Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 18:42:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234151.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_SRR6234151 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234151.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 18:42:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234151.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,586,777
Mapped reads	1,659,631 / 64.16%
Unmapped reads	927,146 / 35.84%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,915 / 0.65%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	113,215 / 4.38%
Duplication rate	5.76%
Clipped reads	949,350 / 36.7%

2.2. ACGT Content

Number/percentage of A's	28,730,485 / 27.22%
Number/percentage of C's	20,042,498 / 18.99%
Number/percentage of T's	32,922,794 / 31.2%
Number/percentage of G's	23,809,100 / 22.56%
Number/percentage of N's	25,672 / 0.02%
GC Percentage	41.55%

2.3. Coverage

Mean	0.0341

Standard Deviation	0.3166

2.4. Mapping Quality

Mean Mapping Quality	45.39

2.5. Mismatches and indels

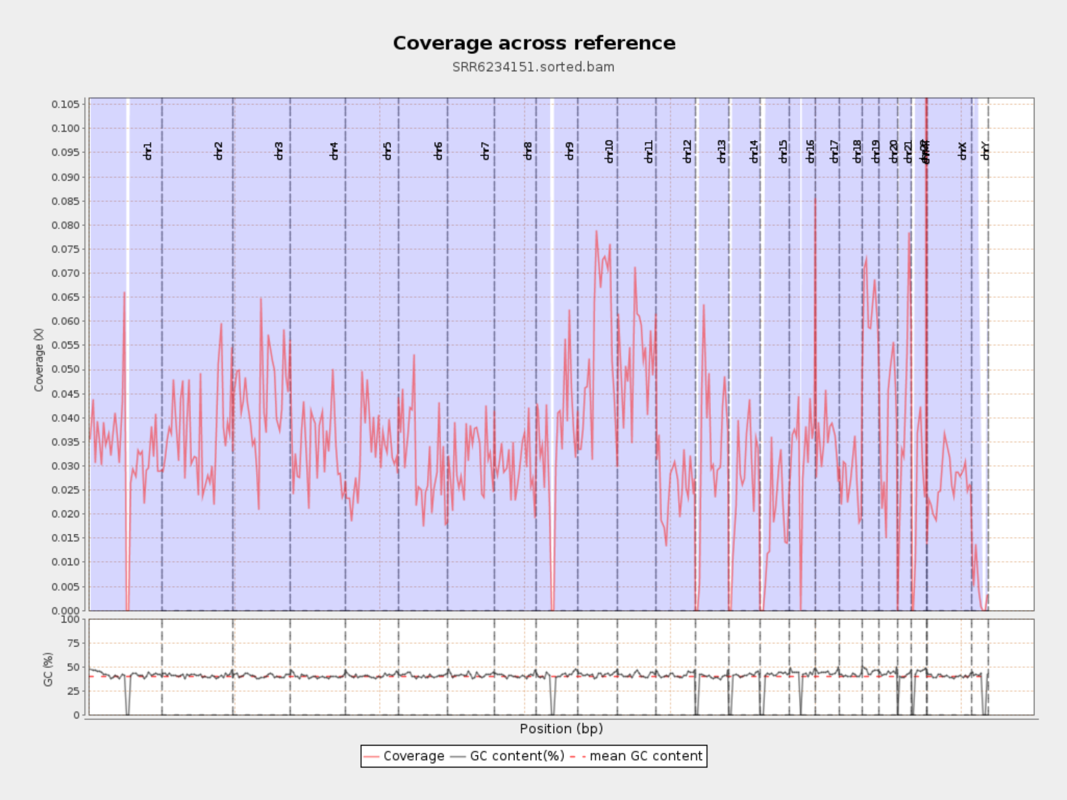
General error rate	0.93%
Mismatches	965,644
Insertions	8,260
Mapped reads with at least one insertion	0.49%
Deletions	51,346
Mapped reads with at least one deletion	3.03%
Homopolymer indels	42.62%

2.6. Chromosome stats

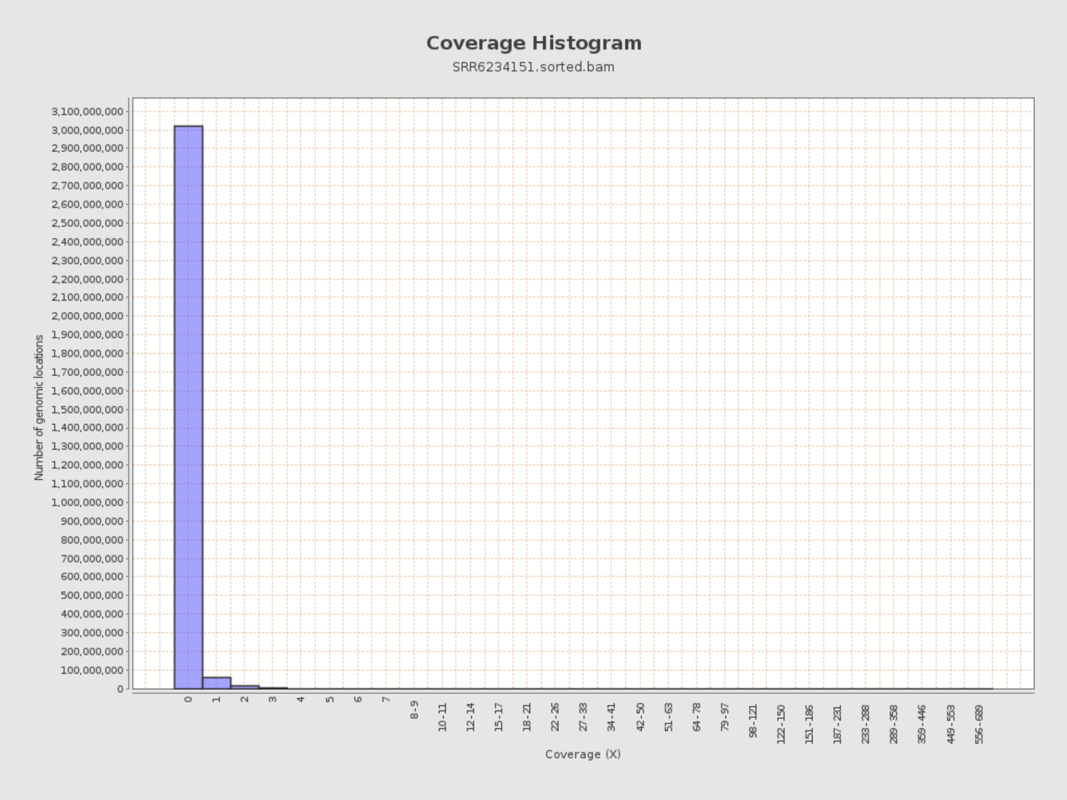
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8116667	0.0326	0.6017
chr2	243199373	8844406	0.0364	0.3259
chr3	198022430	8753862	0.0442	0.2737
chr4	191154276	6432812	0.0337	0.2456
chr5	180915260	5950058	0.0329	0.2369
chr6	171115067	5356808	0.0313	0.2632
chr7	159138663	4965092	0.0312	0.2963

chr8	146364022	4384578	0.03	0.3203
chr9	141213431	4853912	0.0344	0.2655
chr10	135534747	7518743	0.0555	0.3527
chr11	135006516	7069233	0.0524	0.3359
chr12	133851895	3449024	0.0258	0.2104
chr13	115169878	3773189	0.0328	0.2423
chr14	107349540	2777297	0.0259	0.2212
chr15	102531392	1765510	0.0172	0.1734
chr16	90354753	3031839	0.0336	0.2454
chr17	81195210	2854305	0.0352	0.2633
chr18	78077248	2099296	0.0269	0.3559
chr19	59128983	3743637	0.0633	0.501
chr20	63025520	2357001	0.0374	0.2541
chr21	48129895	1958726	0.0407	0.2675
chr22	51304566	1158590	0.0226	0.1931
chrMT	16571	38458	2.3208	2.265
chrX	155270560	4113899	0.0265	0.2196
chrY	59373566	253733	0.0043	0.1002

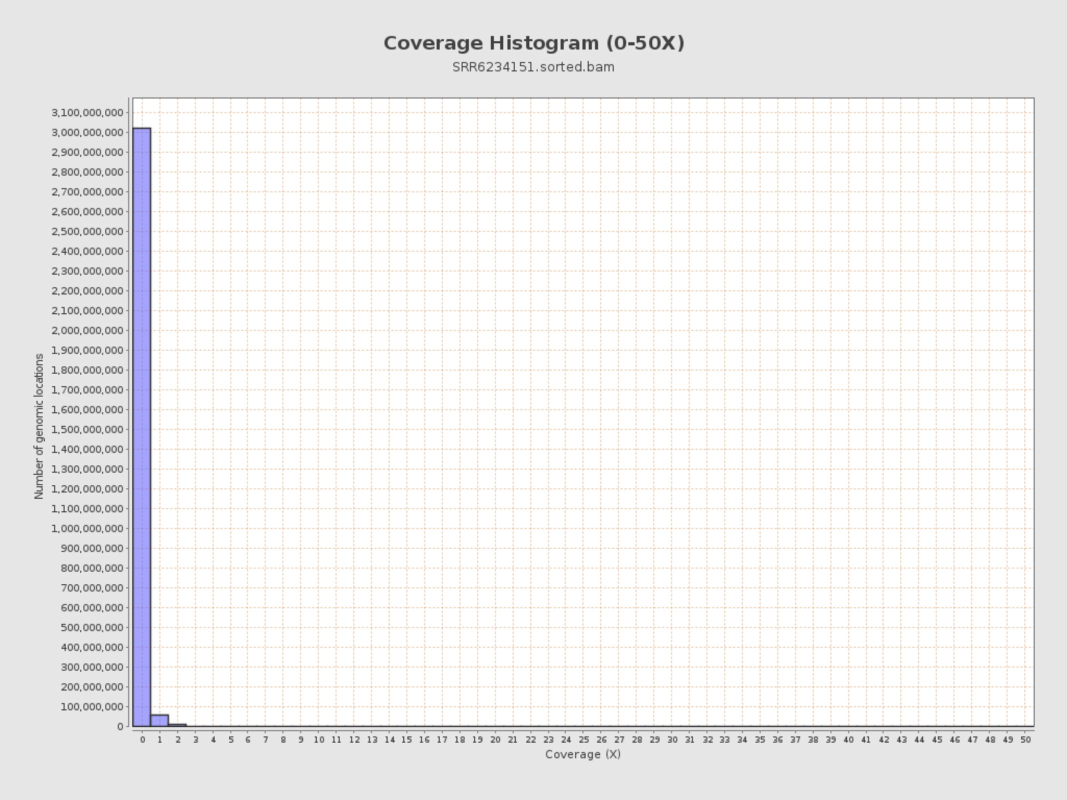
3. Results : Coverage across reference



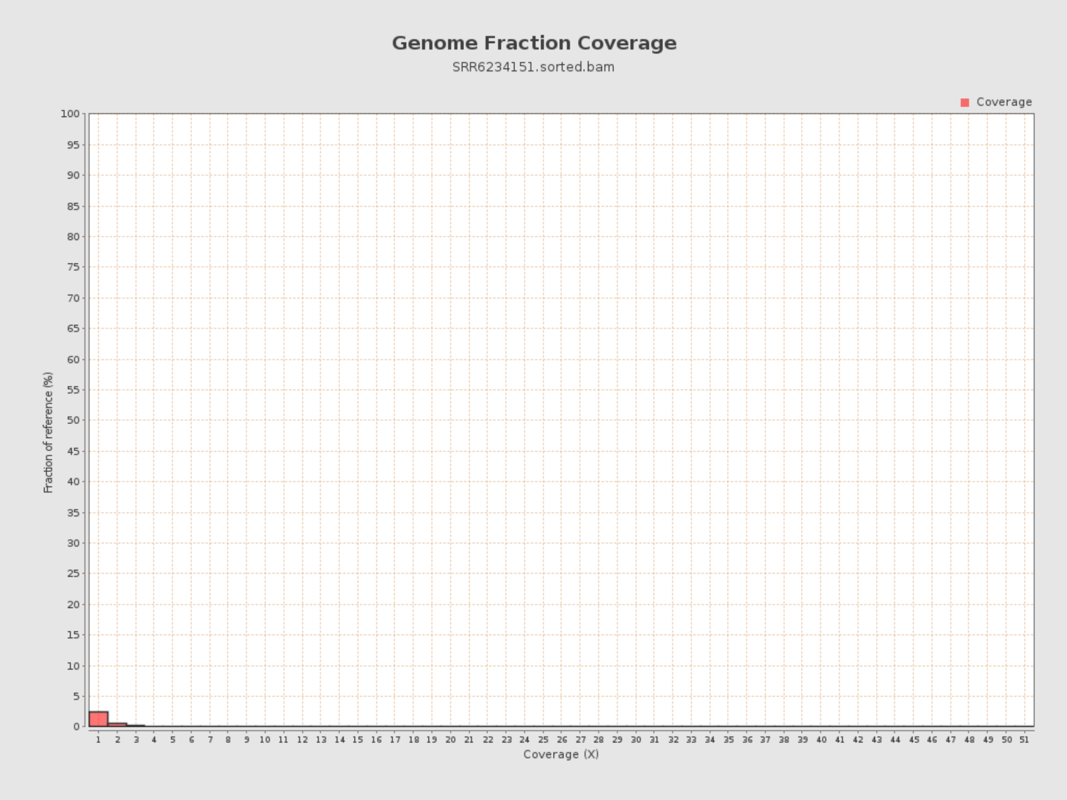
4. Results : Coverage Histogram



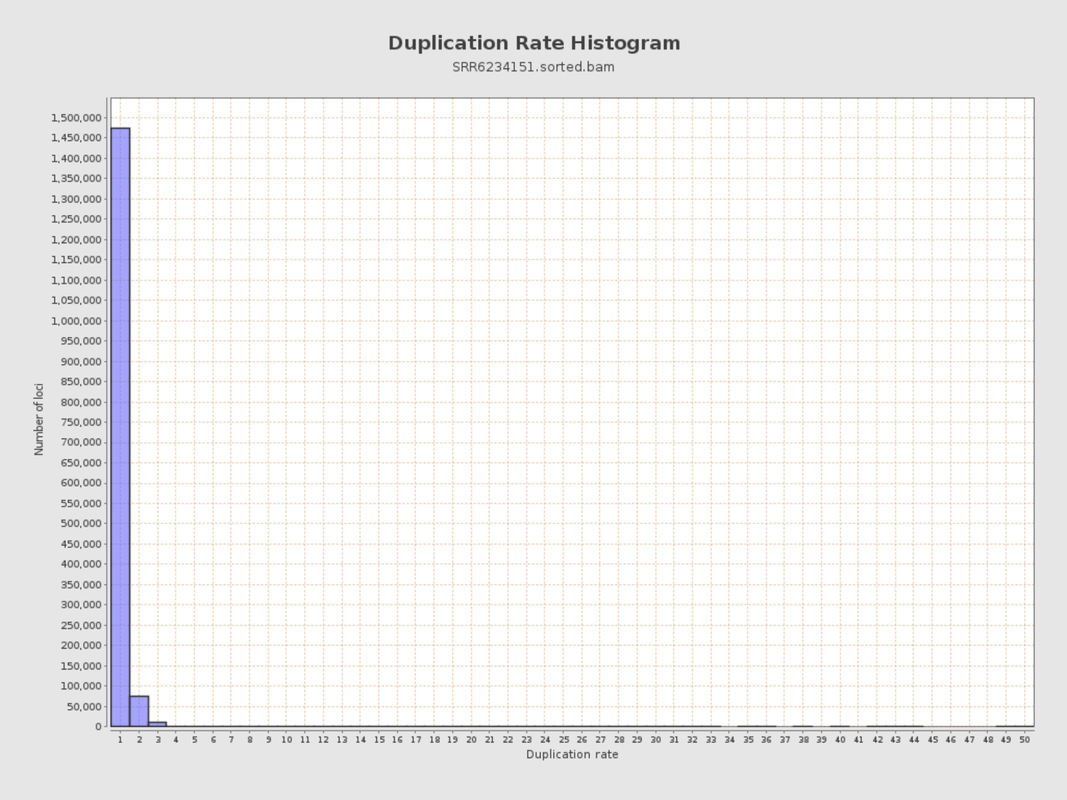
5. Results : Coverage Histogram (0-50X)



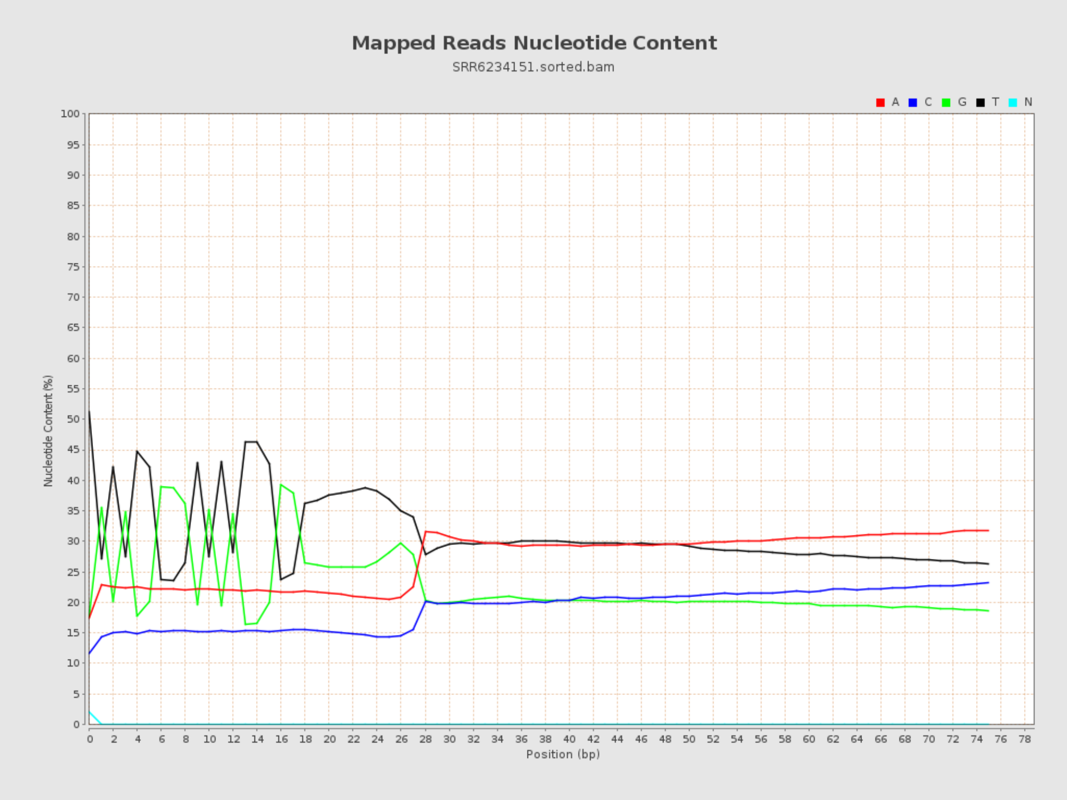
6. Results : Genome Fraction Coverage



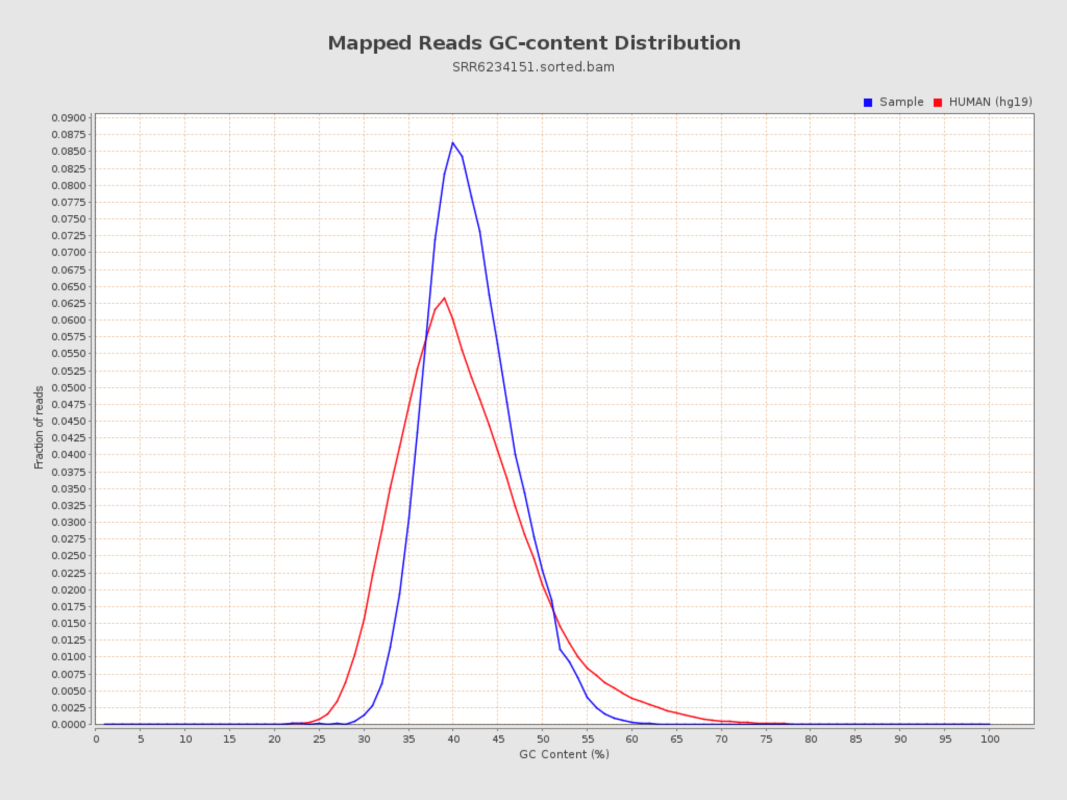
7. Results : Duplication Rate Histogram



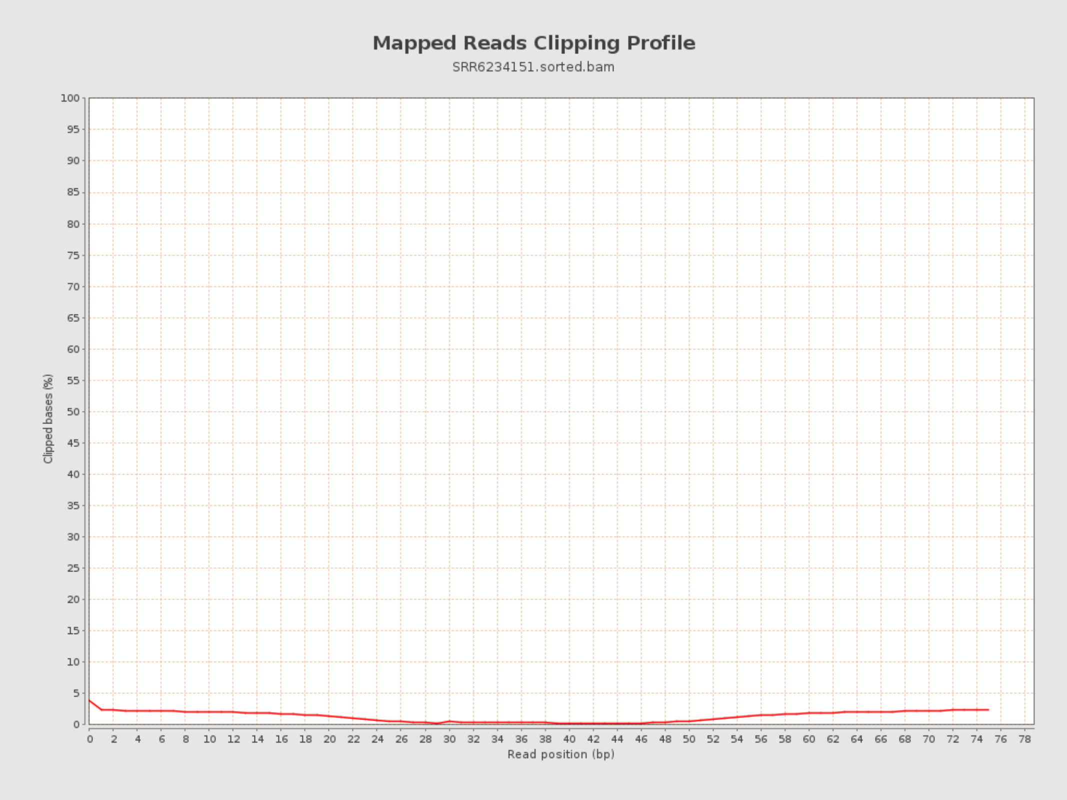
8. Results : Mapped Reads Nucleotide Content



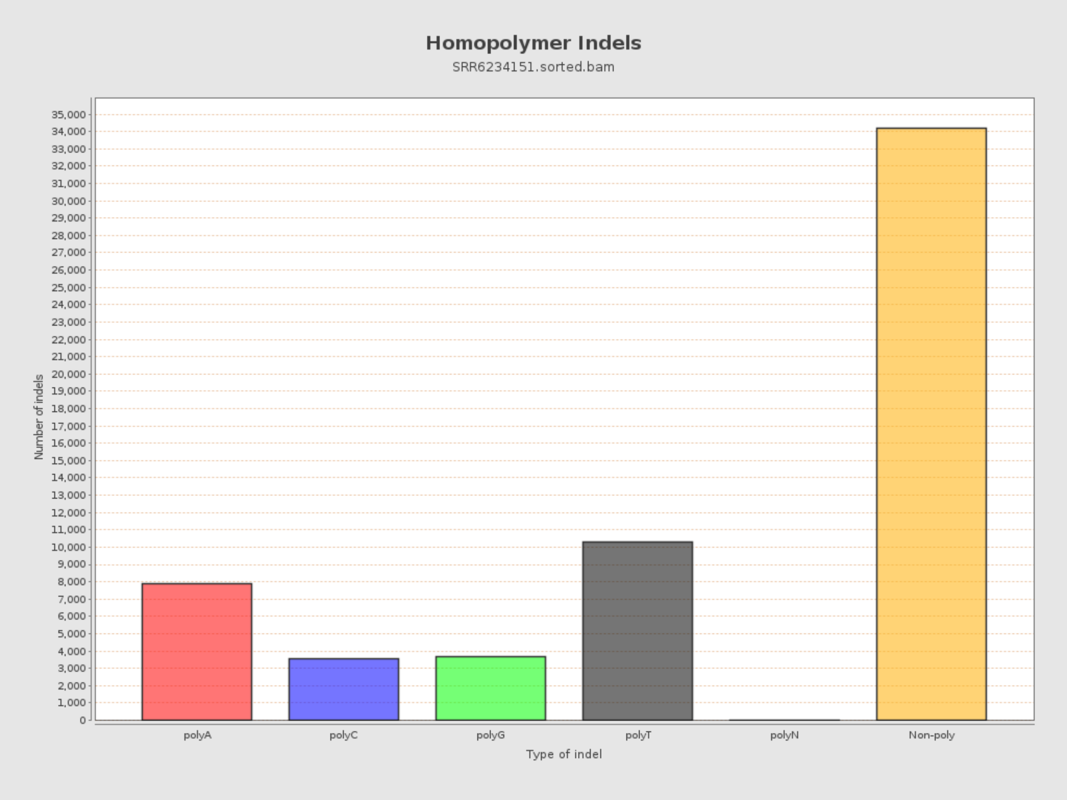
9. Results : Mapped Reads GC-content Distribution



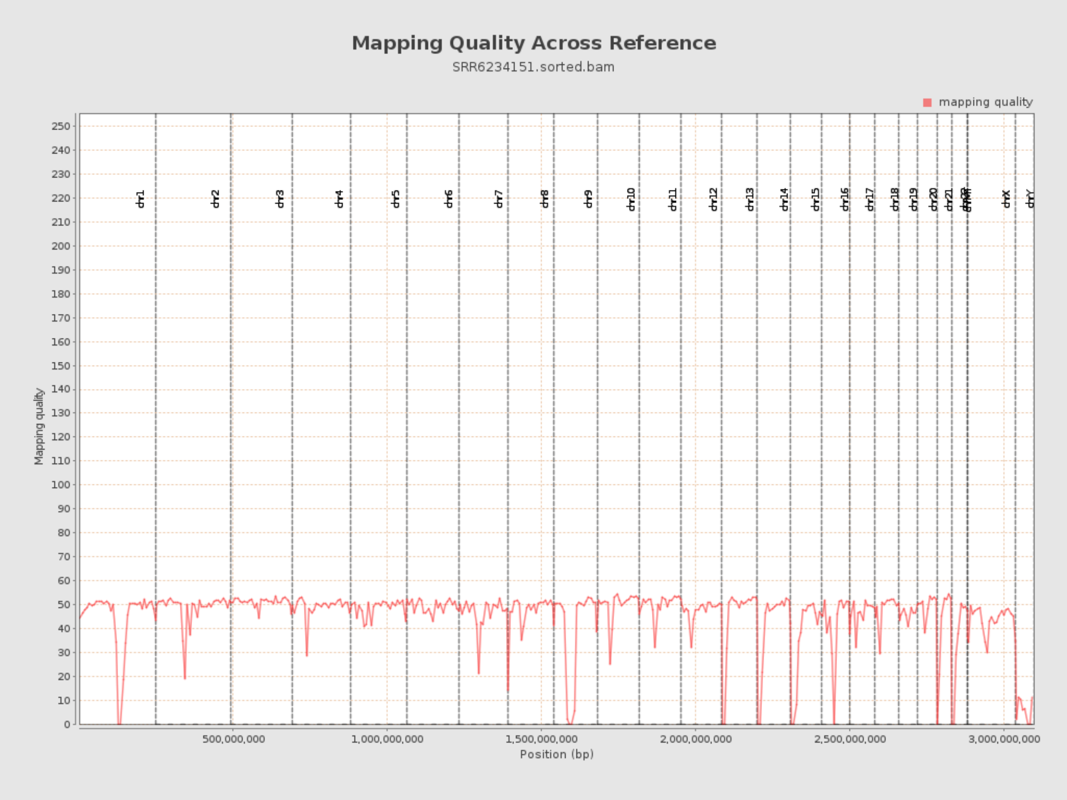
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram