Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 12:26:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234051.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_SRR6234051 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234051.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 12:26:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234051.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,792,089
Mapped reads	2,630,899 / 94.23%
Unmapped reads	161,190 / 5.77%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,362 / 0.62%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	247,173 / 8.85%
Duplication rate	7.28%
Clipped reads	1,351,097 / 48.39%

2.2. ACGT Content

Number/percentage of A's	44,181,882 / 25.71%
Number/percentage of C's	31,951,322 / 18.59%
Number/percentage of T's	54,622,205 / 31.78%
Number/percentage of G's	41,106,699 / 23.92%
Number/percentage of N's	16,178 / 0.01%
GC Percentage	42.51%

2.3. Coverage

Mean	0.0556

Standard Deviation	0.8483

2.4. Mapping Quality

Mean Mapping Quality	40.28

2.5. Mismatches and indels

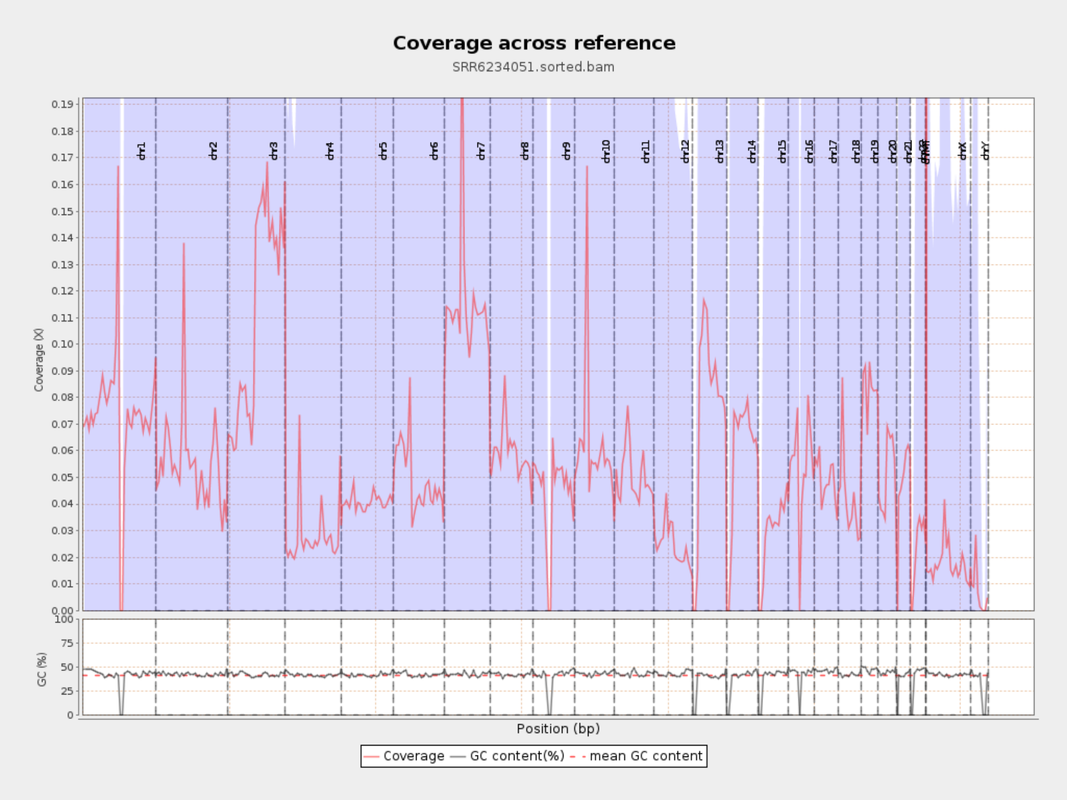
General error rate	0.76%
Mismatches	1,275,946
Insertions	15,784
Mapped reads with at least one insertion	0.59%
Deletions	56,647
Mapped reads with at least one deletion	2.13%
Homopolymer indels	44.12%

2.6. Chromosome stats

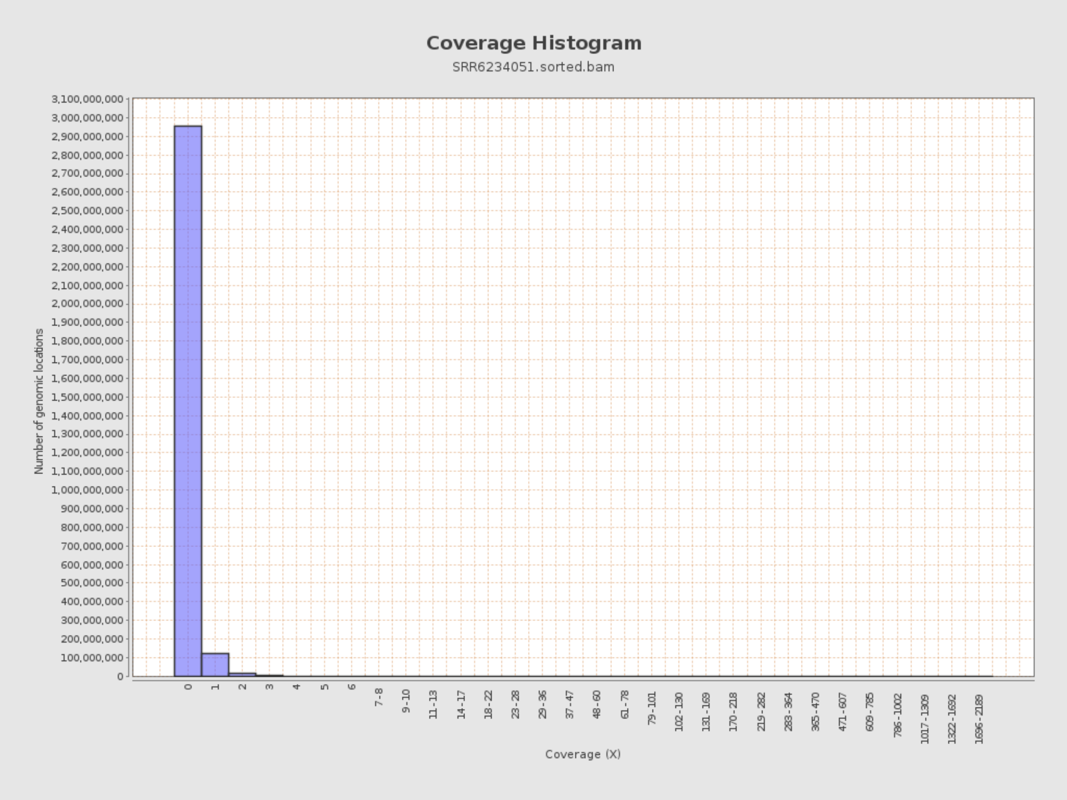
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	18453682	0.074	1.8324
chr2	243199373	13457995	0.0553	0.9016
chr3	198022430	21840429	0.1103	0.4213
chr4	191154276	5403853	0.0283	0.2662
chr5	180915260	7384872	0.0408	0.2453
chr6	171115067	8463511	0.0495	0.4047
chr7	159138663	18477484	0.1161	1.8594

chr8	146364022	8644981	0.0591	0.6799
chr9	141213431	6200465	0.0439	0.4874
chr10	135534747	8455226	0.0624	0.9217
chr11	135006516	6820419	0.0505	0.4631
chr12	133851895	3295635	0.0246	0.2073
chr13	115169878	8838680	0.0767	0.3445
chr14	107349540	6307408	0.0588	0.3628
chr15	102531392	2918631	0.0285	0.2396
chr16	90354753	4744137	0.0525	0.3753
chr17	81195210	4018509	0.0495	0.3279
chr18	78077248	3337776	0.0427	1.348
chr19	59128983	4897441	0.0828	1.1198
chr20	63025520	3213998	0.051	0.3606
chr21	48129895	2319686	0.0482	0.2974
chr22	51304566	1160624	0.0226	0.1725
chrMT	16571	127117	7.6711	7.811
chrX	155270560	2755208	0.0177	0.2776
chrY	59373566	436710	0.0074	0.2141

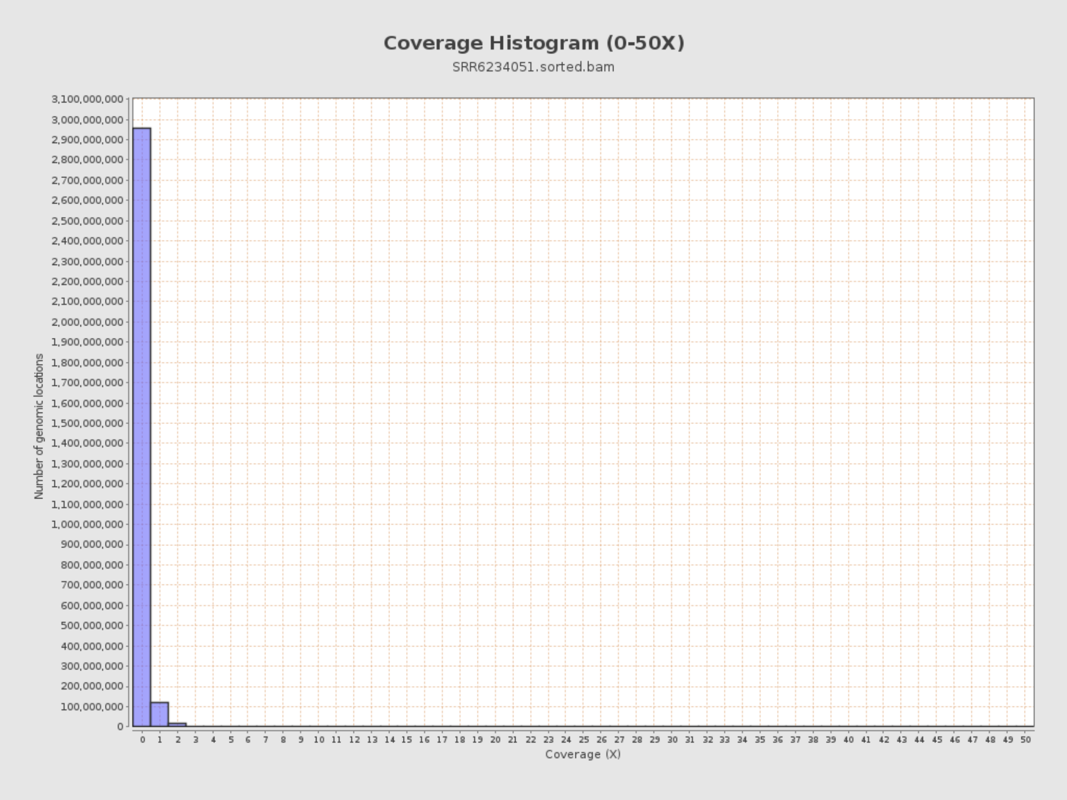
3. Results : Coverage across reference



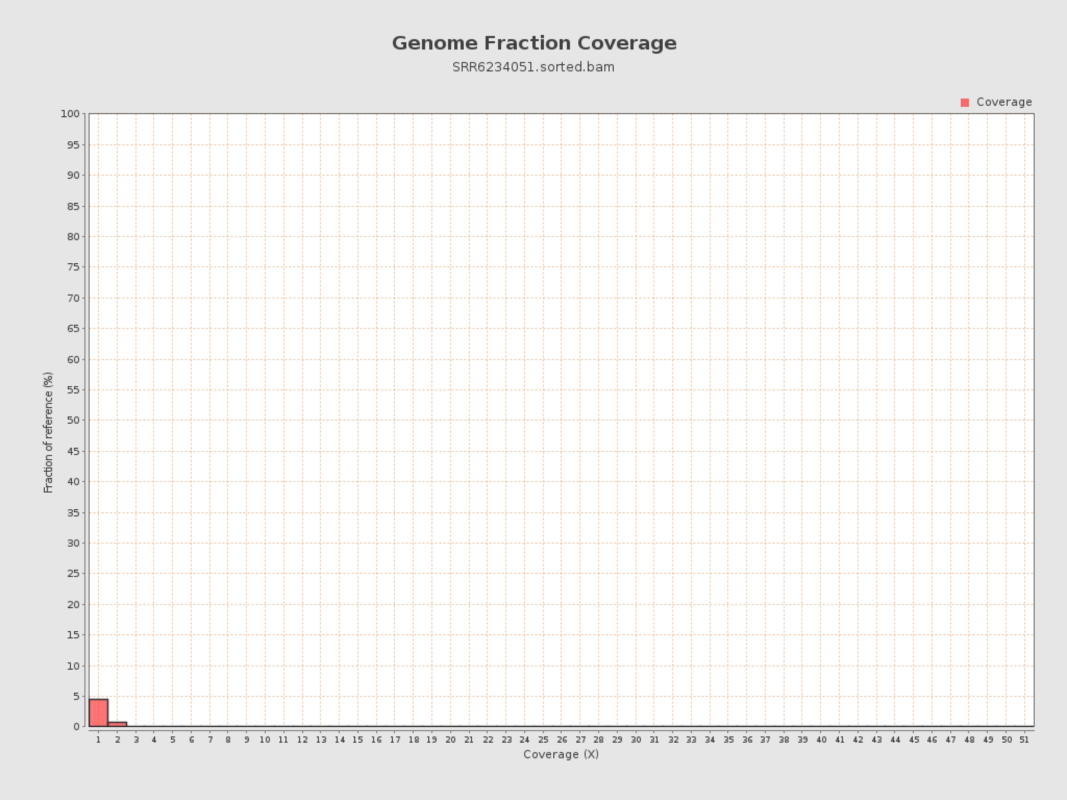
4. Results : Coverage Histogram



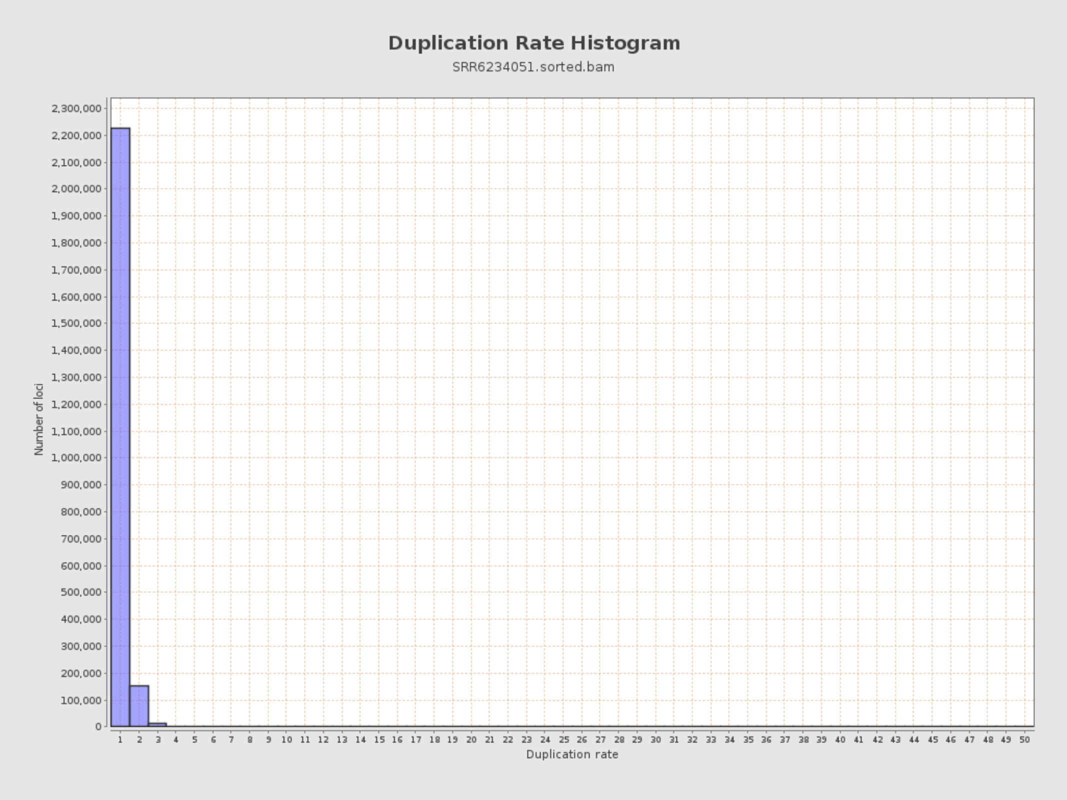
5. Results : Coverage Histogram (0-50X)



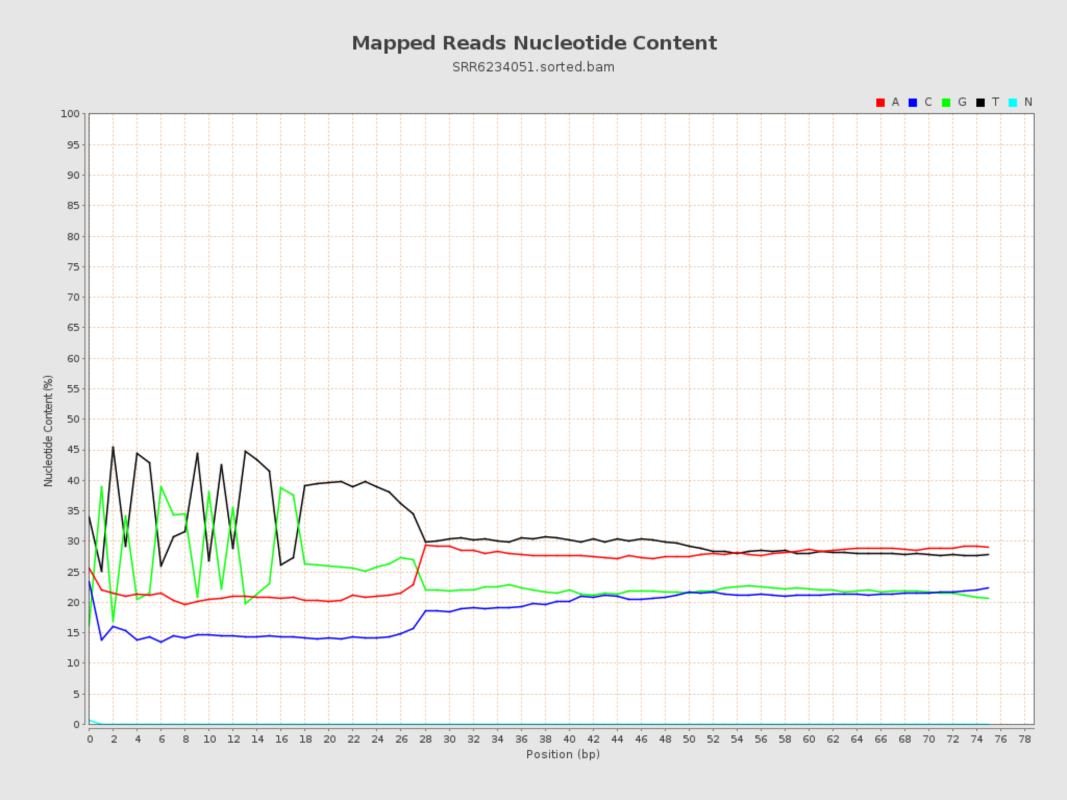
6. Results : Genome Fraction Coverage



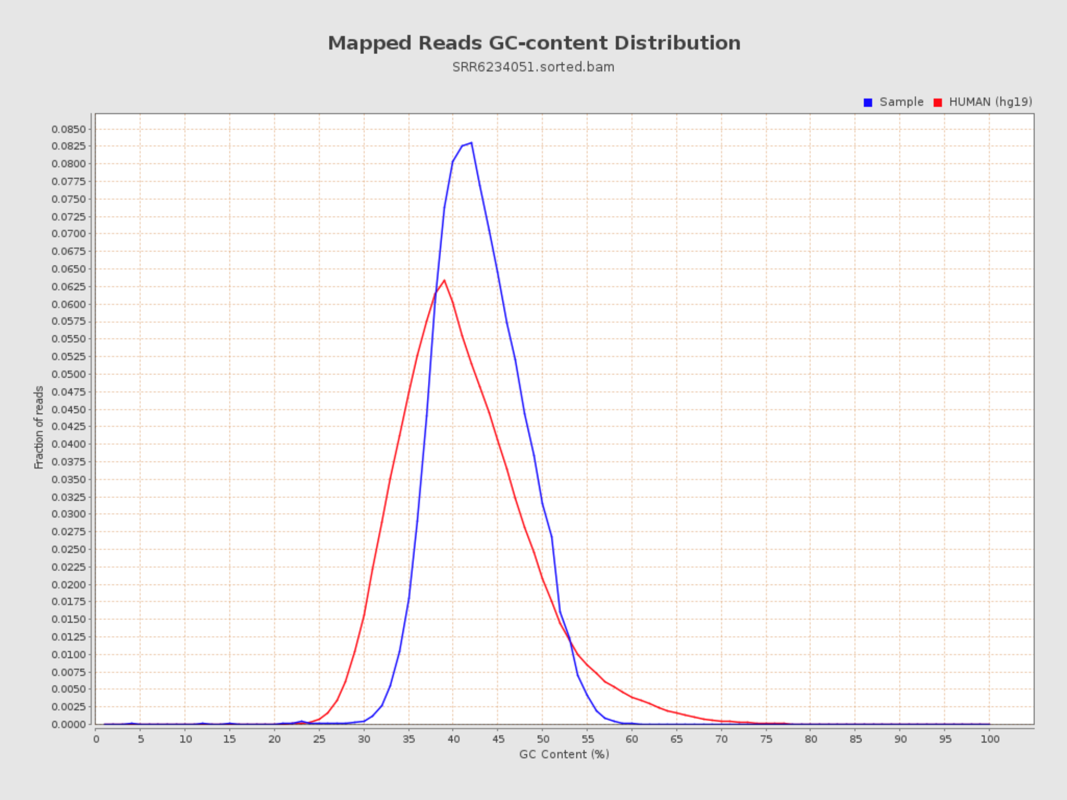
7. Results : Duplication Rate Histogram



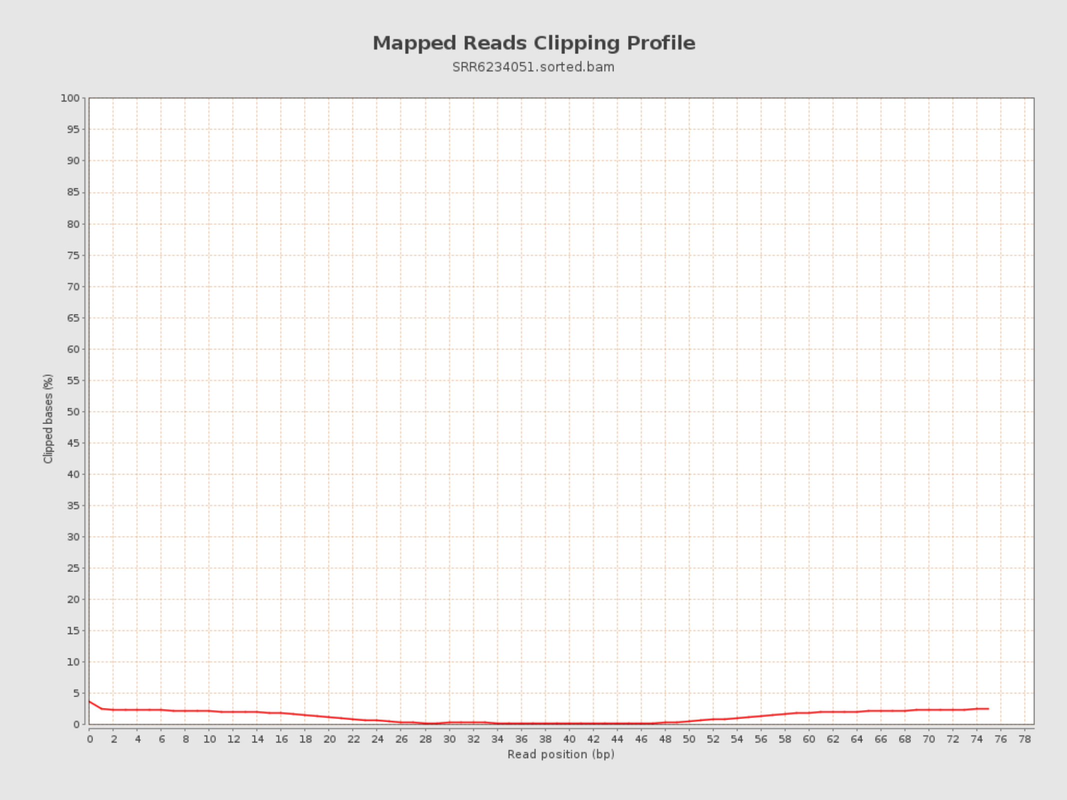
8. Results : Mapped Reads Nucleotide Content



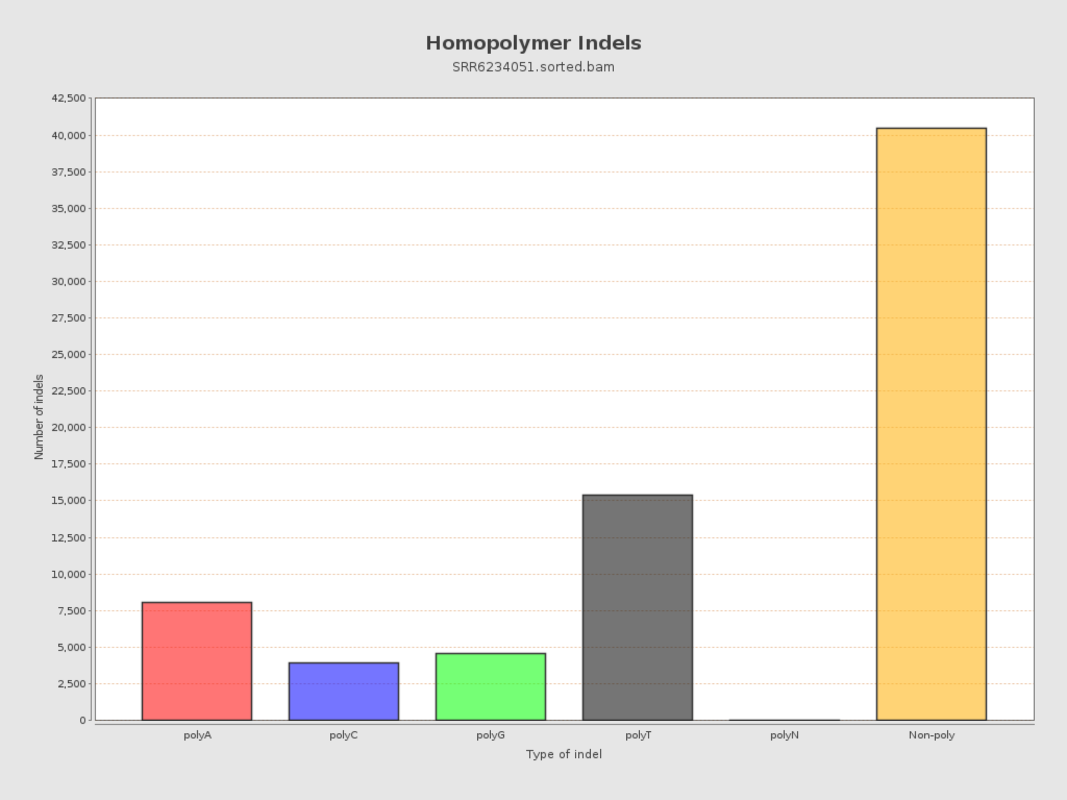
9. Results : Mapped Reads GC-content Distribution



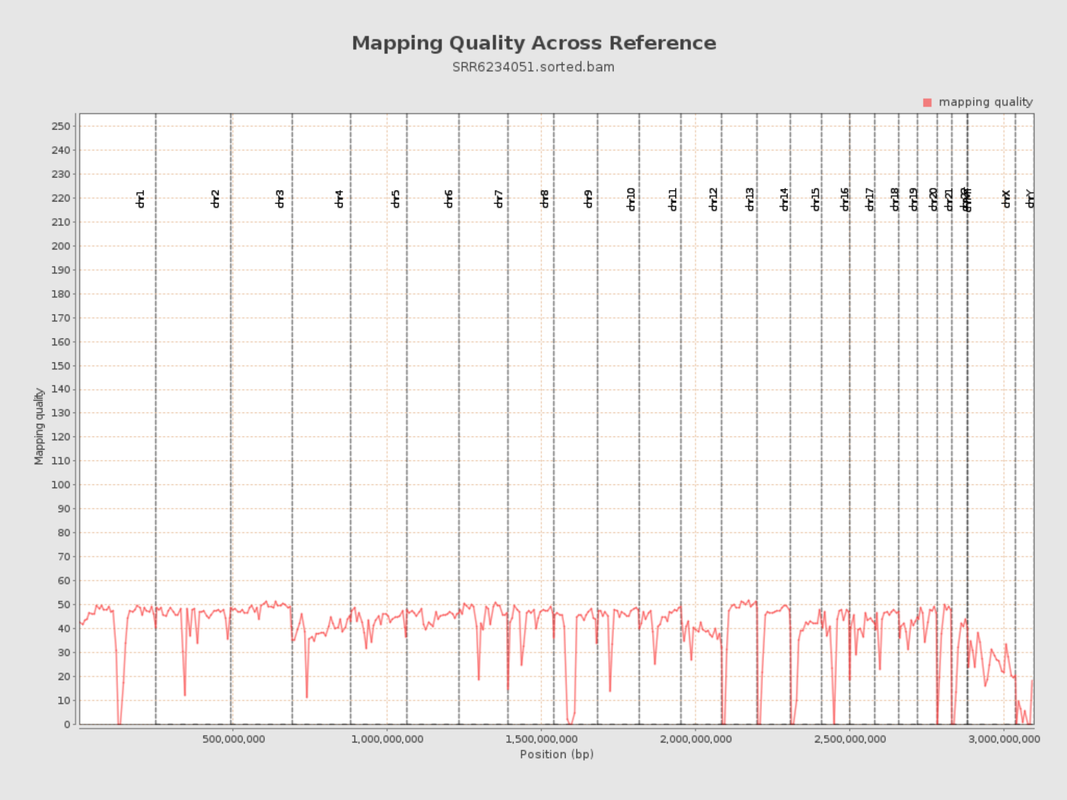
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram