Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 17:52:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234129.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_SRR6234129 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234129.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 17:52:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234129.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,892,015
Mapped reads	3,461,314 / 88.93%
Unmapped reads	430,701 / 11.07%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	36,694 / 0.94%
Read min/max/mean length	30 / 76 / 76.33
Duplicated reads (estimated)	1,209,228 / 31.07%
Duplication rate	13.97%
Clipped reads	1,164,528 / 29.92%

2.2. ACGT Content

Number/percentage of A's	54,584,447 / 22.8%
Number/percentage of C's	39,889,463 / 16.66%
Number/percentage of T's	58,062,426 / 24.25%
Number/percentage of G's	86,867,584 / 36.28%
Number/percentage of N's	49,864 / 0.02%
GC Percentage	52.94%

2.3. Coverage

Mean	0.0774

Standard Deviation	85.4043

2.4. Mapping Quality

Mean Mapping Quality	42.41

2.5. Mismatches and indels

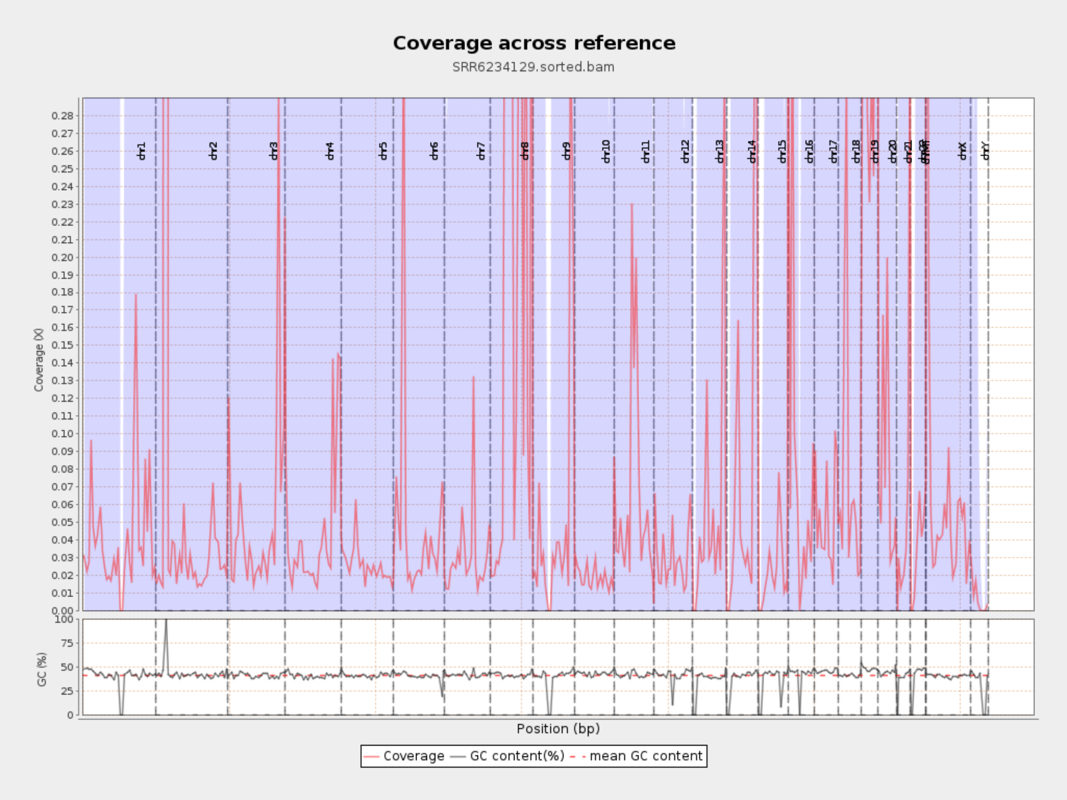
General error rate	0.57%
Mismatches	1,341,284
Insertions	14,287
Mapped reads with at least one insertion	0.41%
Deletions	45,434
Mapped reads with at least one deletion	1.3%
Homopolymer indels	47.76%

2.6. Chromosome stats

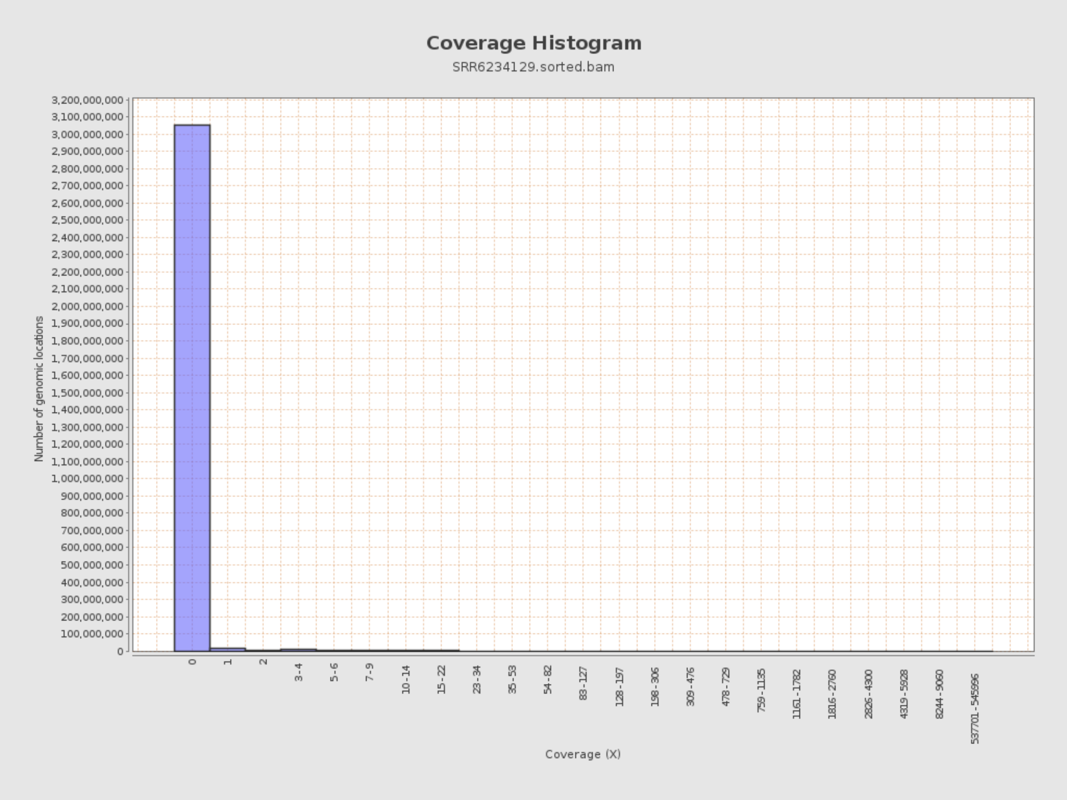
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10191532	0.0409	0.8371
chr2	243199373	48794384	0.2006	304.6614
chr3	198022430	10679535	0.0539	0.7295
chr4	191154276	8304441	0.0434	0.6654
chr5	180915260	4705381	0.026	0.5124
chr6	171115067	8406452	0.0491	2.9115
chr7	159138663	5072328	0.0319	0.6766

chr8	146364022	33764933	0.2307	1.656
chr9	141213431	7421797	0.0526	0.7499
chr10	135534747	2554586	0.0188	0.4159
chr11	135006516	8919064	0.0661	0.9162
chr12	133851895	4099165	0.0306	3.1726
chr13	115169878	7540224	0.0655	0.8482
chr14	107349540	9231265	0.086	1.0167
chr15	102531392	2238268	0.0218	3.7186
chr16	90354753	8473937	0.0938	0.9593
chr17	81195210	4314613	0.0531	0.7224
chr18	78077248	6531810	0.0837	0.9607
chr19	59128983	27117154	0.4586	2.325
chr20	63025520	5071890	0.0805	0.9239
chr21	48129895	3100227	0.0644	0.8313
chr22	51304566	1762721	0.0344	0.569
chrMT	16571	199072	12.0133	12.9655
chrX	155270560	10642206	0.0685	0.836
chrY	59373566	391194	0.0066	0.2267

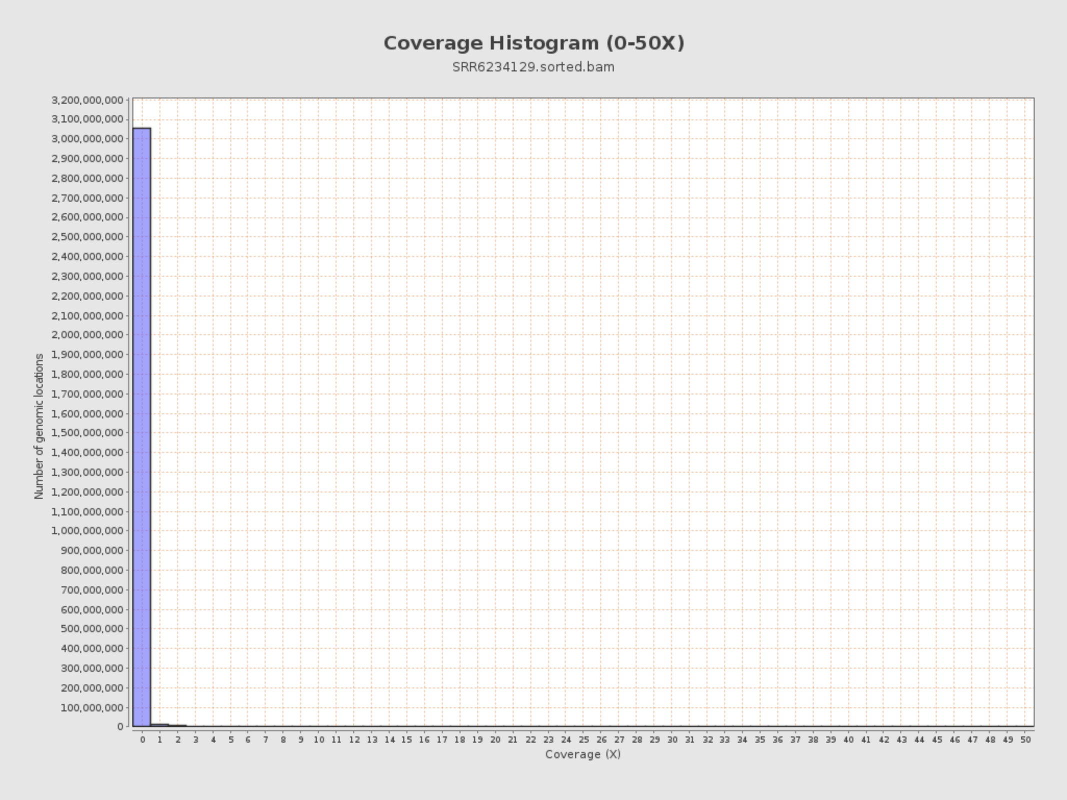
3. Results : Coverage across reference



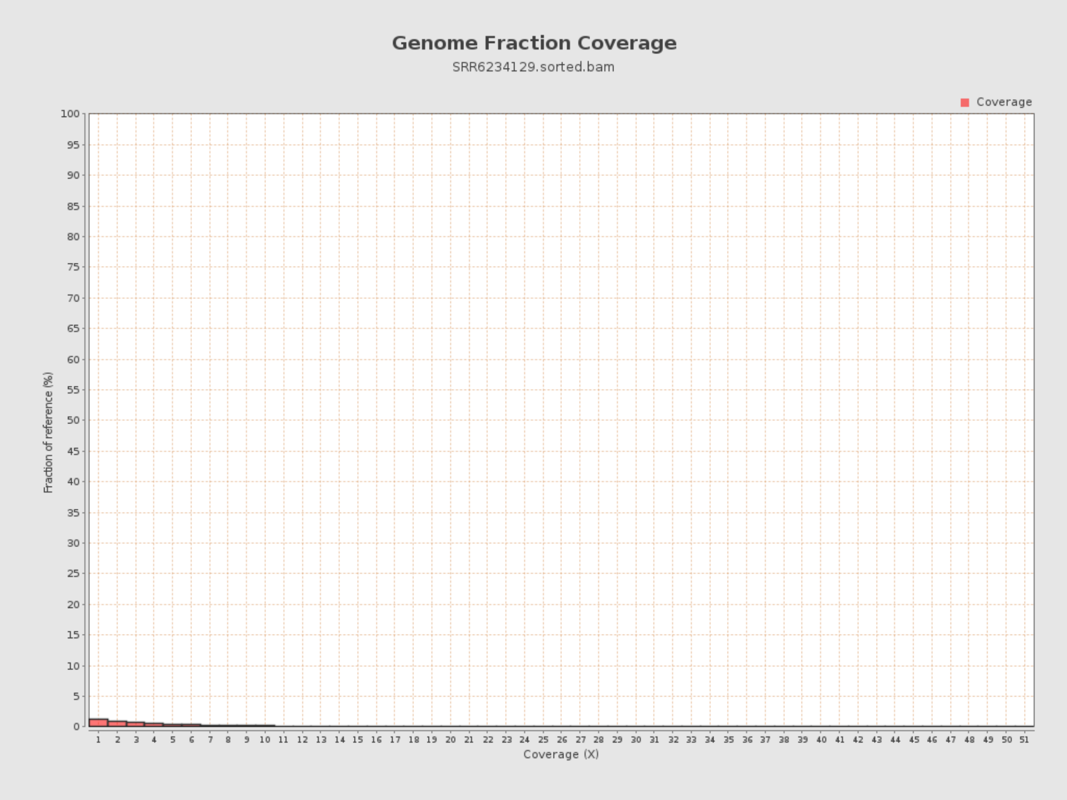
4. Results : Coverage Histogram



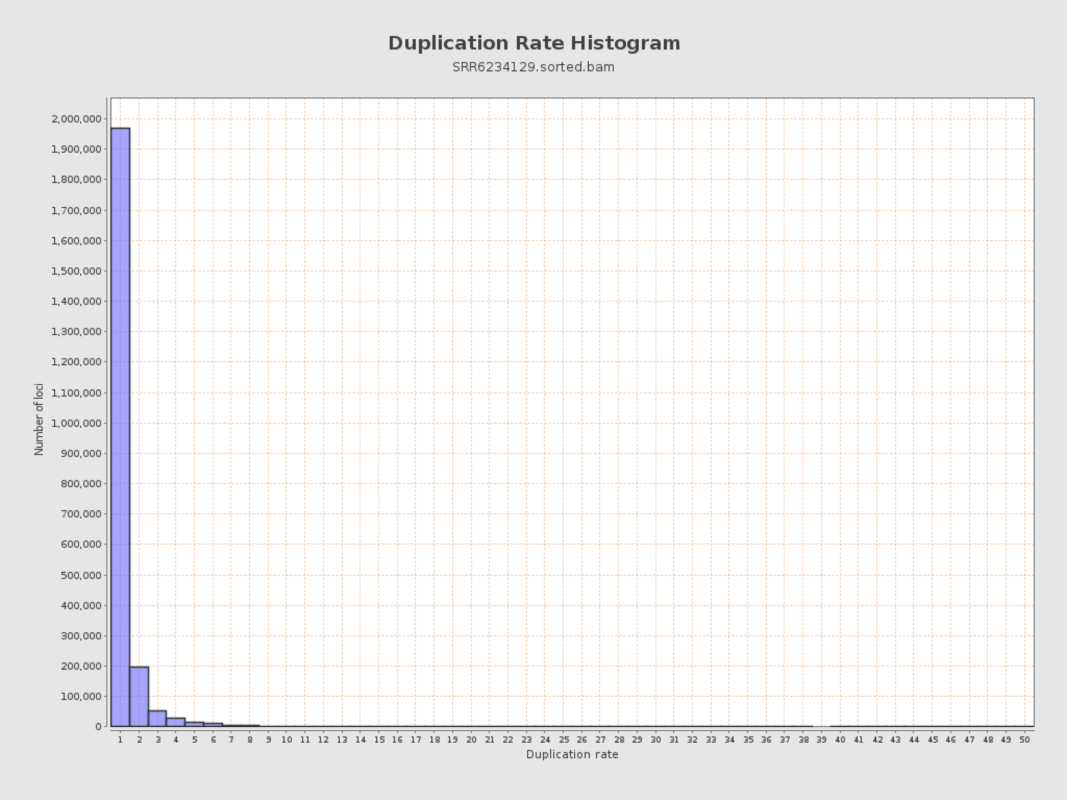
5. Results : Coverage Histogram (0-50X)



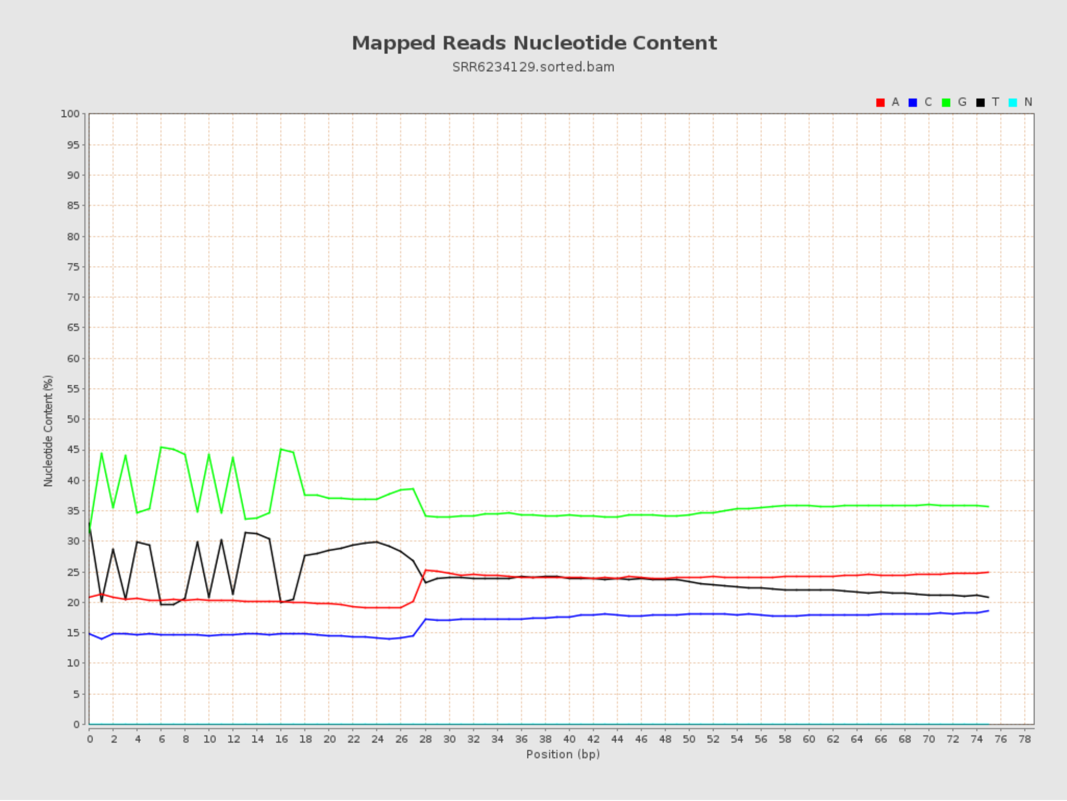
6. Results : Genome Fraction Coverage



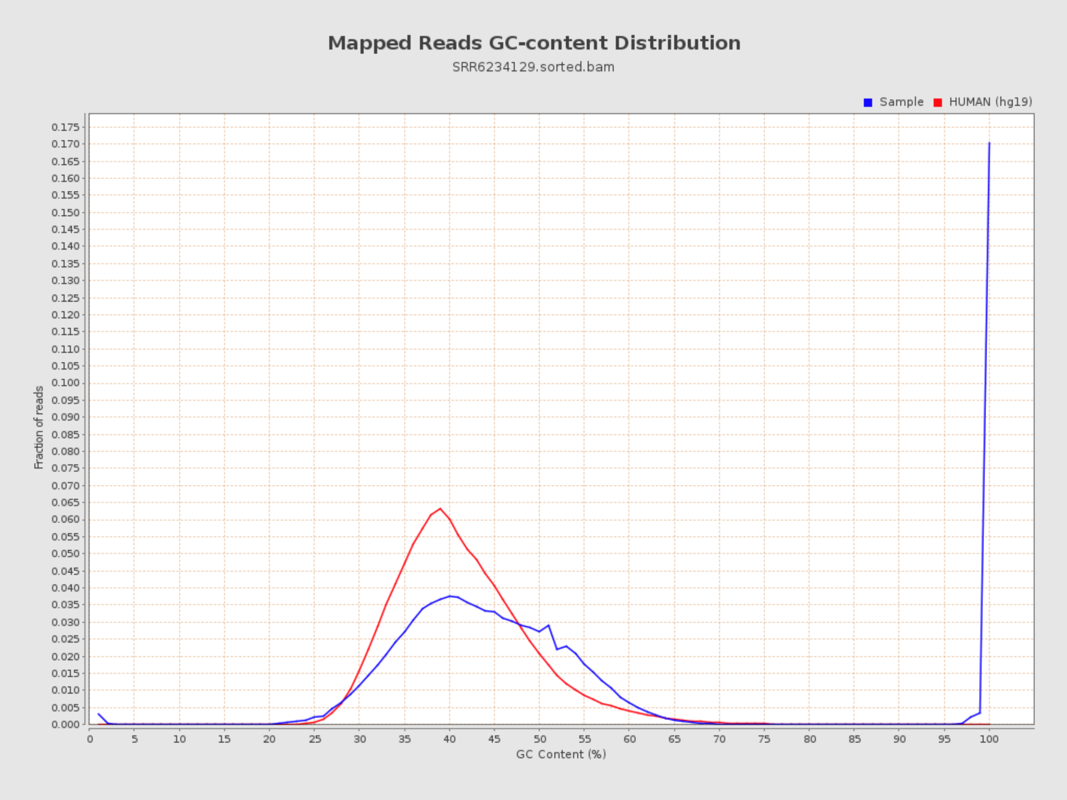
7. Results : Duplication Rate Histogram



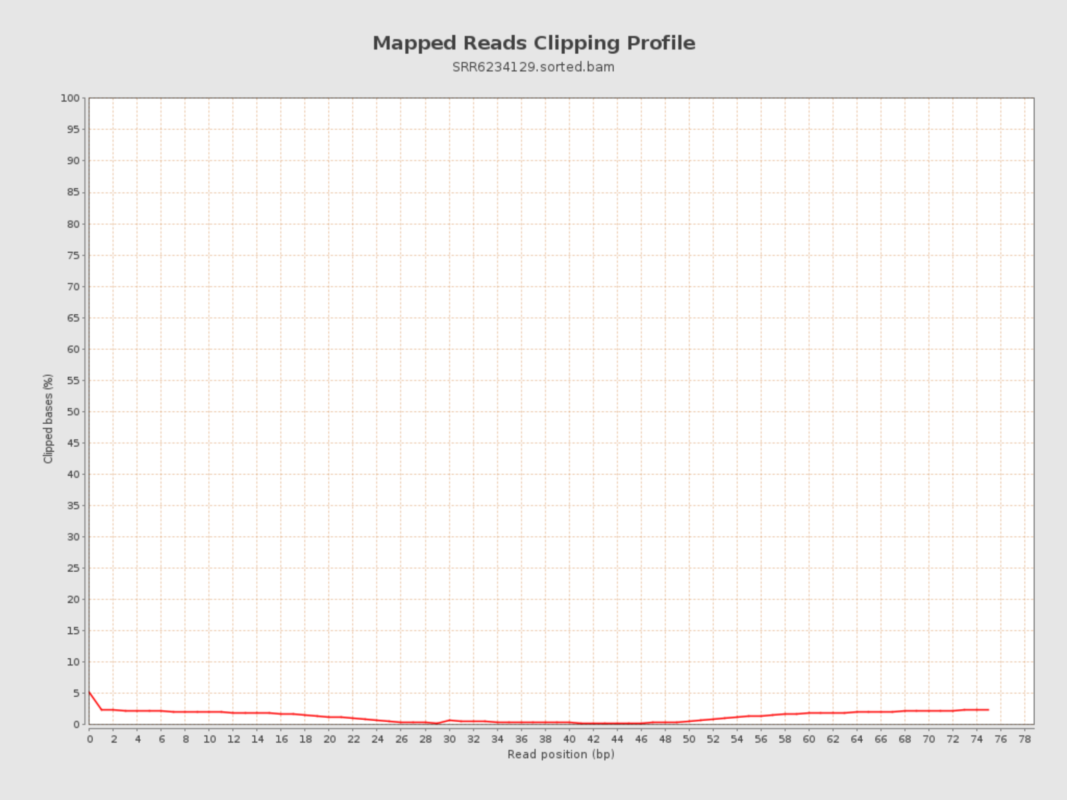
8. Results : Mapped Reads Nucleotide Content



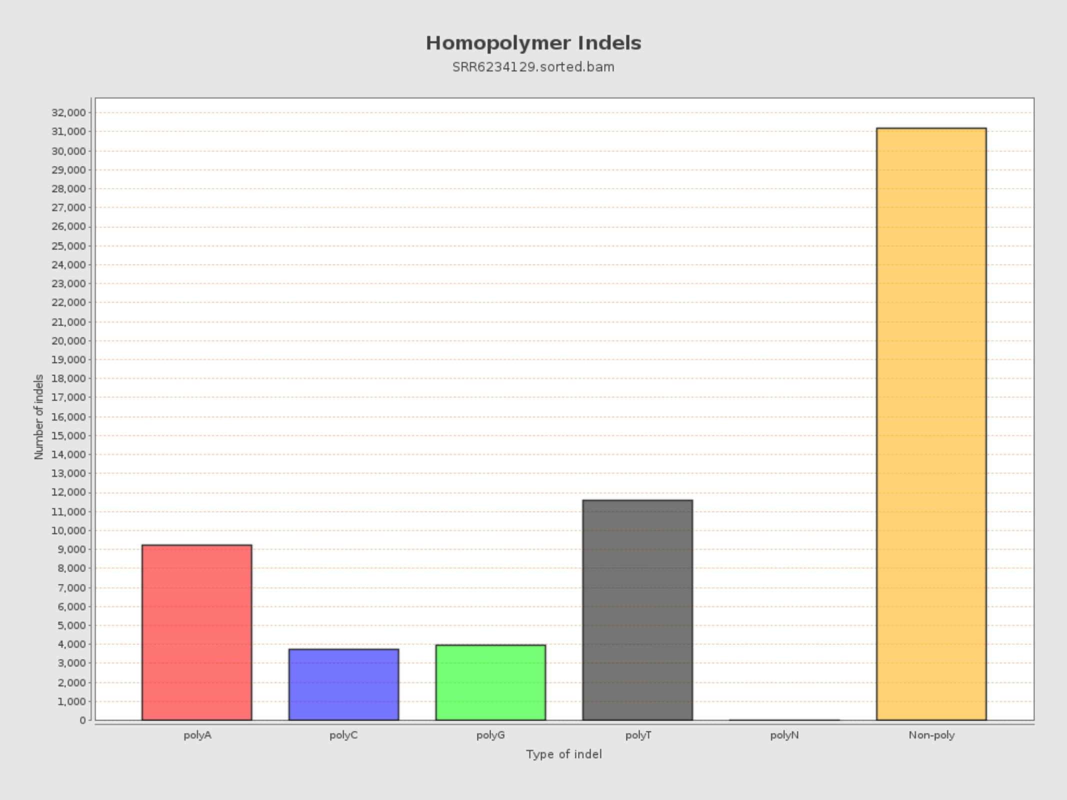
9. Results : Mapped Reads GC-content Distribution



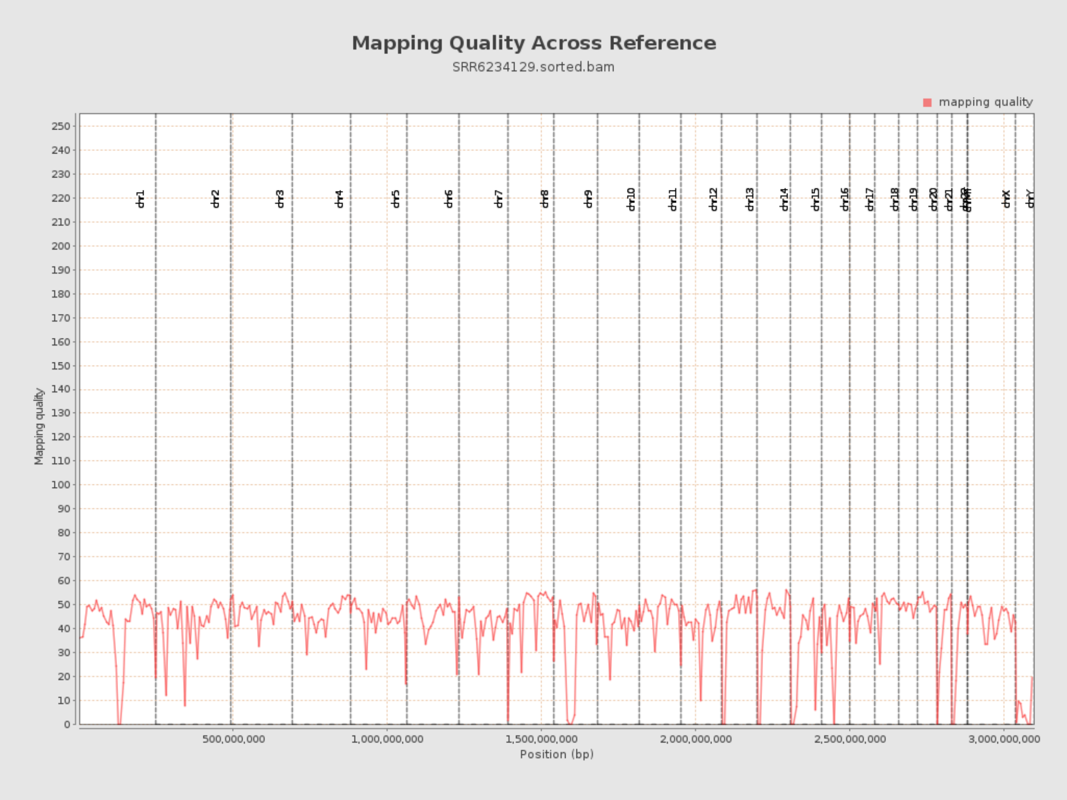
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram