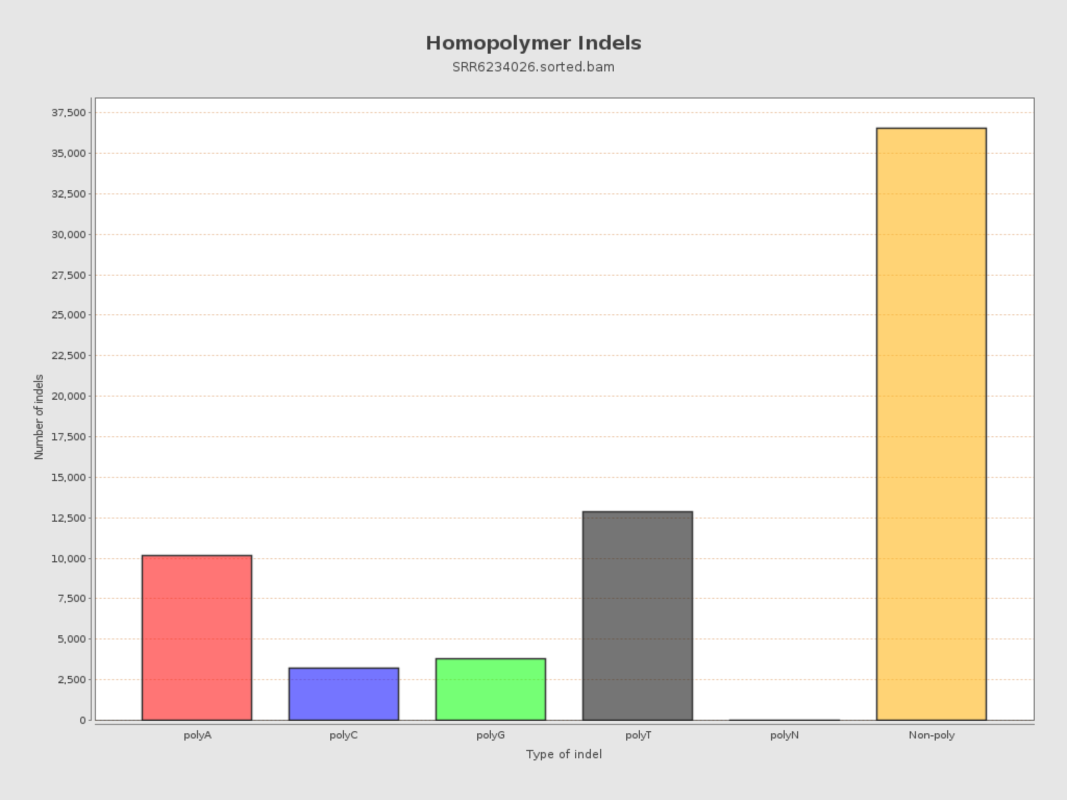
9. Results : Mapped Reads GC-content Distribution



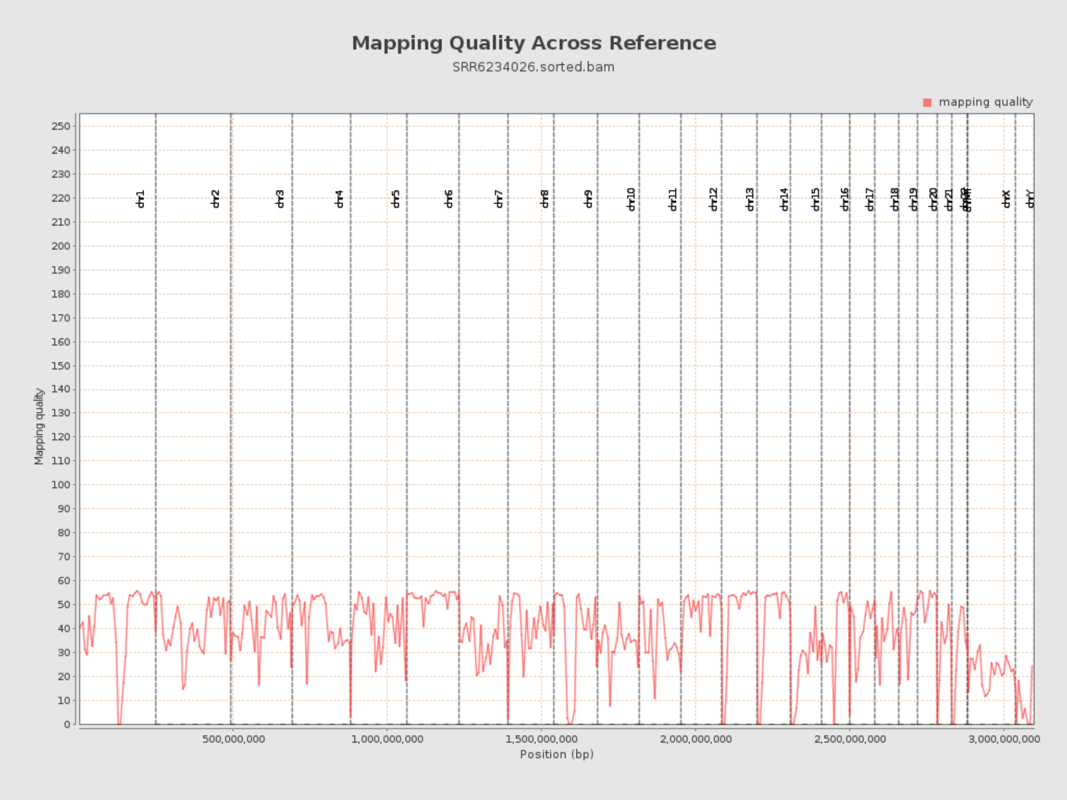
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram