Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 17:06:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234117.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_SRR6234117 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234117.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 17:06:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234117.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	802,854
Mapped reads	347,542 / 43.29%
Unmapped reads	455,312 / 56.71%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,388 / 0.17%
Read min/max/mean length	30 / 76 / 76.06
Duplicated reads (estimated)	9,595 / 1.2%
Duplication rate	2.23%
Clipped reads	231,637 / 28.85%

2.2. ACGT Content

Number/percentage of A's	5,801,567 / 27.53%
Number/percentage of C's	3,486,852 / 16.55%
Number/percentage of T's	6,777,085 / 32.16%
Number/percentage of G's	5,004,708 / 23.75%
Number/percentage of N's	1,648 / 0.01%
GC Percentage	40.3%

2.3. Coverage

Mean	0.0068

Standard Deviation	0.0985

2.4. Mapping Quality

Mean Mapping Quality	44.22

2.5. Mismatches and indels

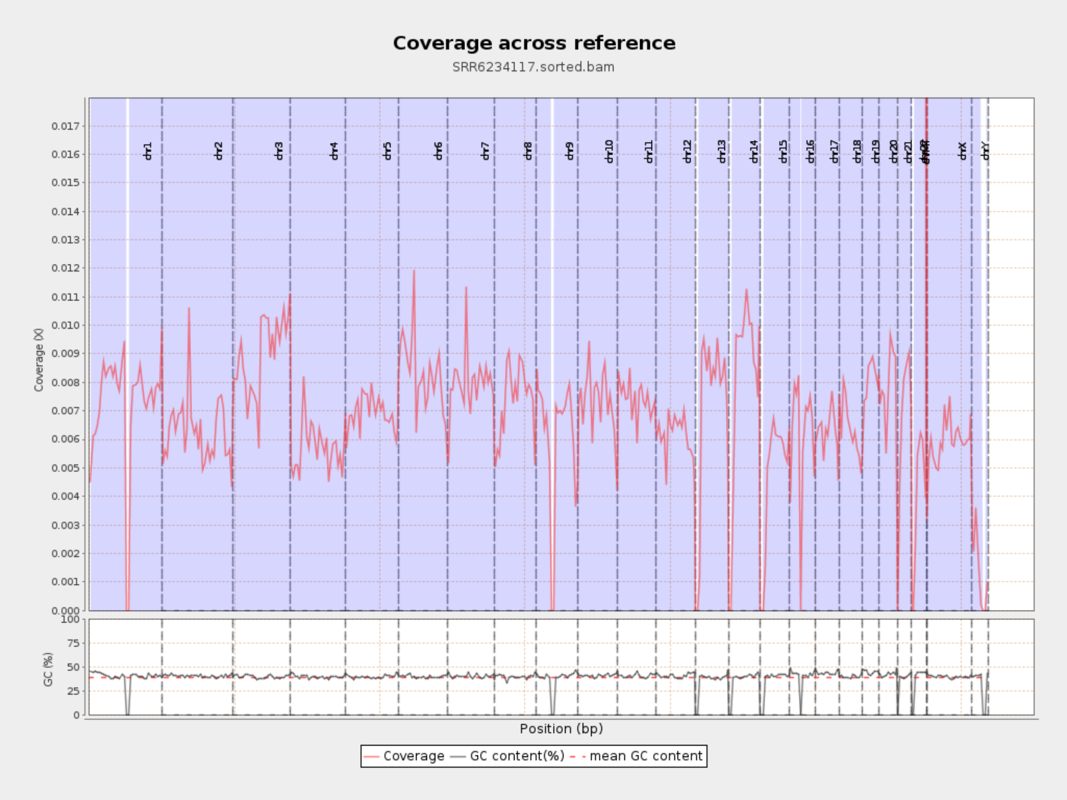
General error rate	1.18%
Mismatches	244,407
Insertions	1,861
Mapped reads with at least one insertion	0.53%
Deletions	8,425
Mapped reads with at least one deletion	2.39%
Homopolymer indels	46.41%

2.6. Chromosome stats

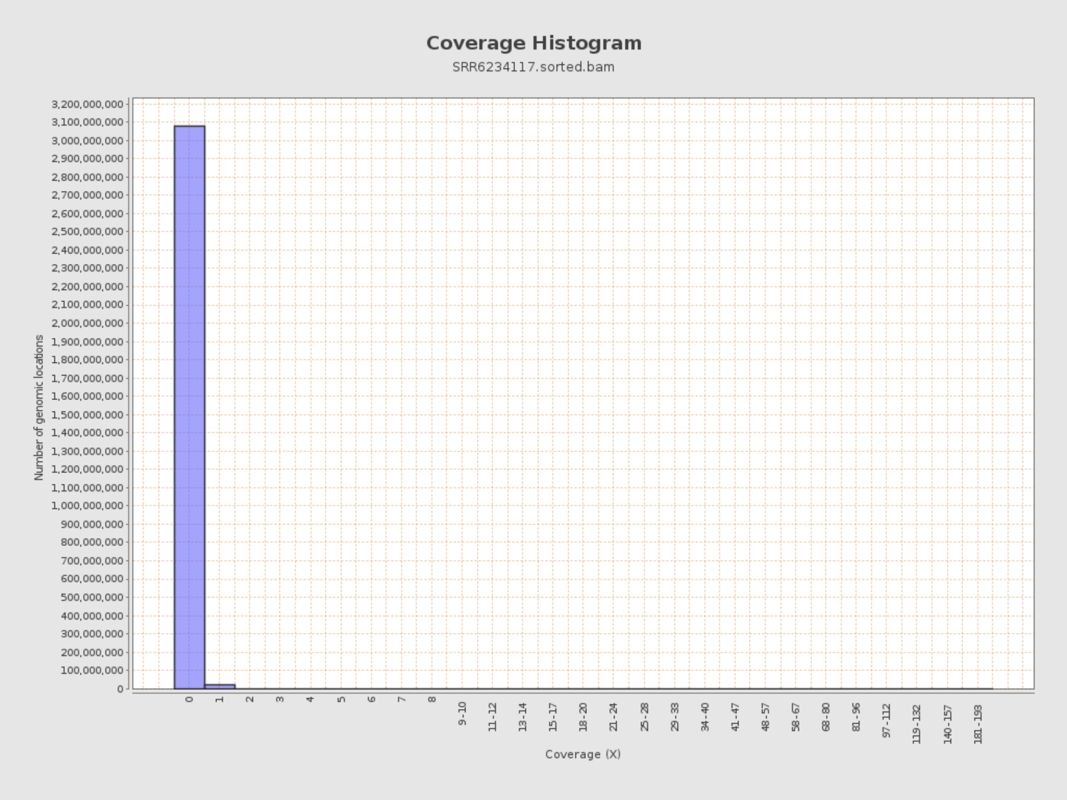
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1798001	0.0072	0.1153
chr2	243199373	1528125	0.0063	0.0973
chr3	198022430	1763471	0.0089	0.101
chr4	191154276	1084695	0.0057	0.0812
chr5	180915260	1251592	0.0069	0.0898
chr6	171115067	1422892	0.0083	0.1038
chr7	159138663	1279207	0.008	0.1155

chr8	146364022	1075951	0.0074	0.1443
chr9	141213431	851038	0.006	0.0905
chr10	135534747	1004448	0.0074	0.0965
chr11	135006516	994692	0.0074	0.1045
chr12	133851895	826194	0.0062	0.0842
chr13	115169878	816523	0.0071	0.0915
chr14	107349540	850042	0.0079	0.0959
chr15	102531392	482311	0.0047	0.0729
chr16	90354753	554825	0.0061	0.0837
chr17	81195210	509177	0.0063	0.0859
chr18	78077248	500579	0.0064	0.1203
chr19	59128983	477173	0.0081	0.101
chr20	63025520	489548	0.0078	0.0947
chr21	48129895	323504	0.0067	0.088
chr22	51304566	197717	0.0039	0.0651
chrMT	16571	15921	0.9608	1.4333
chrX	155270560	912033	0.0059	0.083
chrY	59373566	77211	0.0013	0.0399

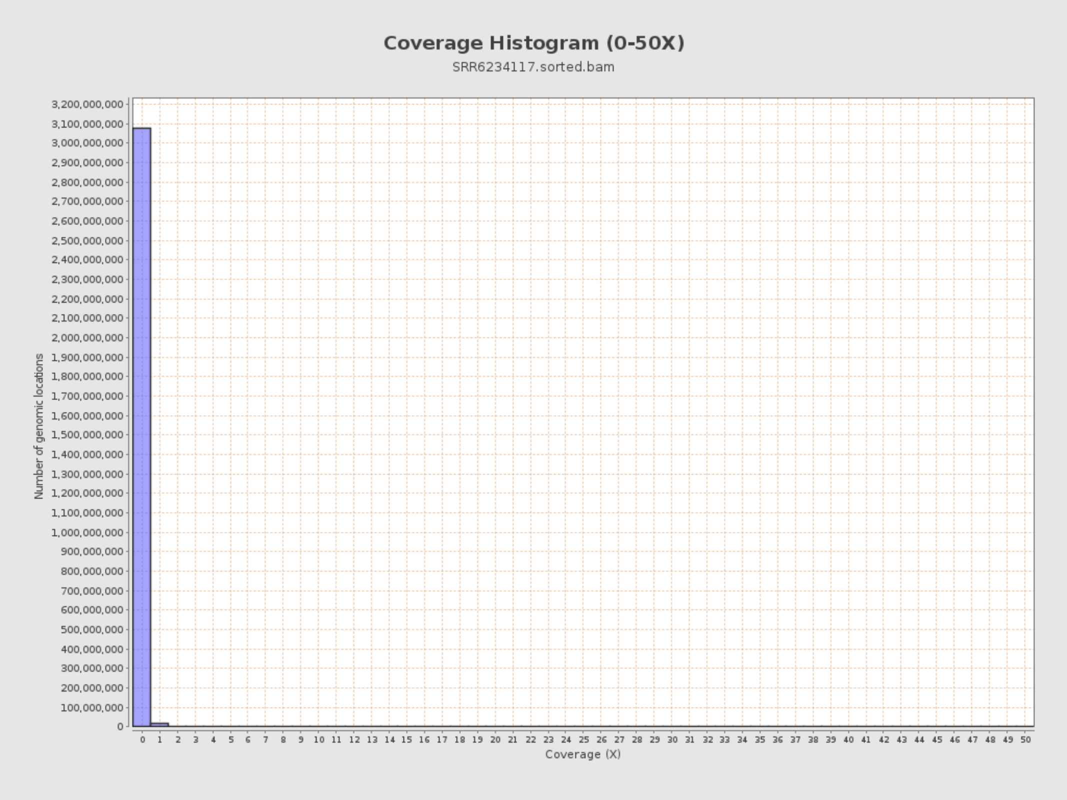
3. Results : Coverage across reference



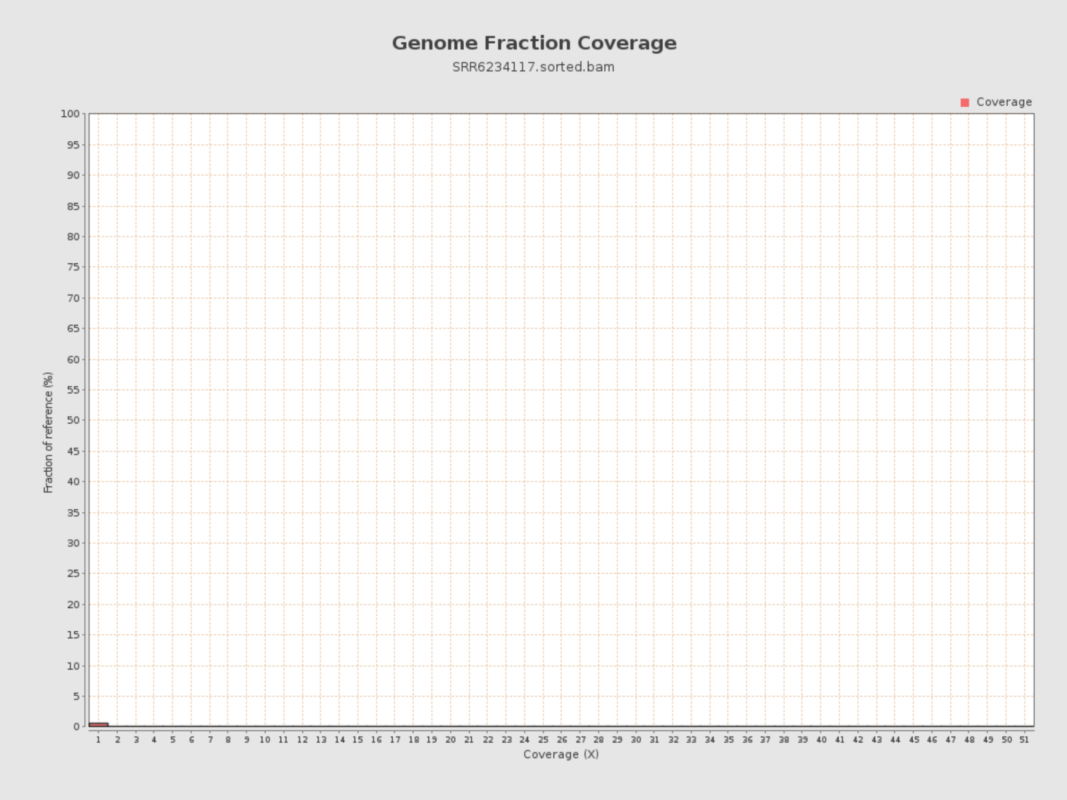
4. Results : Coverage Histogram



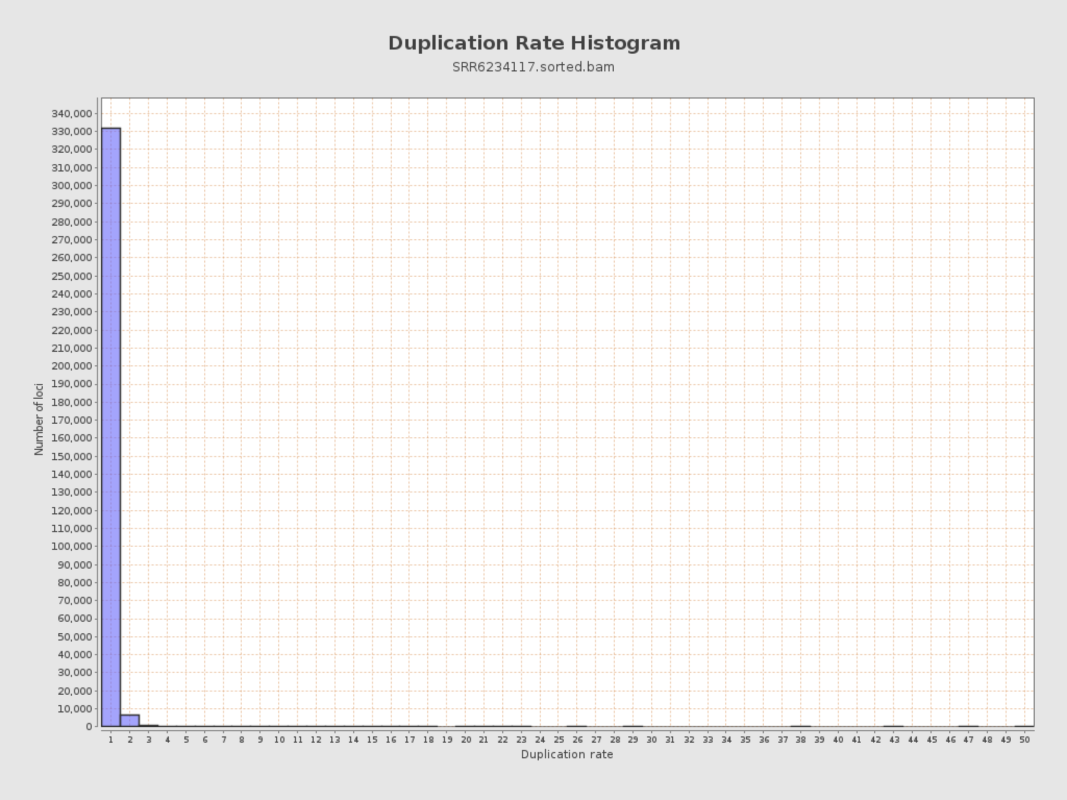
5. Results : Coverage Histogram (0-50X)



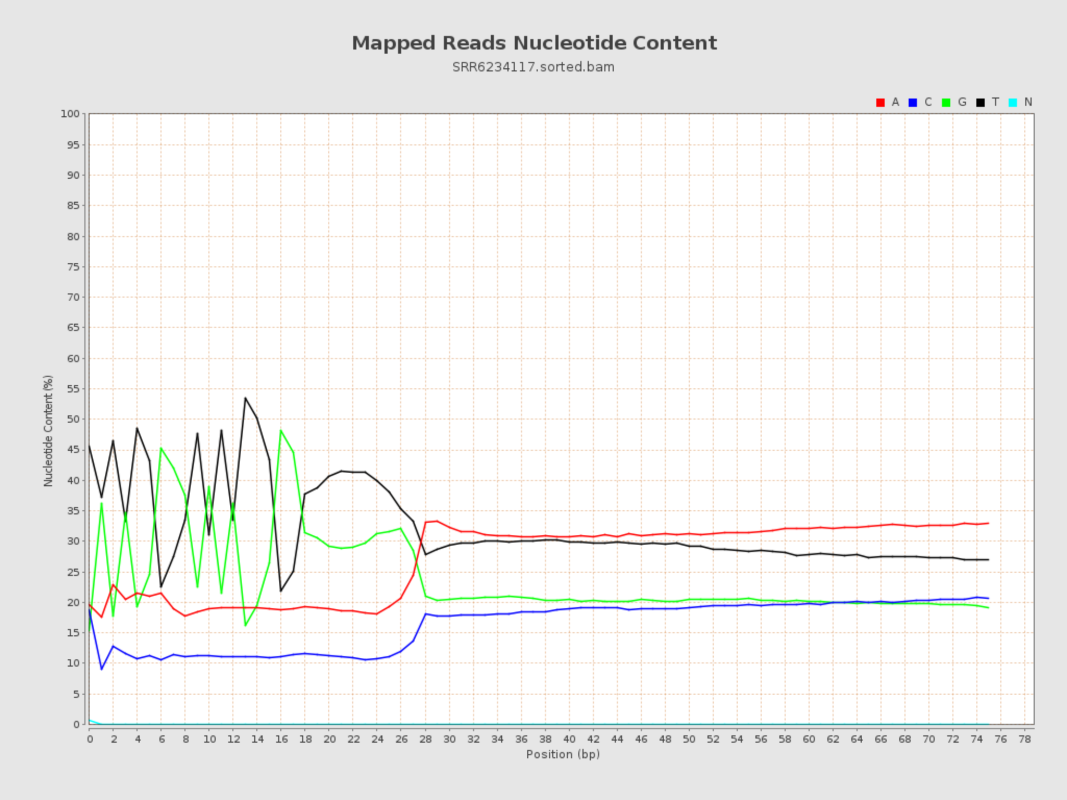
6. Results : Genome Fraction Coverage



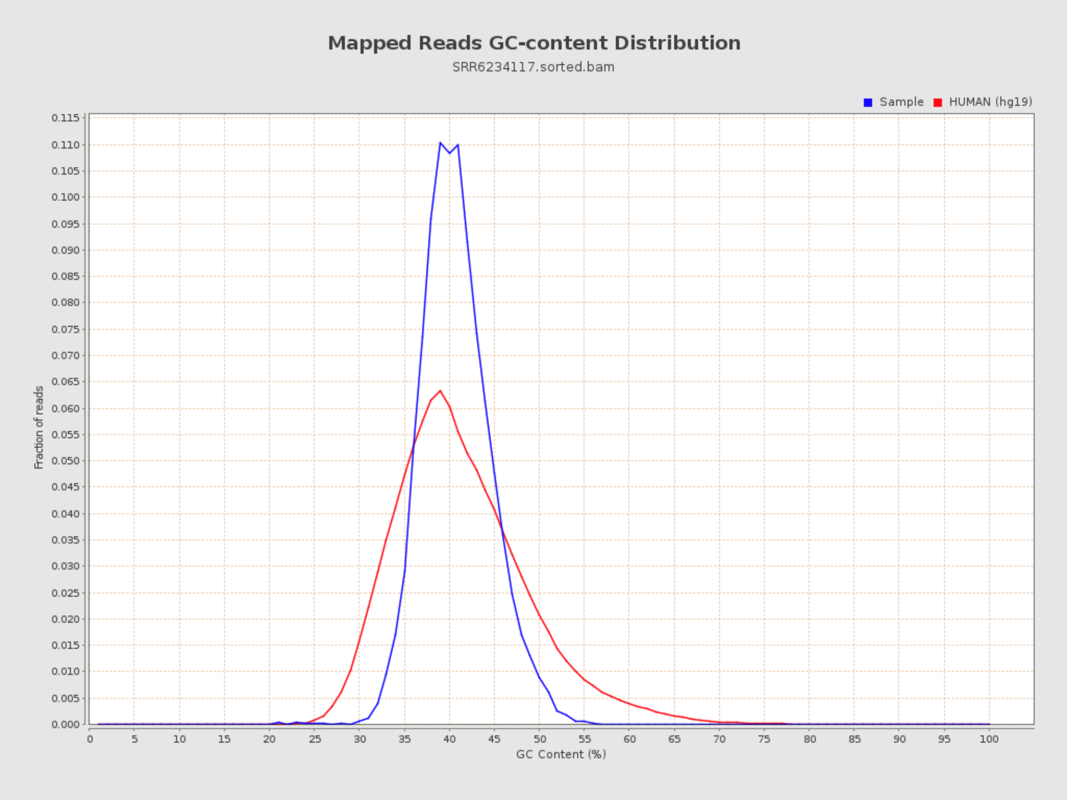
7. Results : Duplication Rate Histogram



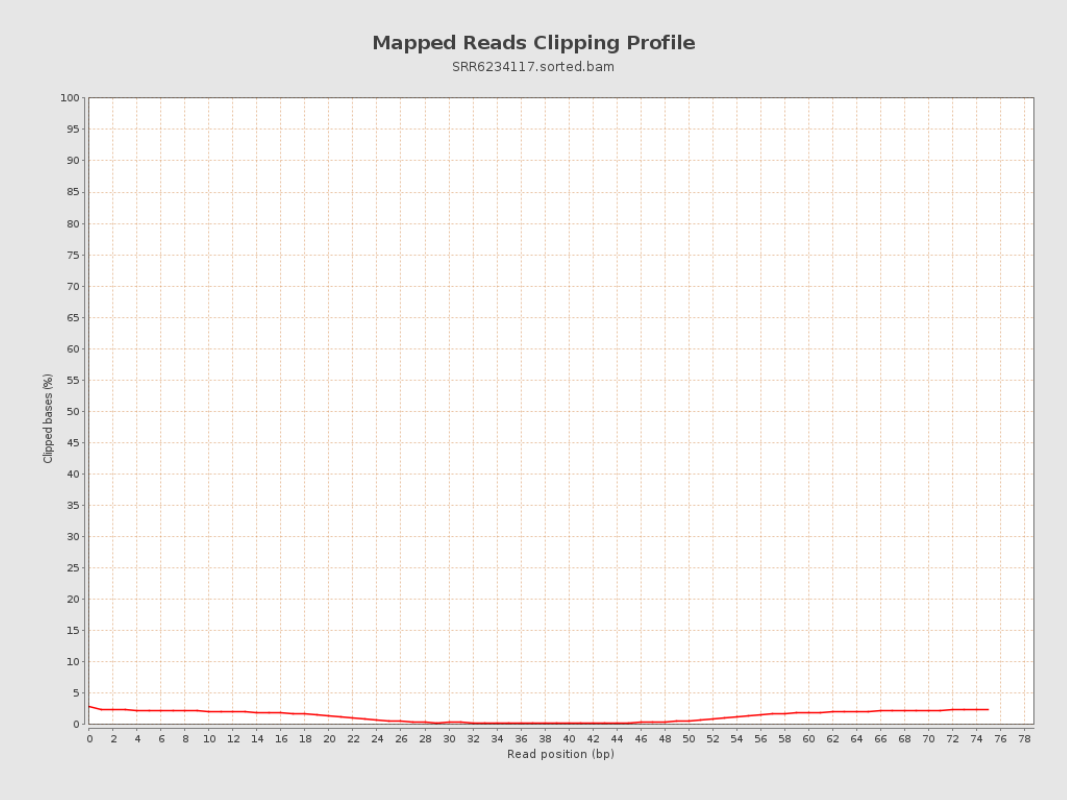
8. Results : Mapped Reads Nucleotide Content



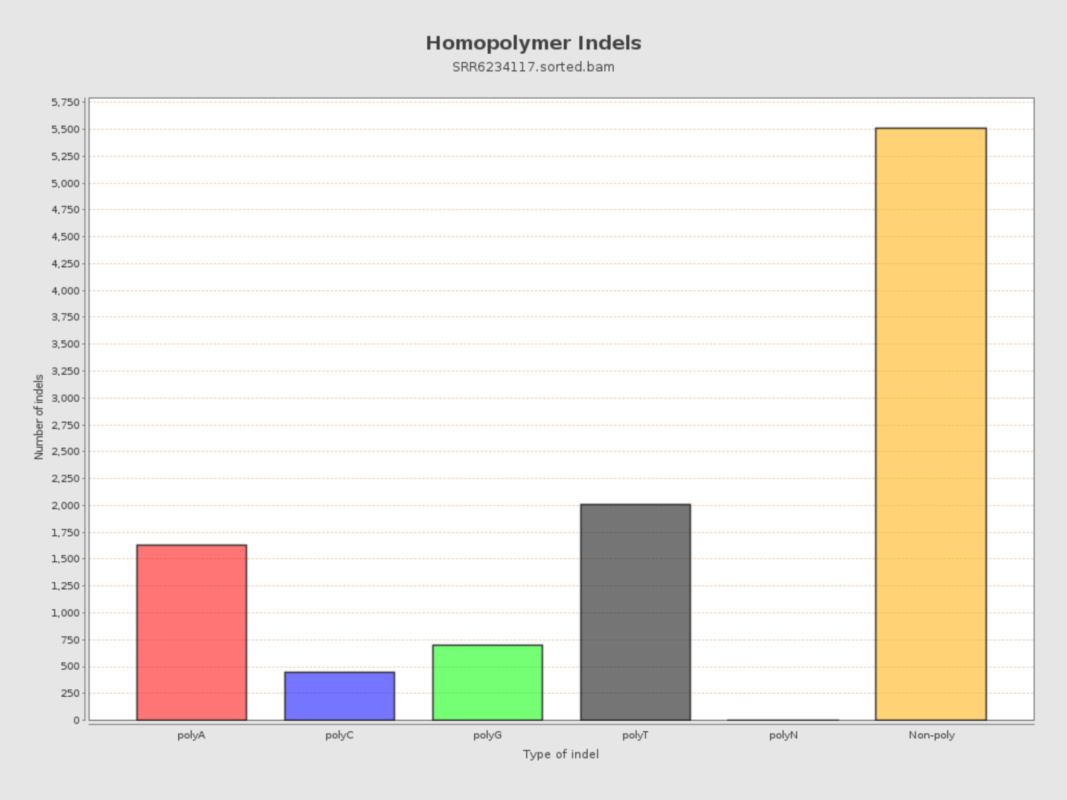
9. Results : Mapped Reads GC-content Distribution



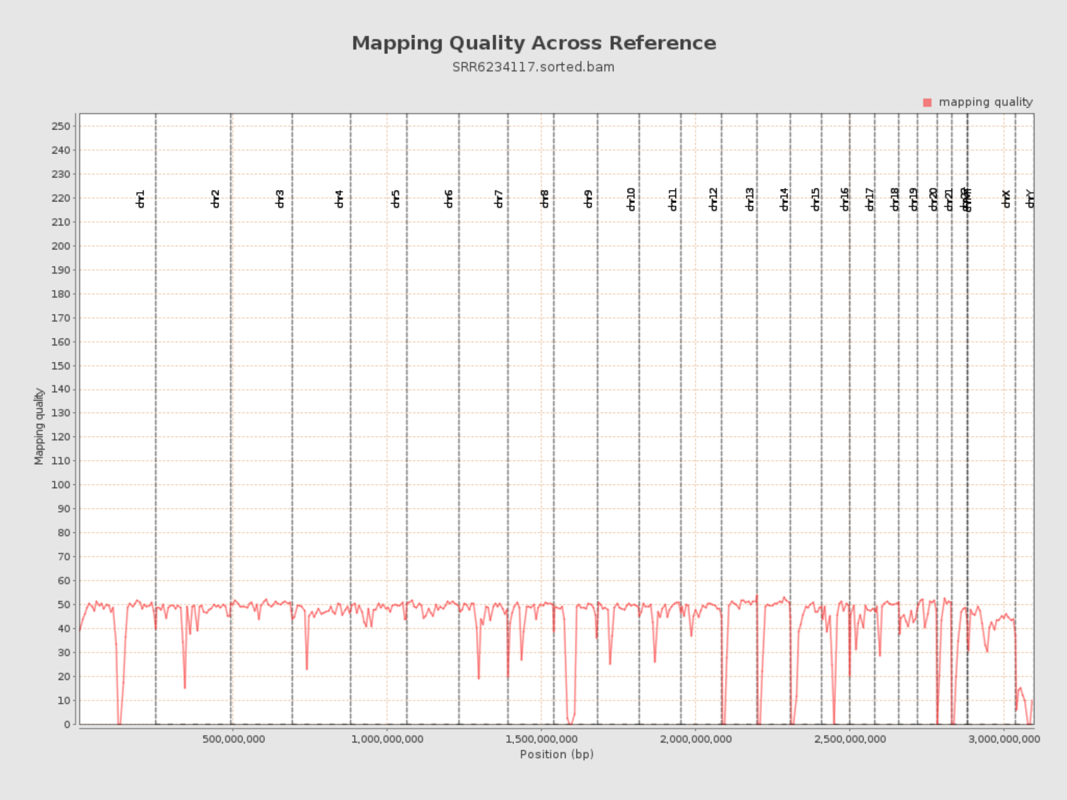
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram