Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 16:59:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234113.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_SRR6234113 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234113.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 16:59:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234113.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	997,926
Mapped reads	703,255 / 70.47%
Unmapped reads	294,671 / 29.53%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,861 / 0.49%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	21,201 / 2.12%
Duplication rate	2.47%
Clipped reads	322,609 / 32.33%

2.2. ACGT Content

Number/percentage of A's	13,201,751 / 28.51%
Number/percentage of C's	7,939,647 / 17.15%
Number/percentage of T's	15,167,251 / 32.76%
Number/percentage of G's	9,983,590 / 21.56%
Number/percentage of N's	8,044 / 0.02%
GC Percentage	38.71%

2.3. Coverage

Mean	0.015

Standard Deviation	0.1668

2.4. Mapping Quality

Mean Mapping Quality	46.14

2.5. Mismatches and indels

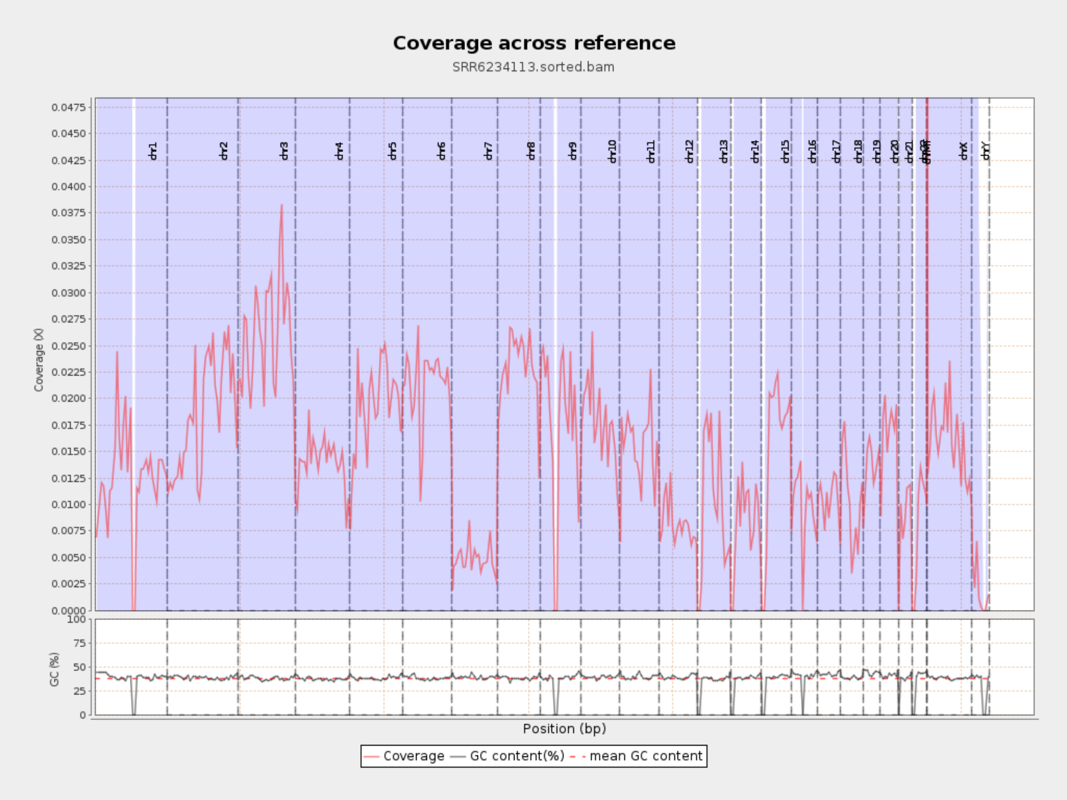
General error rate	0.86%
Mismatches	392,484
Insertions	3,776
Mapped reads with at least one insertion	0.53%
Deletions	13,230
Mapped reads with at least one deletion	1.86%
Homopolymer indels	45.7%

2.6. Chromosome stats

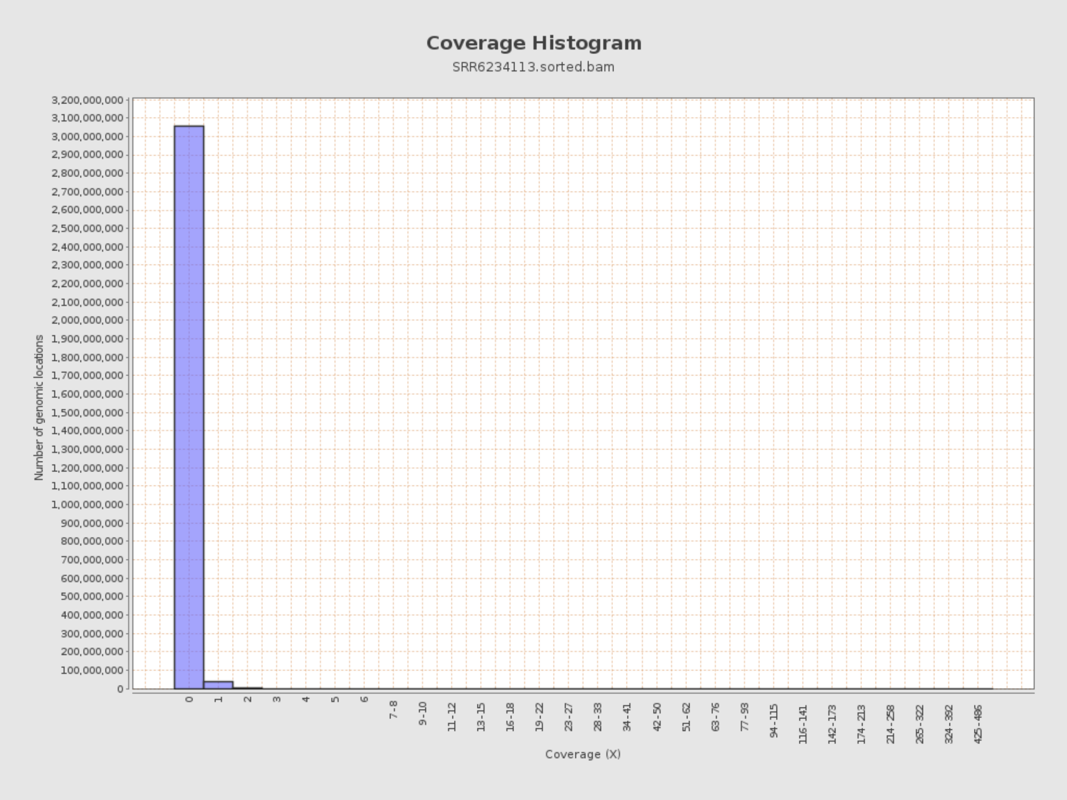
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3115948	0.0125	0.2069
chr2	243199373	4489403	0.0185	0.1831
chr3	198022430	5179771	0.0262	0.1749
chr4	191154276	2667548	0.014	0.131
chr5	180915260	3532870	0.0195	0.1505
chr6	171115067	3655491	0.0214	0.1693
chr7	159138663	762826	0.0048	0.0899

chr8	146364022	3363646	0.023	0.3504
chr9	141213431	2483783	0.0176	0.1581
chr10	135534747	2396118	0.0177	0.1634
chr11	135006516	2104746	0.0156	0.1477
chr12	133851895	1103202	0.0082	0.1
chr13	115169878	1137586	0.0099	0.1073
chr14	107349540	881131	0.0082	0.1036
chr15	102531392	1618540	0.0158	0.1363
chr16	90354753	866175	0.0096	0.1112
chr17	81195210	856858	0.0106	0.1146
chr18	78077248	789821	0.0101	0.2406
chr19	59128983	811537	0.0137	0.1591
chr20	63025520	1051428	0.0167	0.1421
chr21	48129895	414355	0.0086	0.1037
chr22	51304566	415655	0.0081	0.0959
chrMT	16571	6025	0.3636	0.6389
chrX	155270560	2503935	0.0161	0.1423
chrY	59373566	115198	0.0019	0.0598

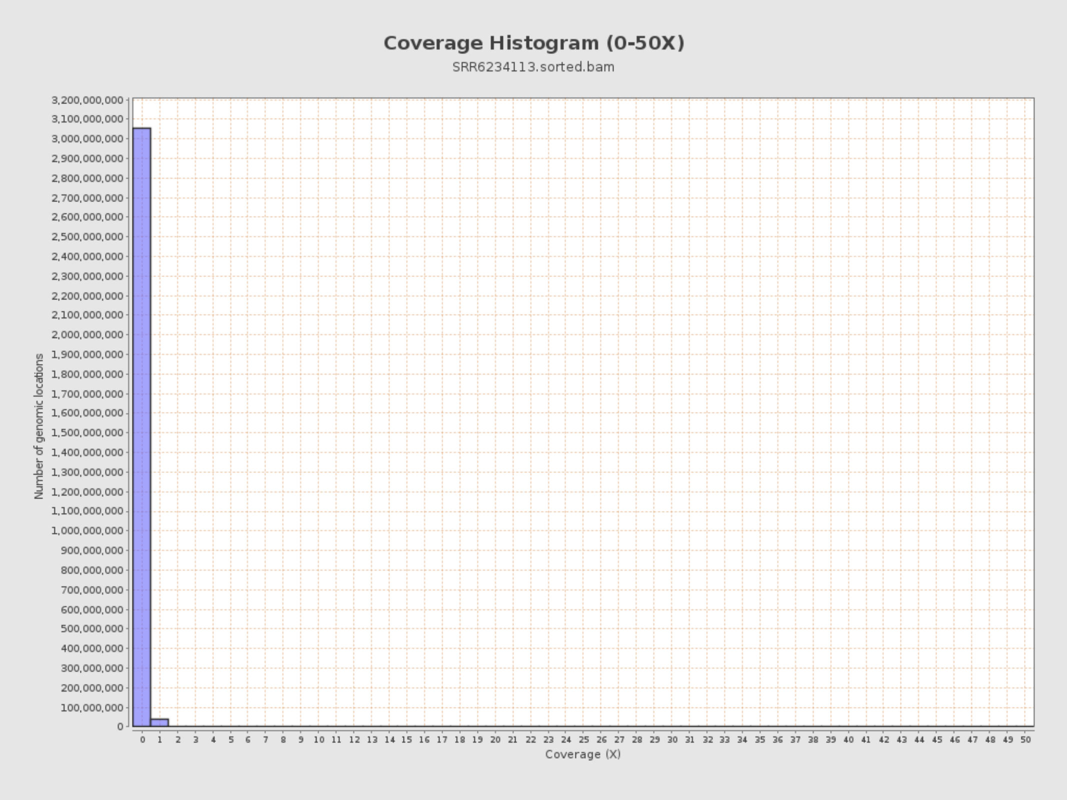
3. Results : Coverage across reference



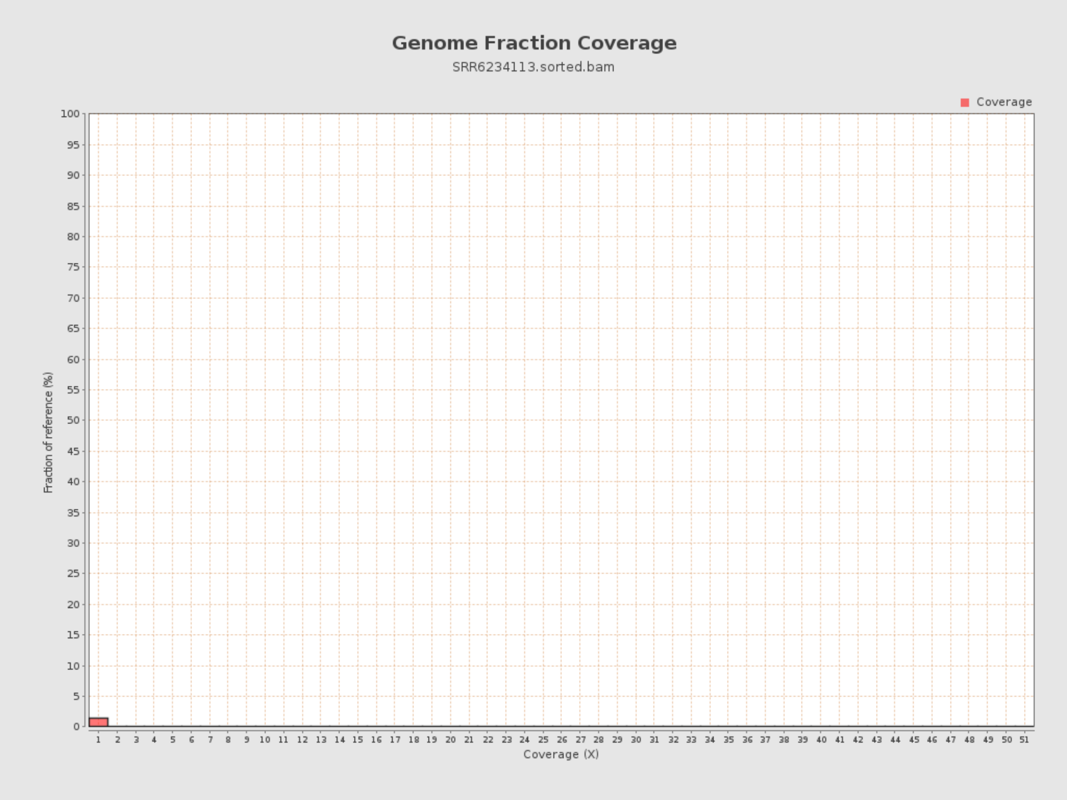
4. Results : Coverage Histogram



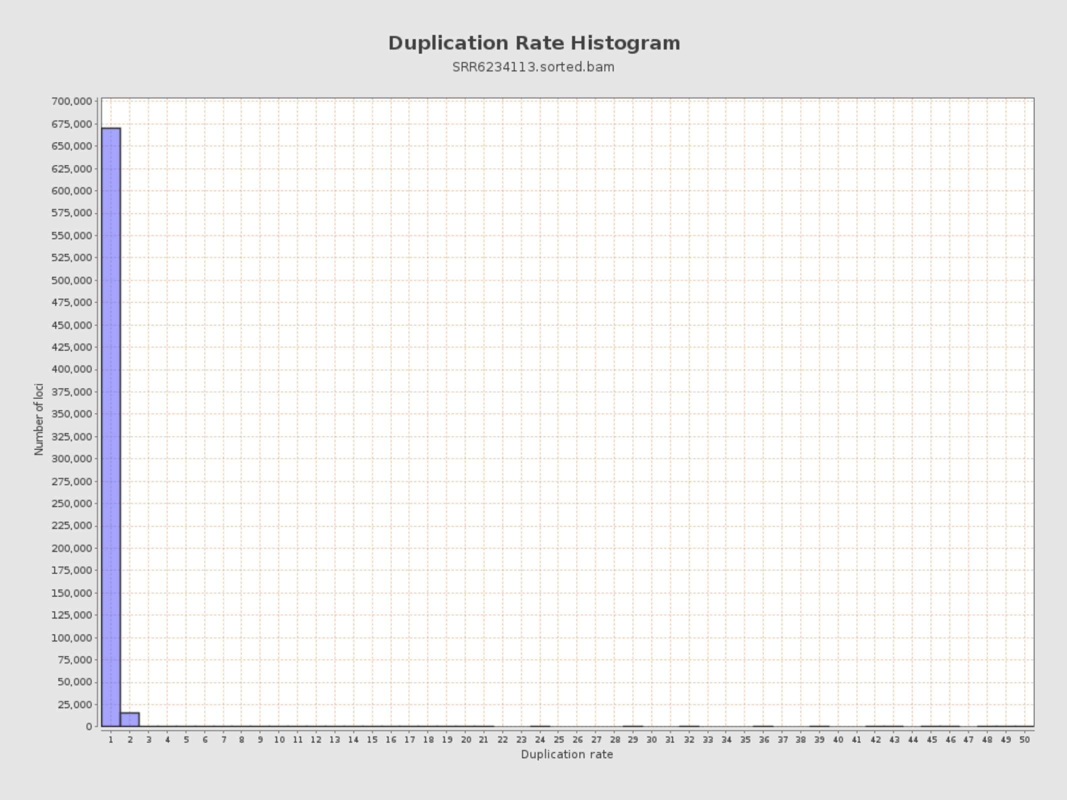
5. Results : Coverage Histogram (0-50X)



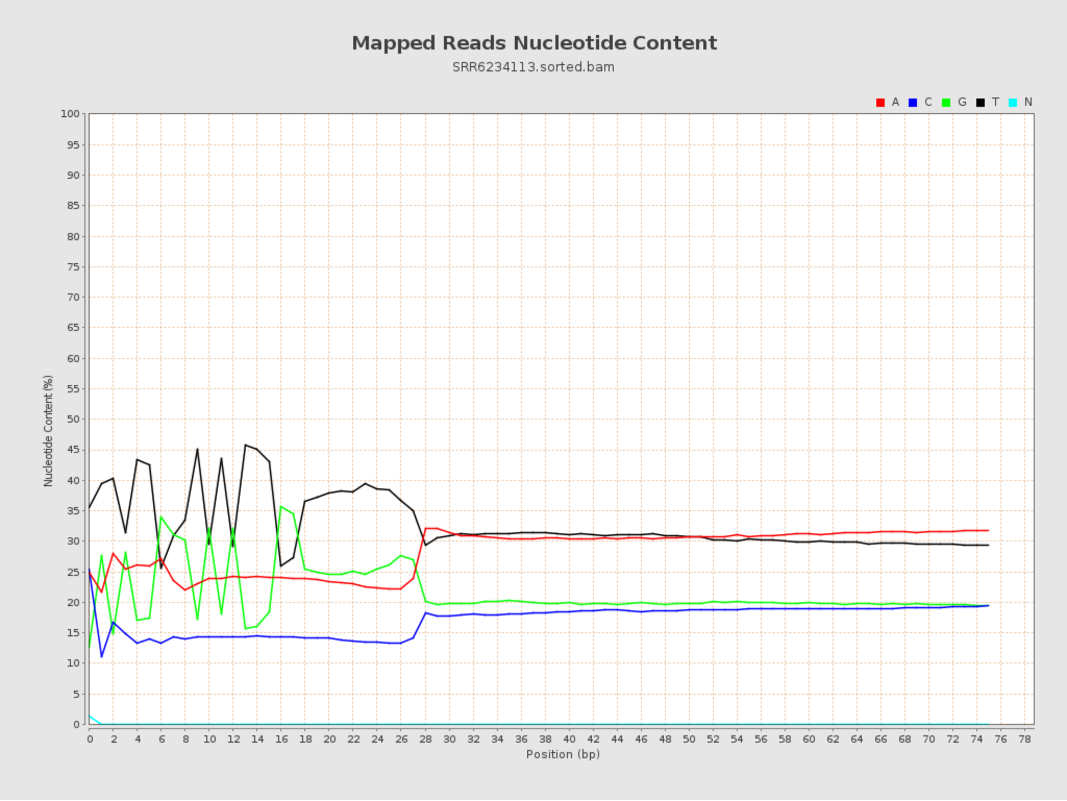
6. Results : Genome Fraction Coverage



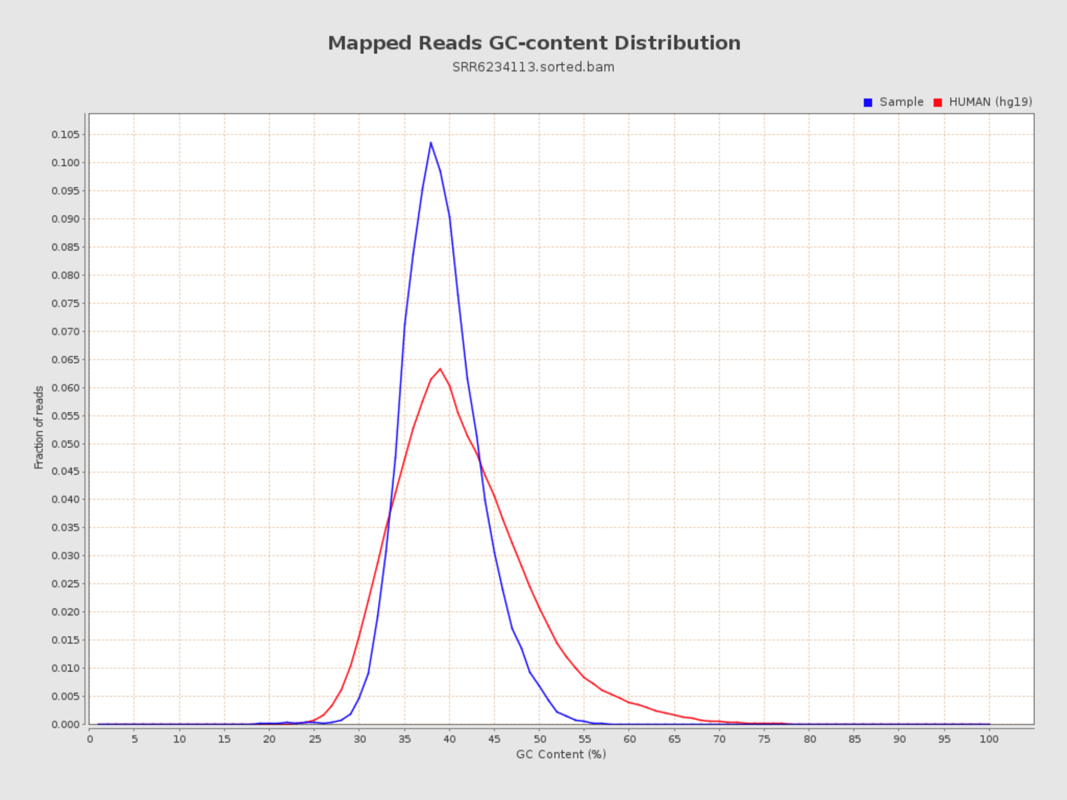
7. Results : Duplication Rate Histogram



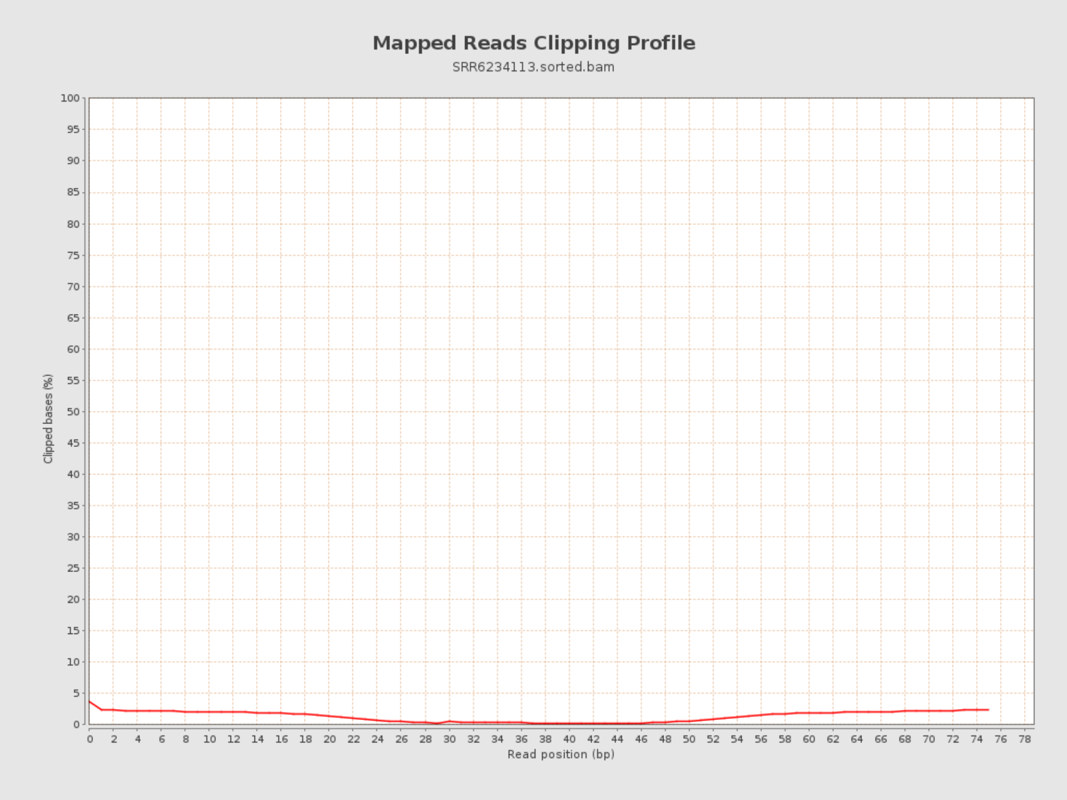
8. Results : Mapped Reads Nucleotide Content



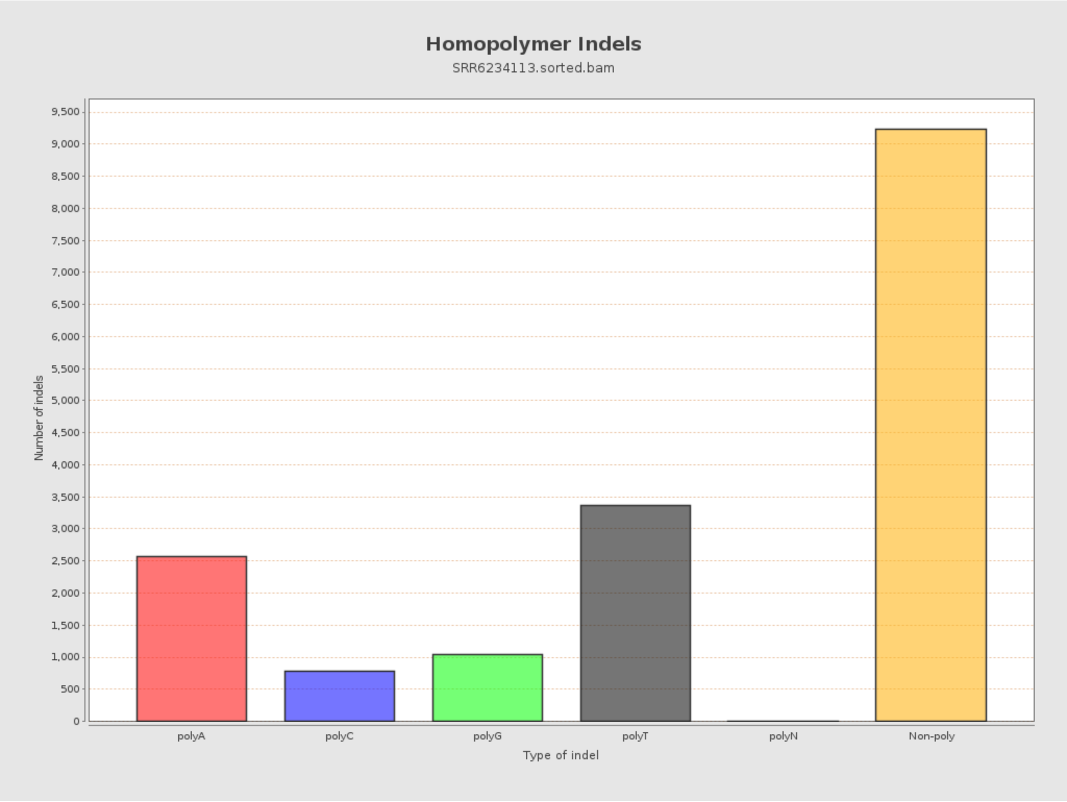
9. Results : Mapped Reads GC-content Distribution



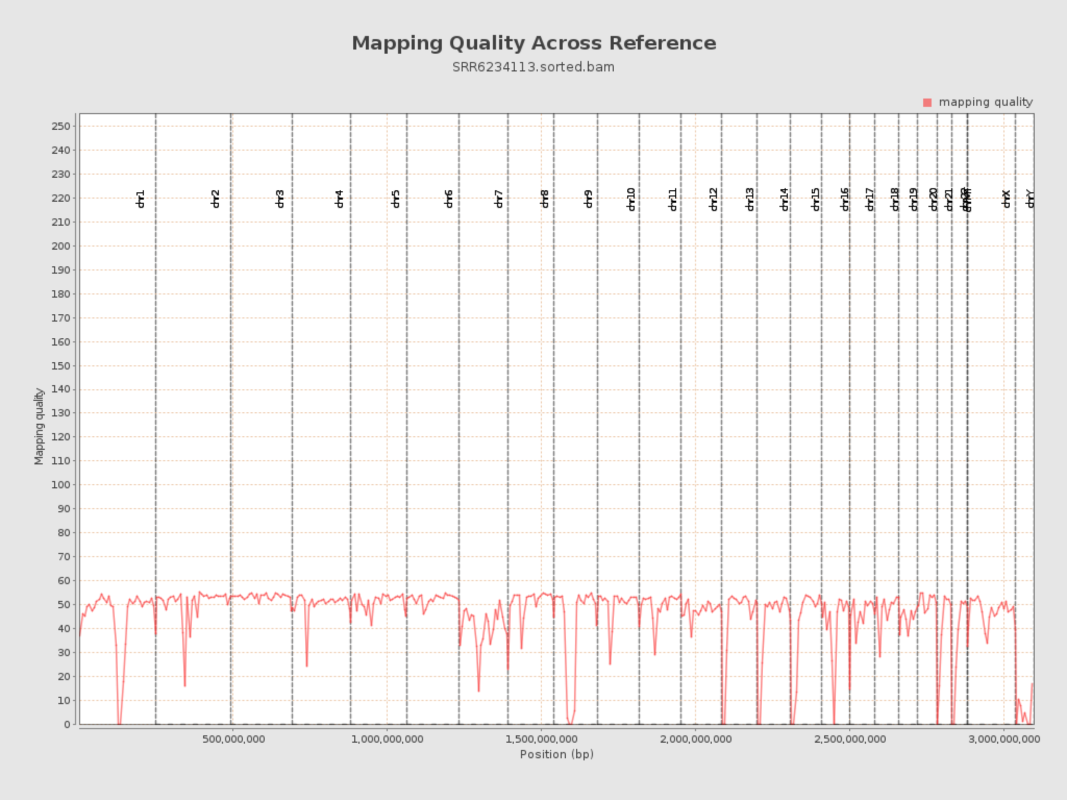
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram