Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 15:44:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234099.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_SRR6234099 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234099.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 15:44:15 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234099.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,139,935
Mapped reads	4,863,570 / 94.62%
Unmapped reads	276,365 / 5.38%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	34,186 / 0.67%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	647,454 / 12.6%
Duplication rate	11.15%
Clipped reads	2,481,901 / 48.29%

2.2. ACGT Content

Number/percentage of A's	82,297,939 / 26.08%
Number/percentage of C's	57,215,488 / 18.13%
Number/percentage of T's	102,222,173 / 32.39%
Number/percentage of G's	73,789,448 / 23.38%
Number/percentage of N's	31,167 / 0.01%
GC Percentage	41.52%

2.3. Coverage

Mean	0.102

Standard Deviation	1.2107

2.4. Mapping Quality

Mean Mapping Quality	44.96

2.5. Mismatches and indels

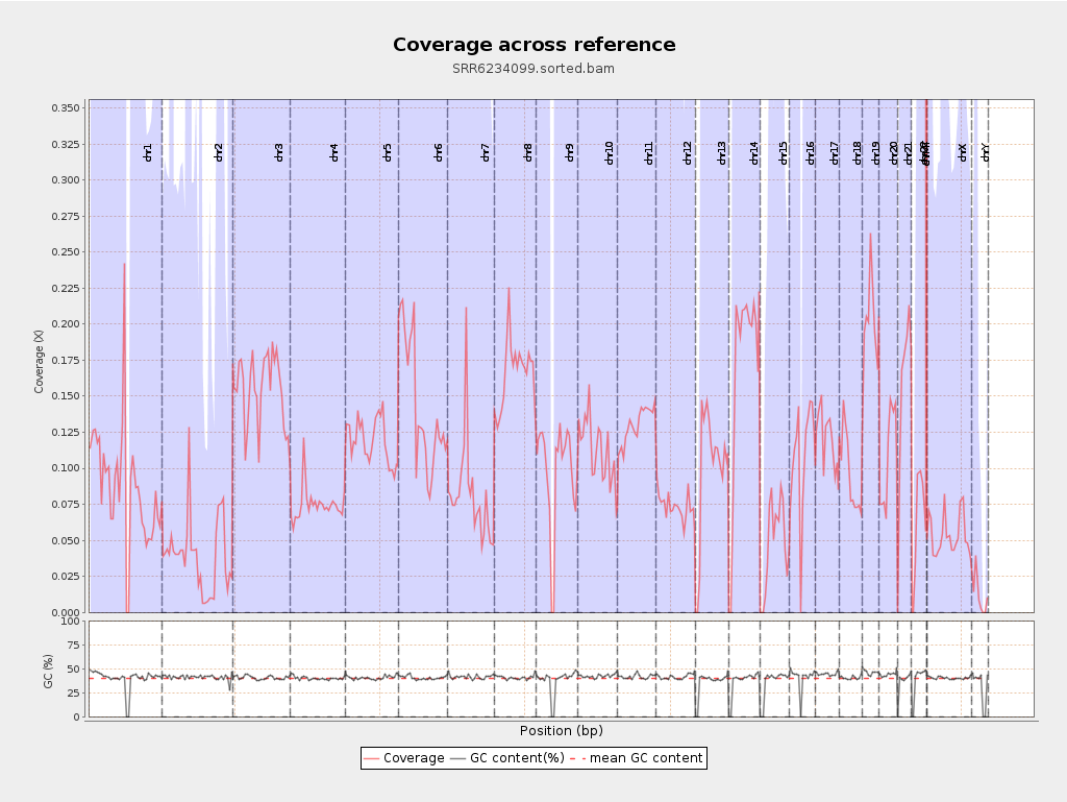
General error rate	0.56%
Mismatches	1,727,090
Insertions	21,377
Mapped reads with at least one insertion	0.43%
Deletions	72,429
Mapped reads with at least one deletion	1.47%
Homopolymer indels	44.54%

2.6. Chromosome stats

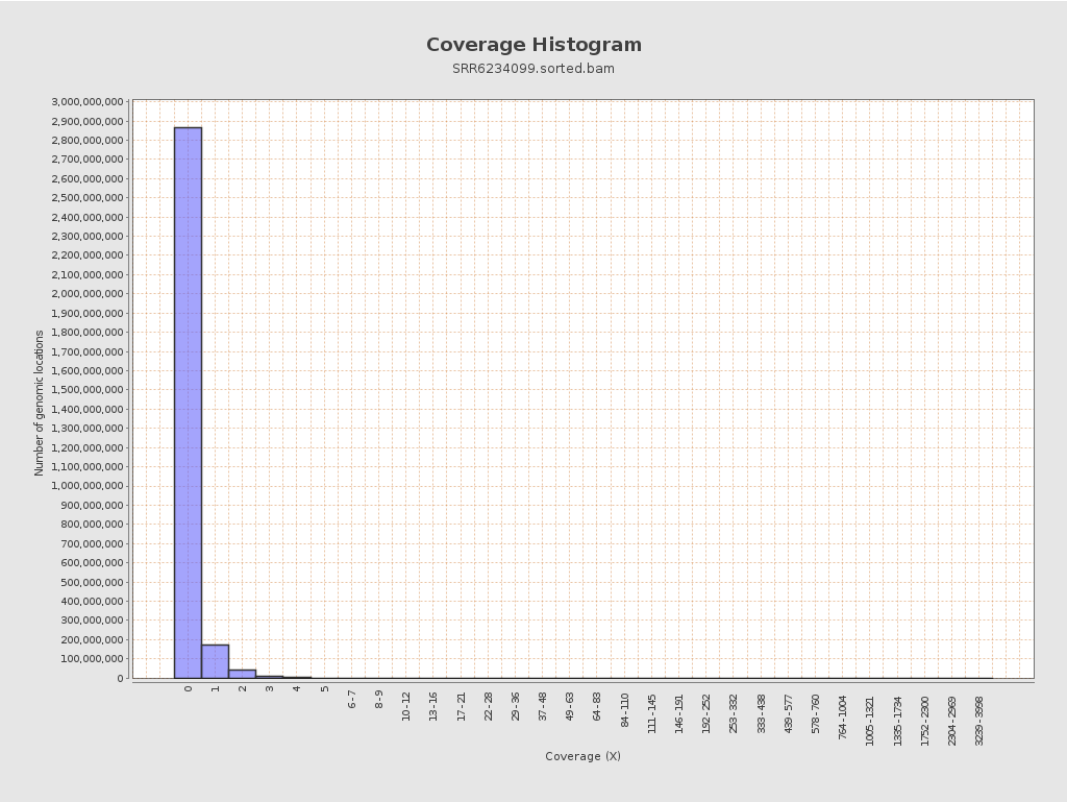
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	21479529	0.0862	2.859
chr2	243199373	9470943	0.0389	1.8494
chr3	198022430	30691870	0.155	0.5145
chr4	191154276	14207027	0.0743	0.4319
chr5	180915260	21523872	0.119	0.4755
chr6	171115067	24444266	0.1429	0.8209
chr7	159138663	12893467	0.081	1.3023

chr8	146364022	24368328	0.1665	1.3728
chr9	141213431	13636841	0.0966	0.7043
chr10	135534747	15344465	0.1132	0.7595
chr11	135006516	17445122	0.1292	0.9736
chr12	133851895	9851332	0.0736	0.3864
chr13	115169878	11440156	0.0993	0.4686
chr14	107349540	18011605	0.1678	0.5823
chr15	102531392	4945846	0.0482	0.3377
chr16	90354753	9924334	0.1098	0.518
chr17	81195210	9788785	0.1206	0.5898
chr18	78077248	7566687	0.0969	1.7297
chr19	59128983	12038562	0.2036	1.5423
chr20	63025520	6739766	0.1069	0.4773
chr21	48129895	7480408	0.1554	0.5474
chr22	51304566	3129954	0.061	0.3109
chrMT	16571	229493	13.8491	8.5901
chrX	155270560	8328934	0.0536	0.4703
chrY	59373566	700146	0.0118	0.2696

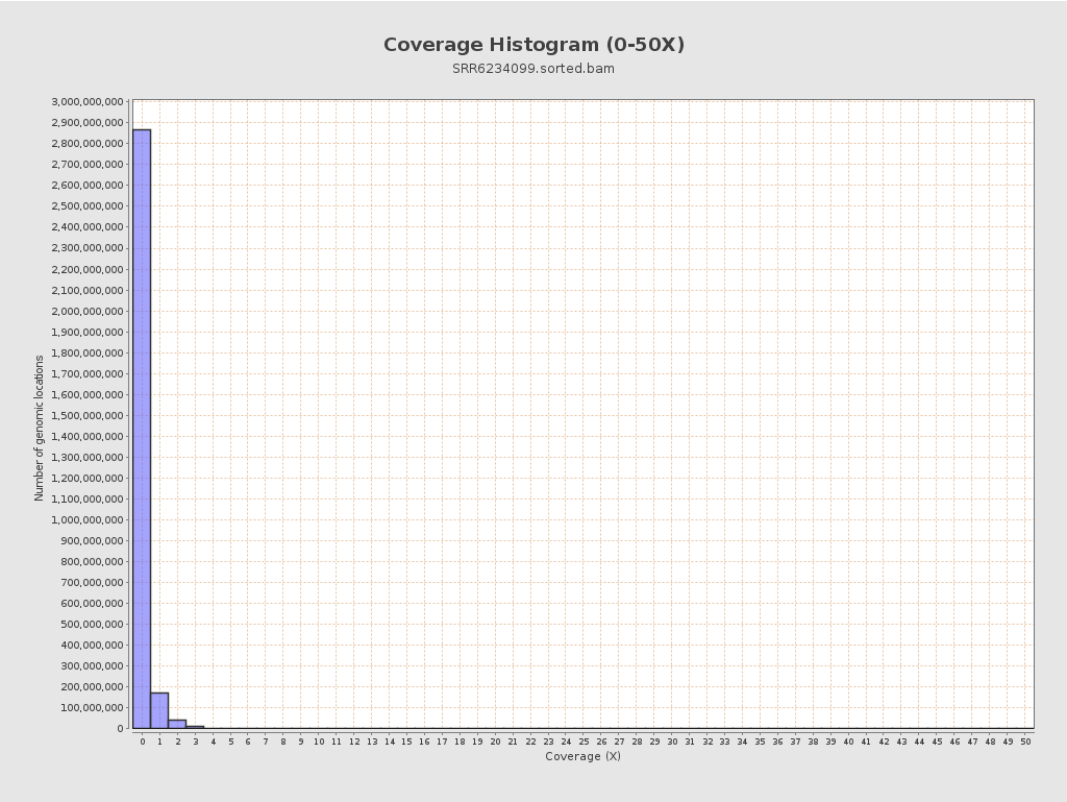
3. Results : Coverage across reference



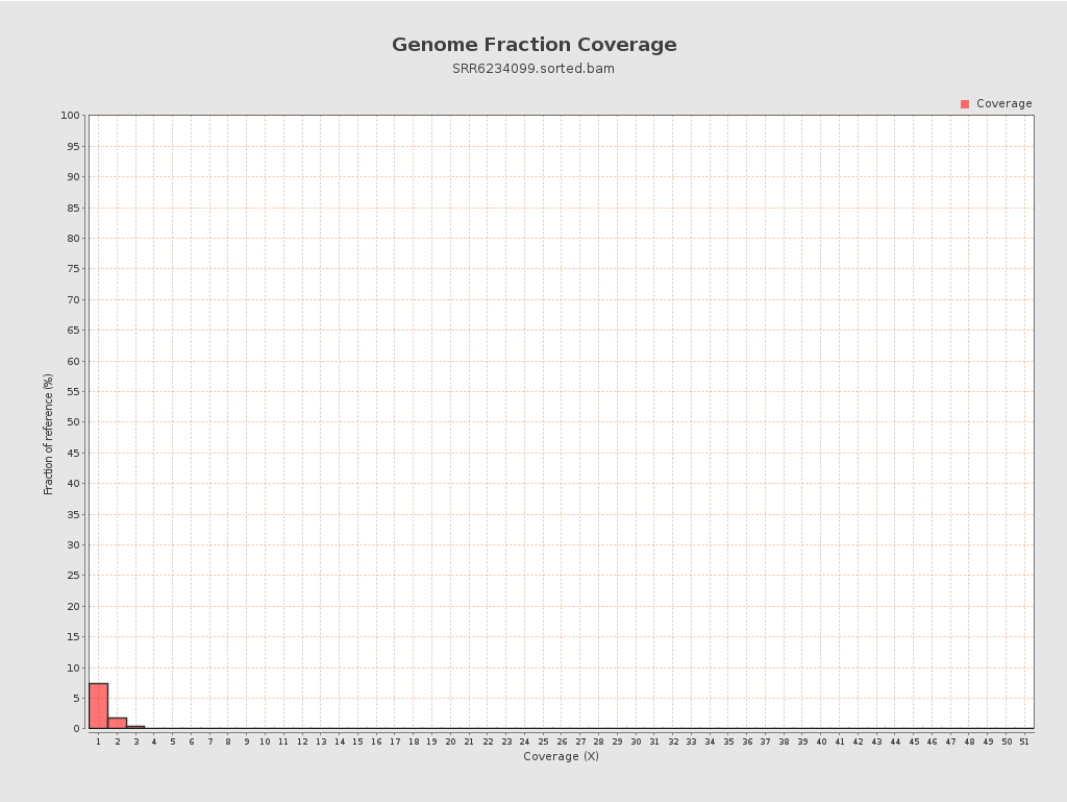
4. Results : Coverage Histogram



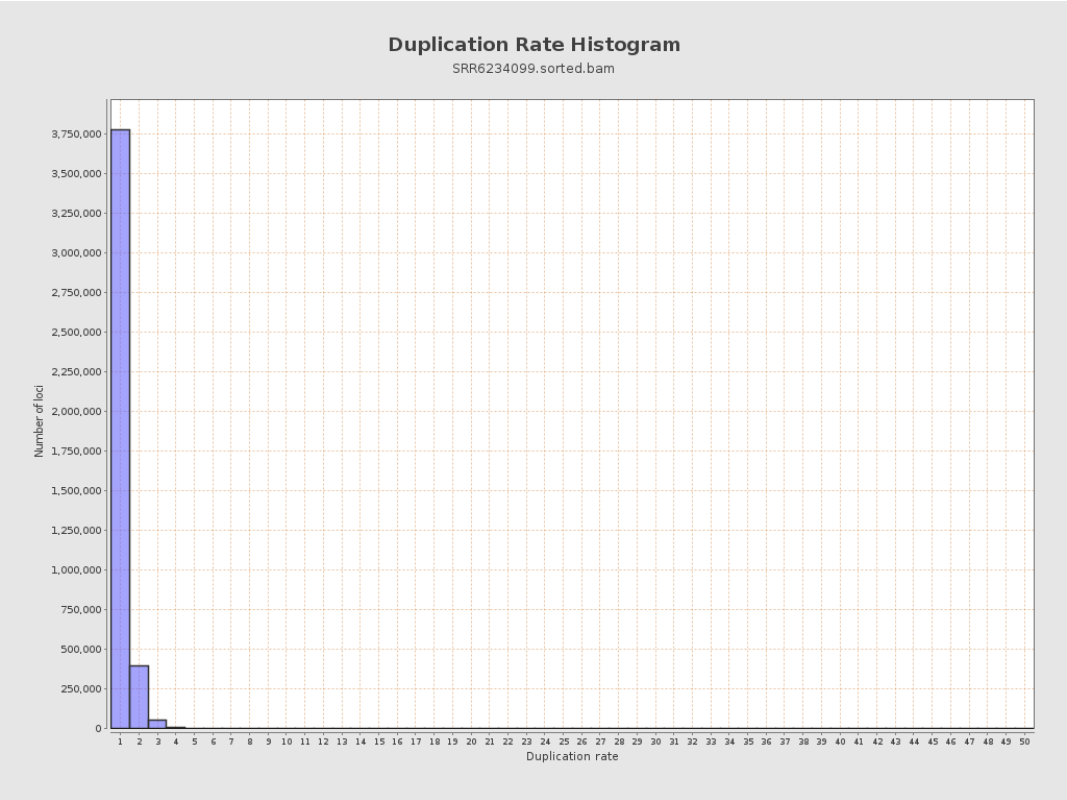
5. Results : Coverage Histogram (0-50X)



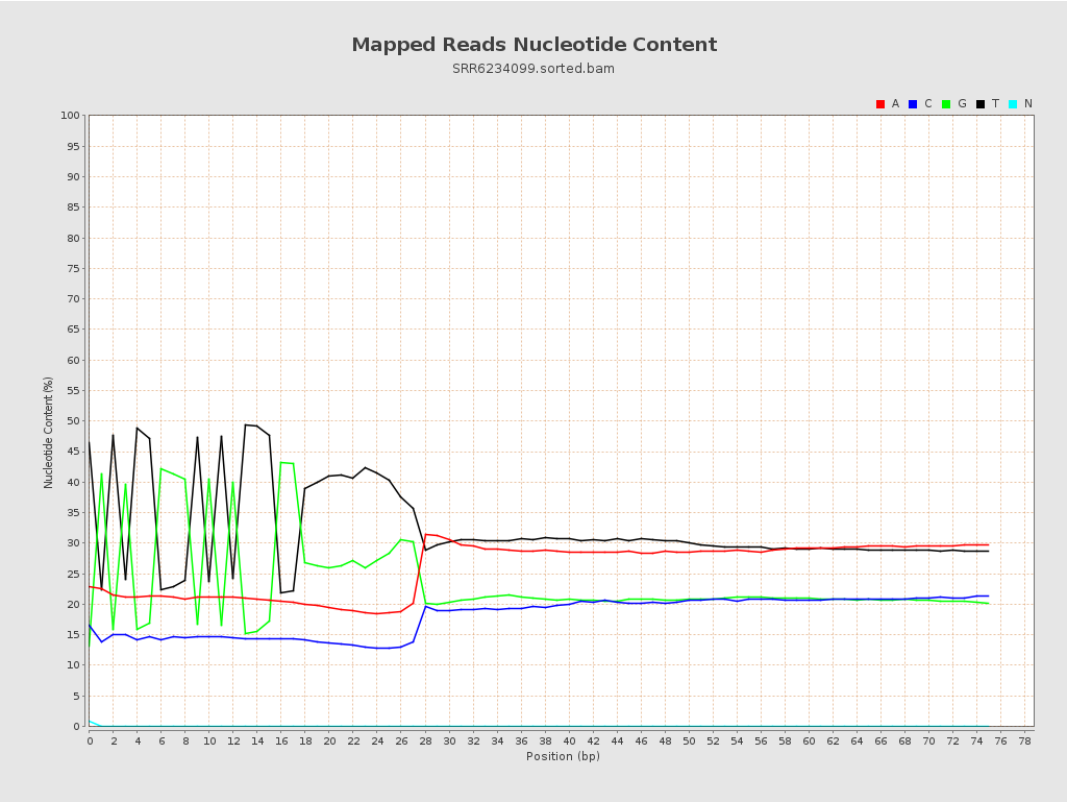
6. Results : Genome Fraction Coverage



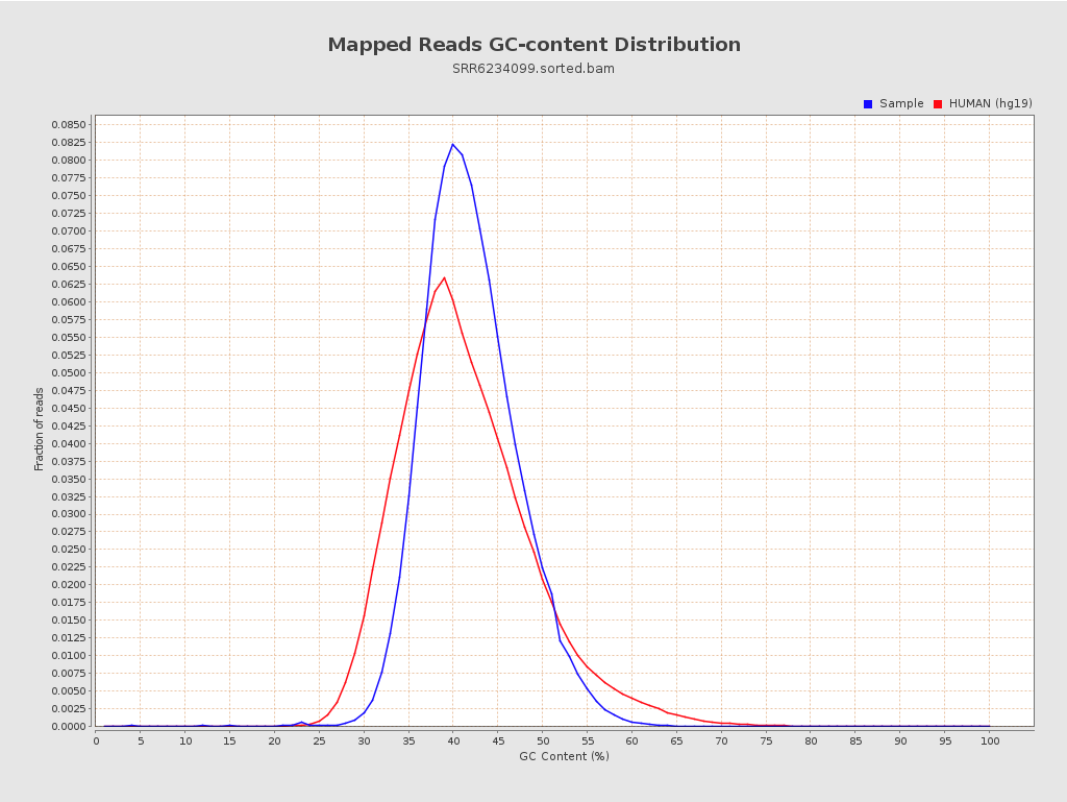
7. Results : Duplication Rate Histogram



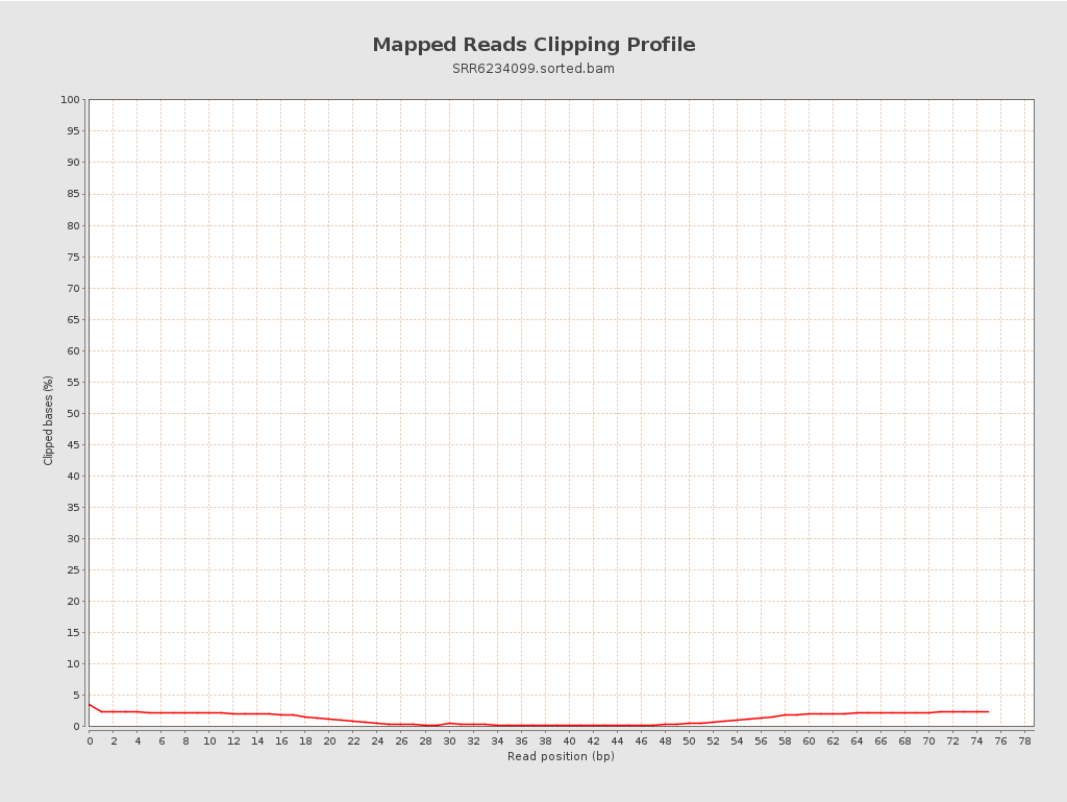
8. Results : Mapped Reads Nucleotide Content



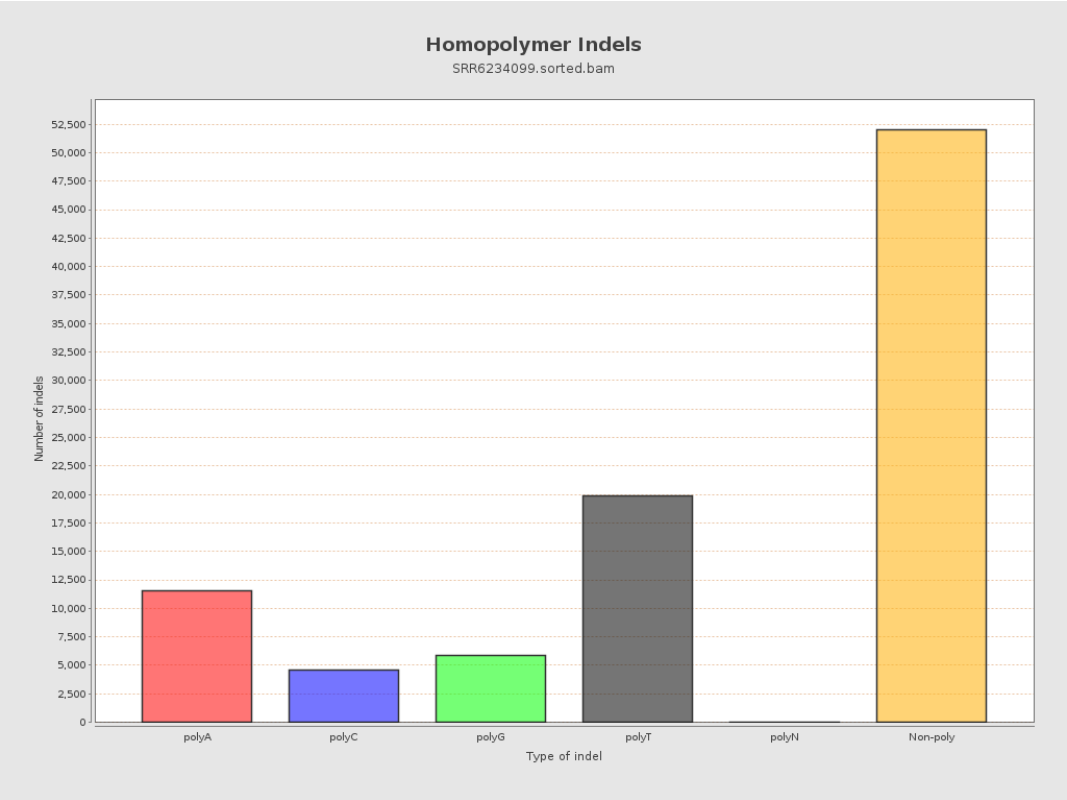
9. Results : Mapped Reads GC-content Distribution



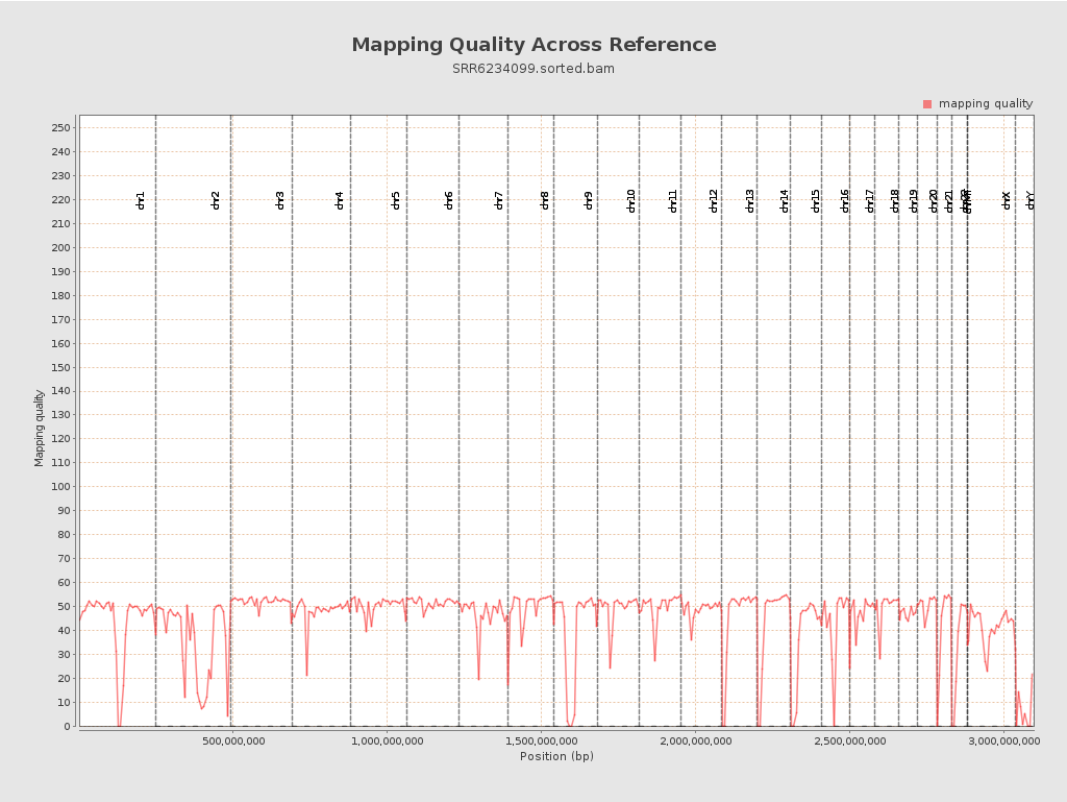
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram