Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 12:39:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234056.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_SRR6234056 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234056.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 12:39:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234056.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,469,253
Mapped reads	988,556 / 67.28%
Unmapped reads	480,697 / 32.72%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,615 / 0.86%
Read min/max/mean length	30 / 76 / 76.3
Duplicated reads (estimated)	120,525 / 8.2%
Duplication rate	10%
Clipped reads	582,559 / 39.65%

2.2. ACGT Content

Number/percentage of A's	16,894,255 / 26.97%
Number/percentage of C's	11,179,422 / 17.85%
Number/percentage of T's	20,378,868 / 32.54%
Number/percentage of G's	14,164,931 / 22.62%
Number/percentage of N's	15,125 / 0.02%
GC Percentage	40.47%

2.3. Coverage

Mean	0.0202

Standard Deviation	0.2679

2.4. Mapping Quality

Mean Mapping Quality	43.84

2.5. Mismatches and indels

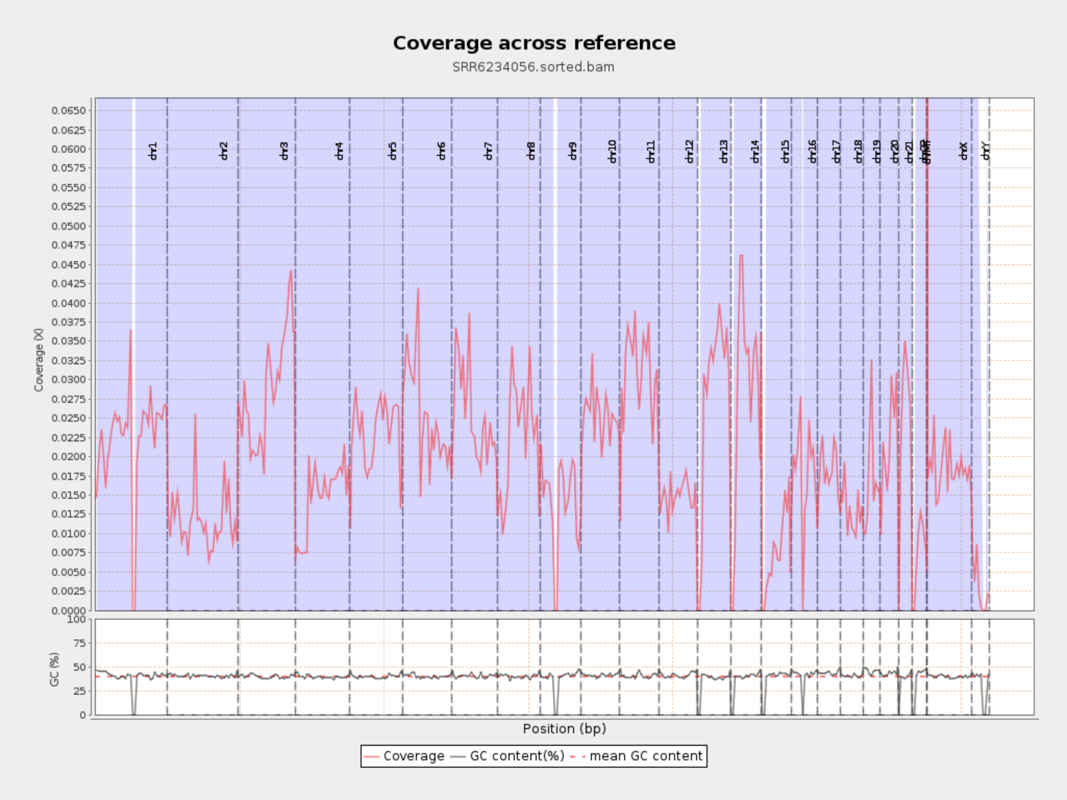
General error rate	0.85%
Mismatches	526,584
Insertions	4,757
Mapped reads with at least one insertion	0.48%
Deletions	25,371
Mapped reads with at least one deletion	2.53%
Homopolymer indels	43.93%

2.6. Chromosome stats

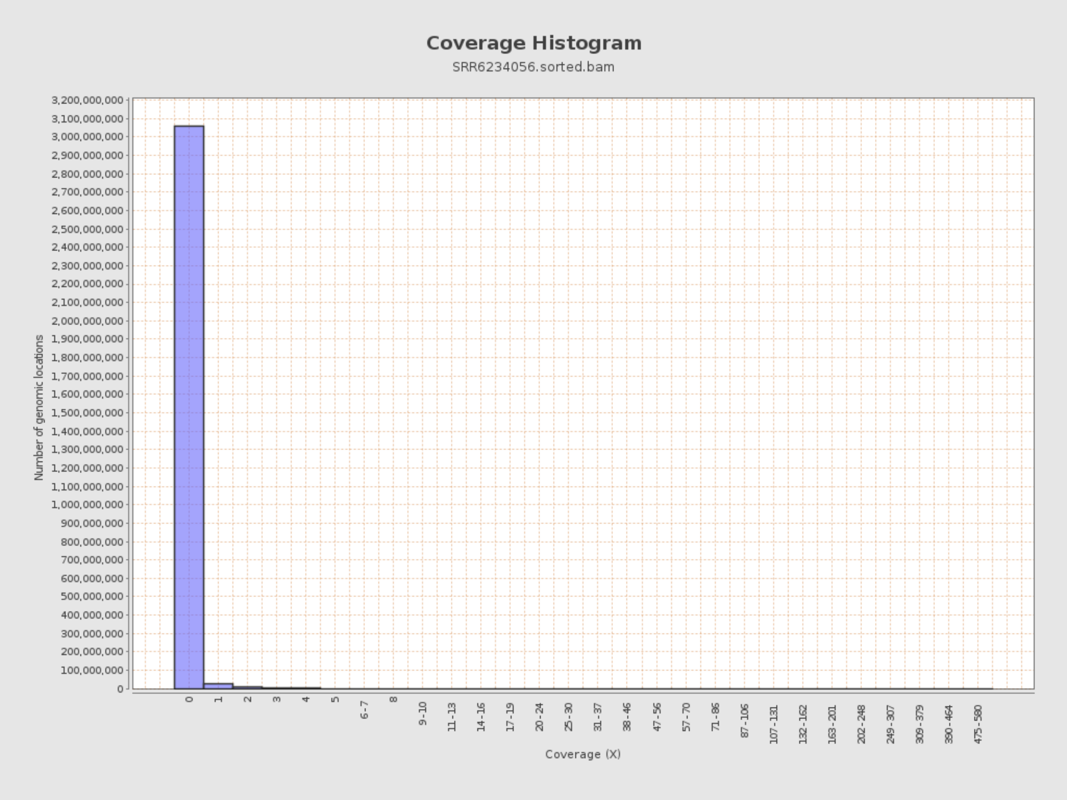
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5541507	0.0222	0.4067
chr2	243199373	2836187	0.0117	0.2961
chr3	198022430	5680483	0.0287	0.251
chr4	191154276	2831153	0.0148	0.1814
chr5	180915260	4218561	0.0233	0.2272
chr6	171115067	4367522	0.0255	0.2657
chr7	159138663	4045195	0.0254	0.2975

chr8	146364022	3360757	0.023	0.3627
chr9	141213431	1993754	0.0141	0.1859
chr10	135534747	3435083	0.0253	0.2637
chr11	135006516	4175939	0.0309	0.3583
chr12	133851895	1989557	0.0149	0.1782
chr13	115169878	3215632	0.0279	0.2527
chr14	107349540	3001728	0.028	0.2544
chr15	102531392	778516	0.0076	0.1273
chr16	90354753	1577546	0.0175	0.2008
chr17	81195210	1477896	0.0182	0.2234
chr18	78077248	1009737	0.0129	0.2994
chr19	59128983	1020037	0.0173	0.2881
chr20	63025520	1378489	0.0219	0.2254
chr21	48129895	1221720	0.0254	0.2379
chr22	51304566	381624	0.0074	0.1228
chrMT	16571	72131	4.3528	4.2011
chrX	155270560	2893135	0.0186	0.2098
chrY	59373566	172600	0.0029	0.0747

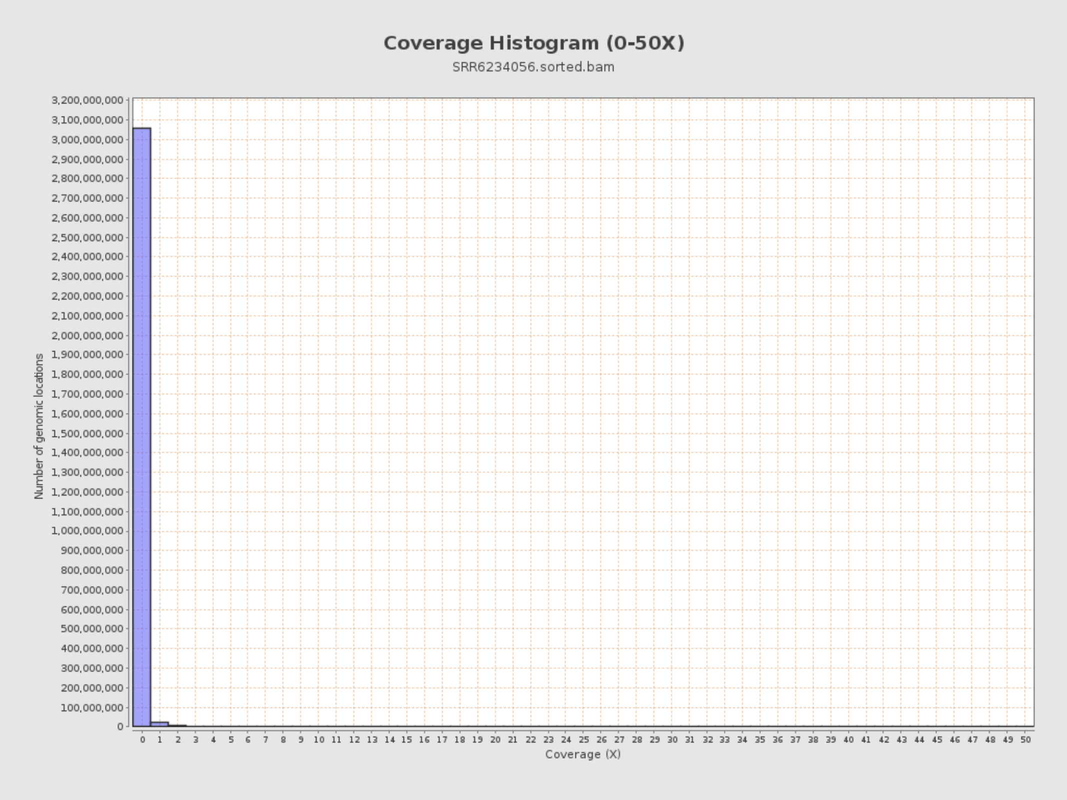
3. Results : Coverage across reference



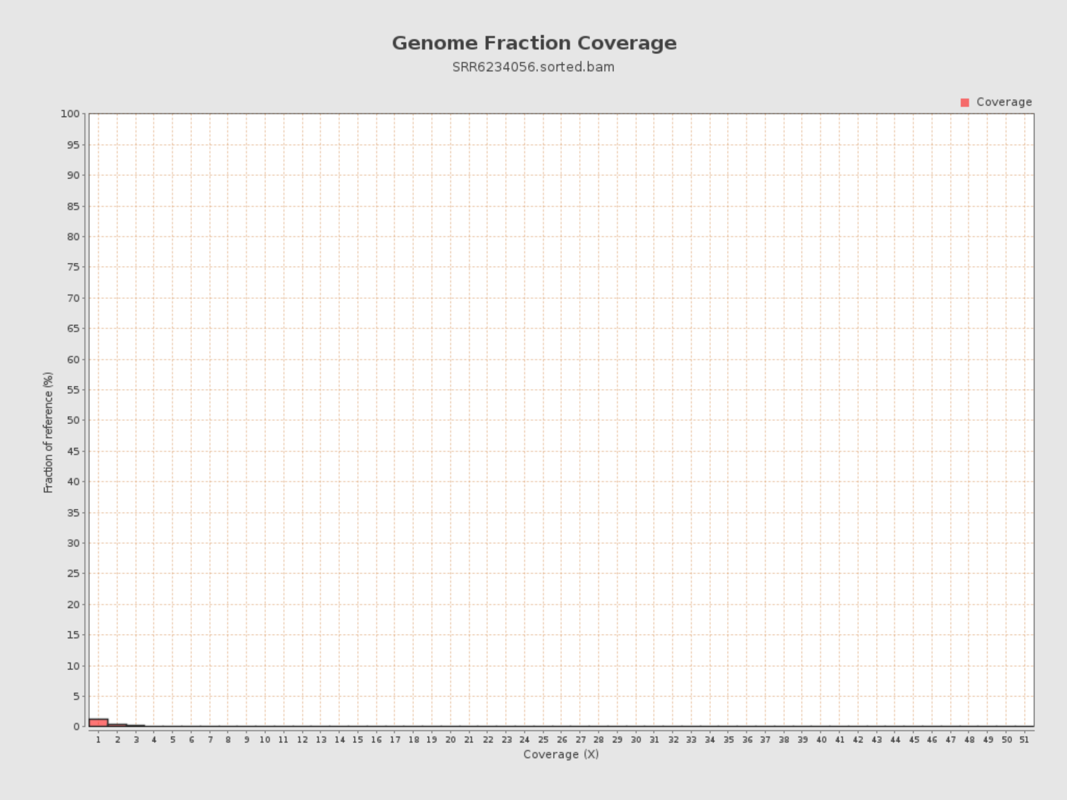
4. Results : Coverage Histogram



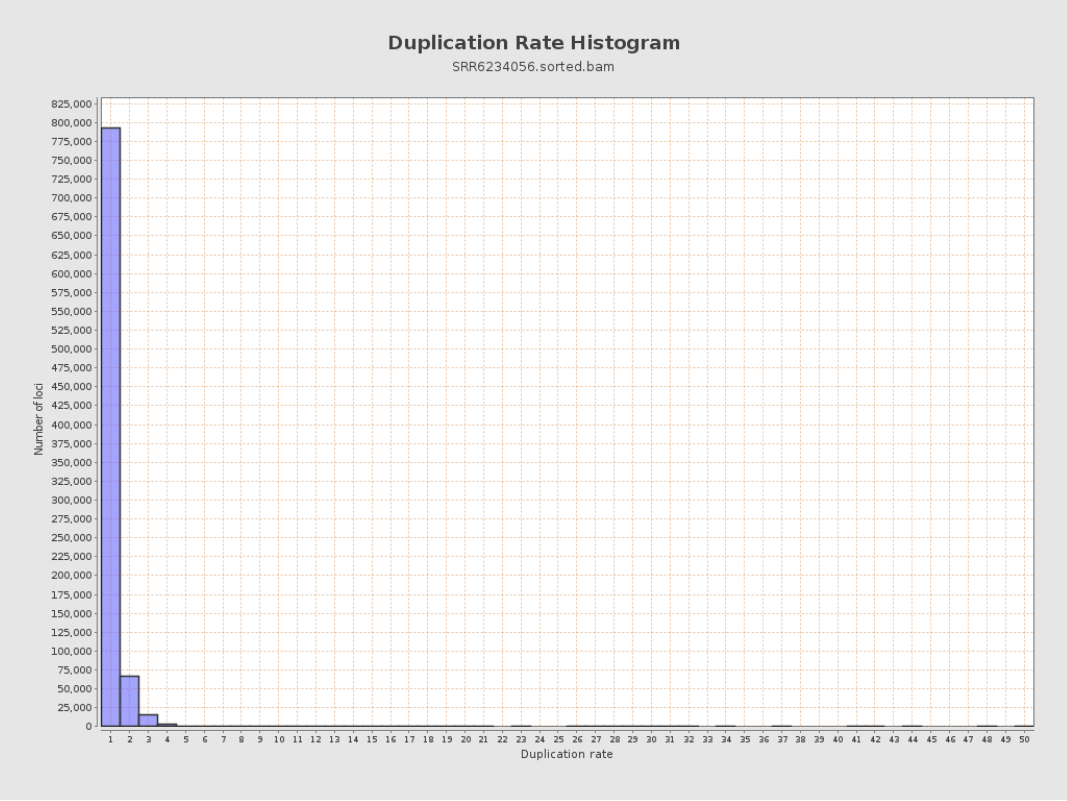
5. Results : Coverage Histogram (0-50X)



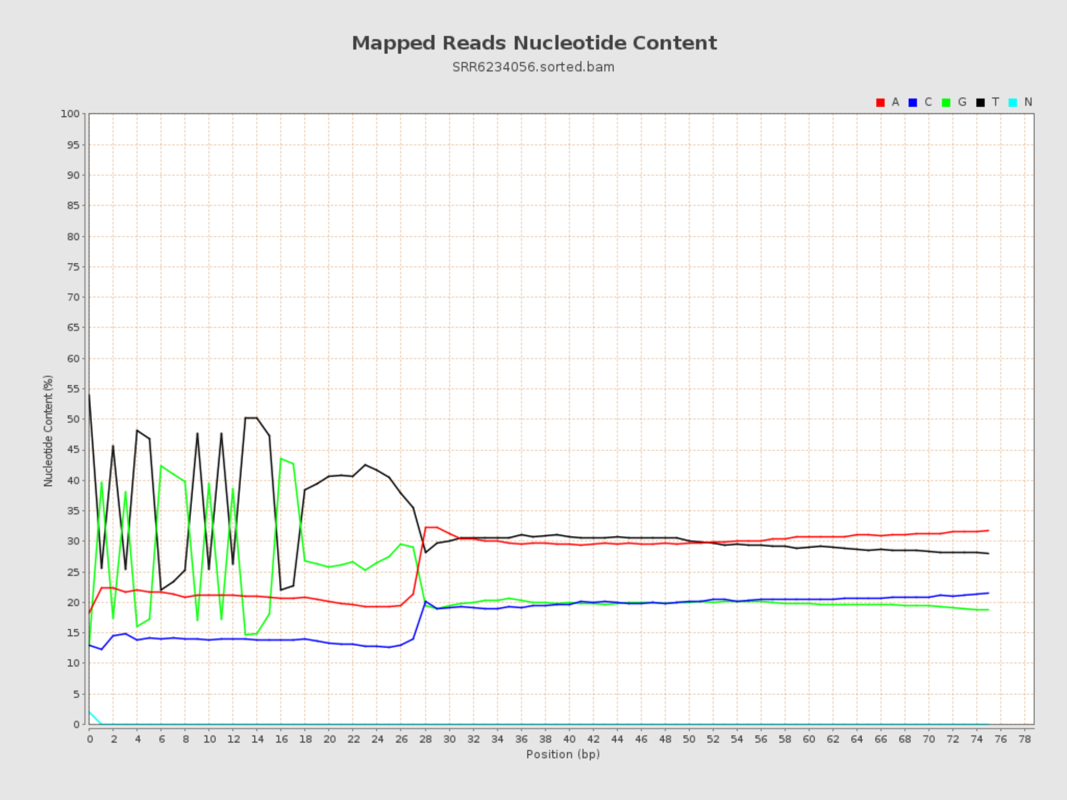
6. Results : Genome Fraction Coverage



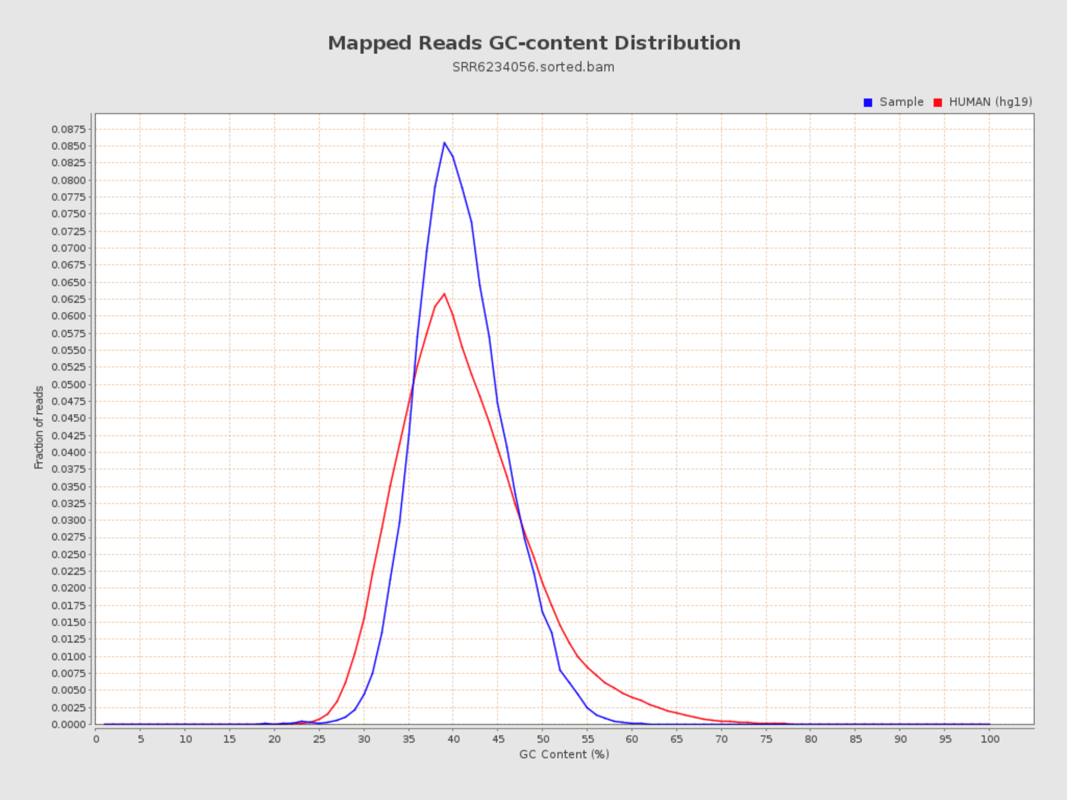
7. Results : Duplication Rate Histogram



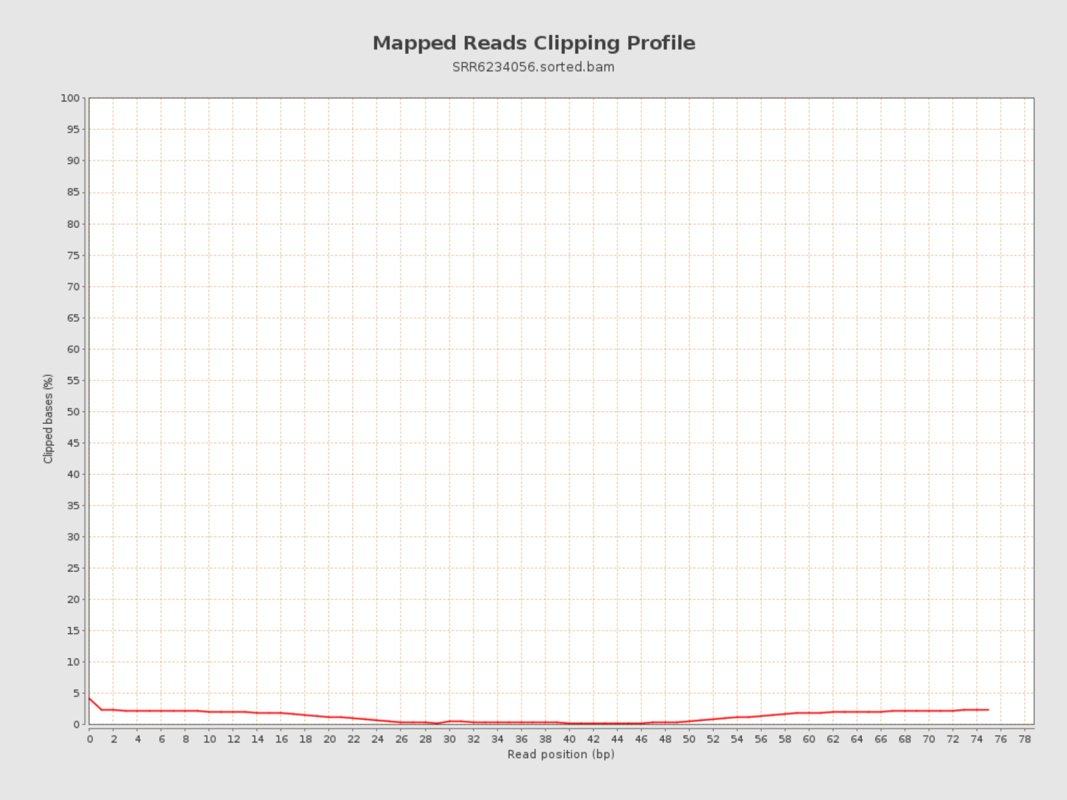
8. Results : Mapped Reads Nucleotide Content



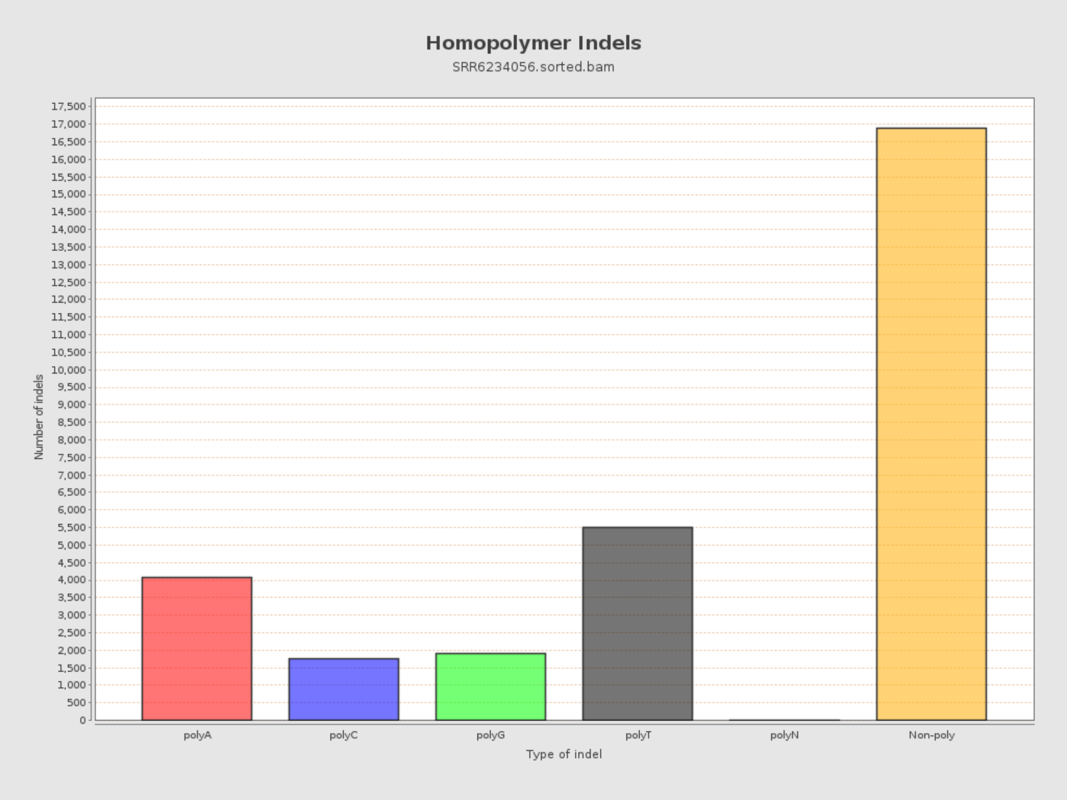
9. Results : Mapped Reads GC-content Distribution



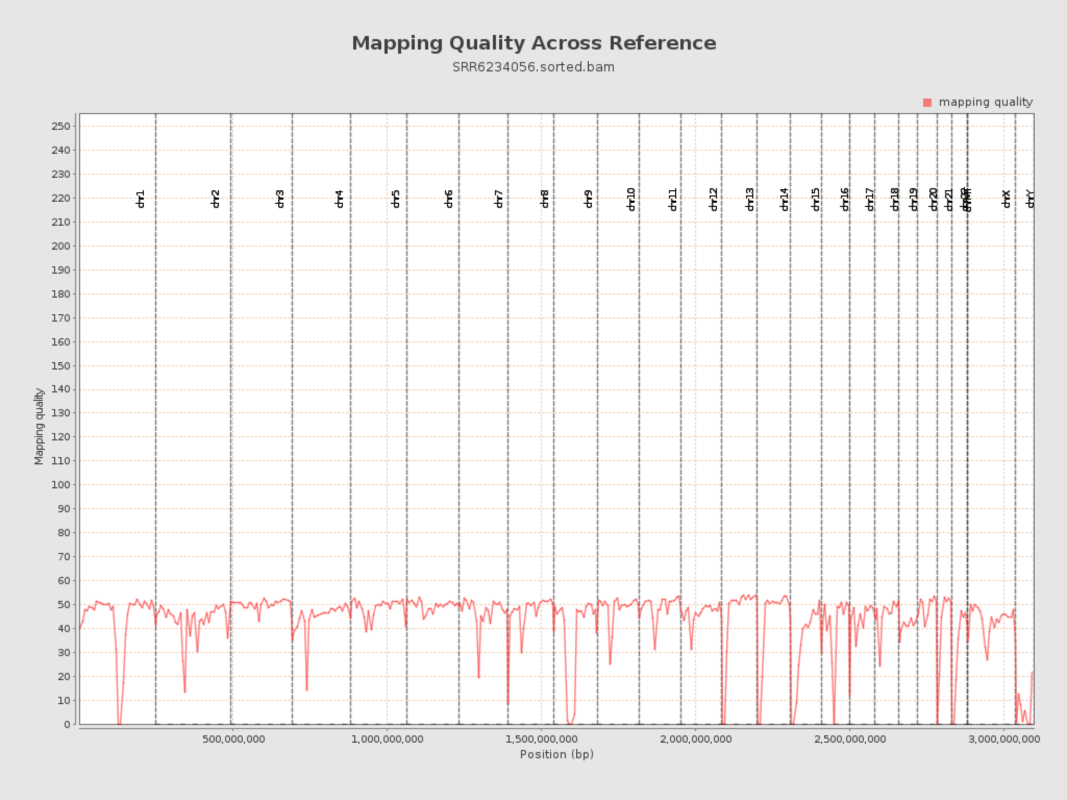
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram