Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 17:01:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234114.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_SRR6234114 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234114.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 17:00:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234114.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,305,794
Mapped reads	846,476 / 64.82%
Unmapped reads	459,318 / 35.18%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,368 / 0.26%
Read min/max/mean length	30 / 76 / 76.09
Duplicated reads (estimated)	40,212 / 3.08%
Duplication rate	3.94%
Clipped reads	587,697 / 45.01%

2.2. ACGT Content

Number/percentage of A's	13,168,945 / 25.63%
Number/percentage of C's	8,938,035 / 17.4%
Number/percentage of T's	16,402,457 / 31.93%
Number/percentage of G's	12,861,866 / 25.03%
Number/percentage of N's	5,402 / 0.01%
GC Percentage	42.43%

2.3. Coverage

Mean	0.0166

Standard Deviation	0.1827

2.4. Mapping Quality

Mean Mapping Quality	42.53

2.5. Mismatches and indels

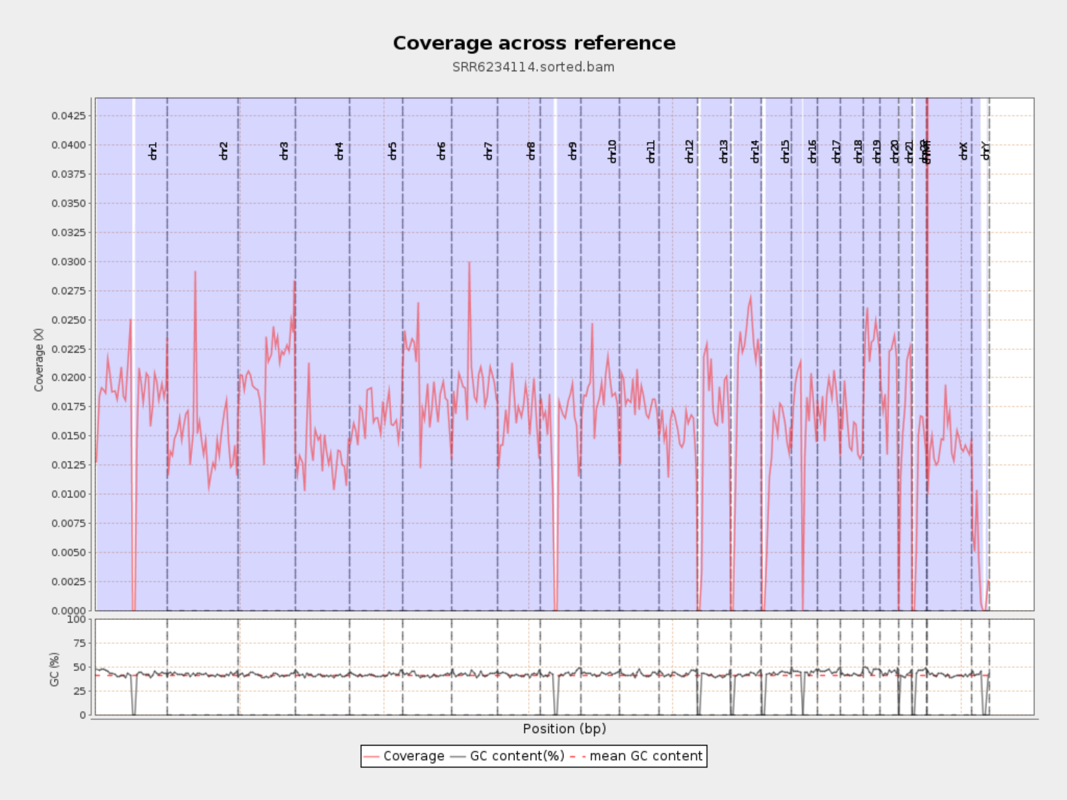
General error rate	0.94%
Mismatches	473,114
Insertions	4,279
Mapped reads with at least one insertion	0.5%
Deletions	19,855
Mapped reads with at least one deletion	2.31%
Homopolymer indels	46.82%

2.6. Chromosome stats

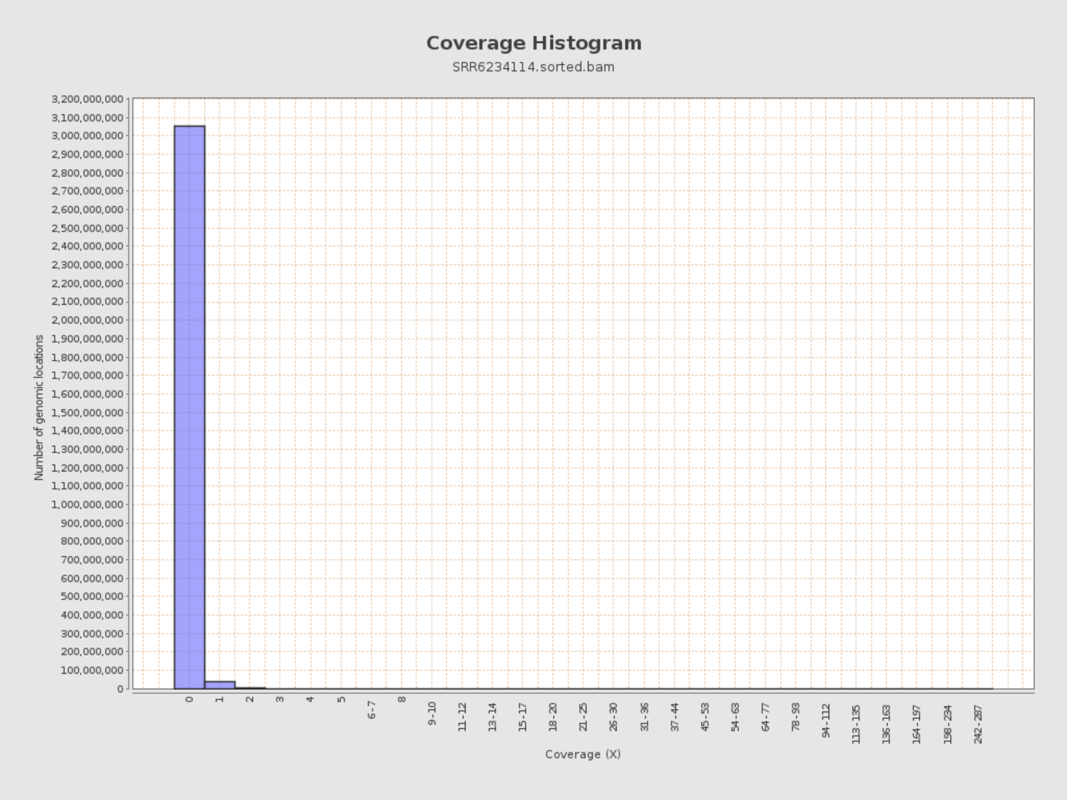
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4456497	0.0179	0.2404
chr2	243199373	3602311	0.0148	0.2061
chr3	198022430	4130556	0.0209	0.1648
chr4	191154276	2585262	0.0135	0.1387
chr5	180915260	3004098	0.0166	0.1481
chr6	171115067	3296716	0.0193	0.1819
chr7	159138663	3115021	0.0196	0.2622

chr8	146364022	2455636	0.0168	0.2001
chr9	141213431	2079884	0.0147	0.1743
chr10	135534747	2542473	0.0188	0.1754
chr11	135006516	2451361	0.0182	0.1969
chr12	133851895	2061073	0.0154	0.1411
chr13	115169878	1804572	0.0157	0.1514
chr14	107349540	2075038	0.0193	0.1649
chr15	102531392	1254584	0.0122	0.1319
chr16	90354753	1467970	0.0162	0.155
chr17	81195210	1441977	0.0178	0.1638
chr18	78077248	1194925	0.0153	0.2541
chr19	59128983	1372819	0.0232	0.2118
chr20	63025520	1229503	0.0195	0.1666
chr21	48129895	776171	0.0161	0.1476
chr22	51304566	545572	0.0106	0.1166
chrMT	16571	33396	2.0153	2.411
chrX	155270560	2222777	0.0143	0.1466
chrY	59373566	211867	0.0036	0.0768

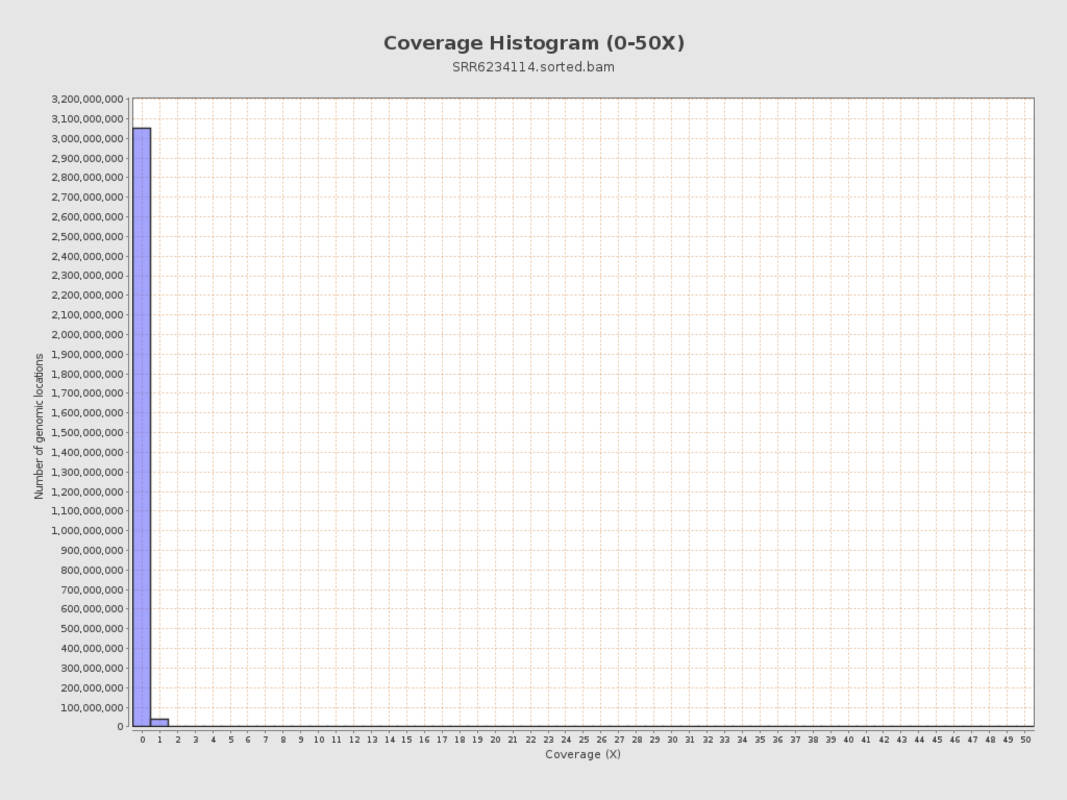
3. Results : Coverage across reference



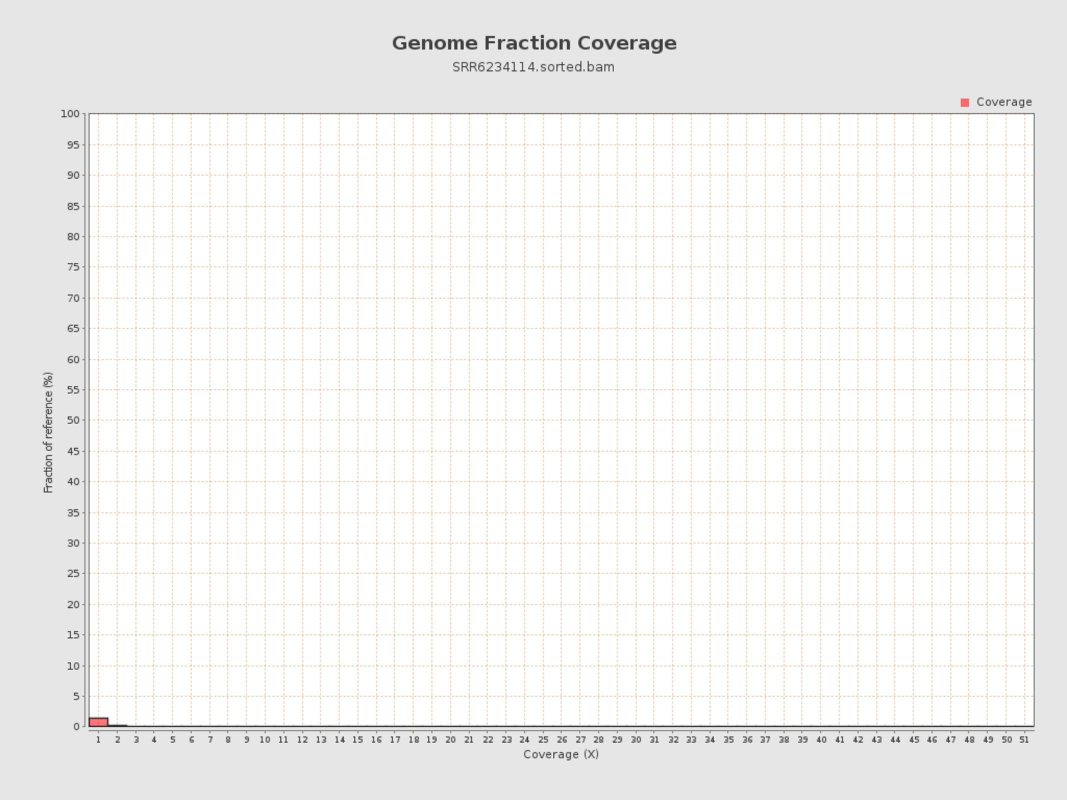
4. Results : Coverage Histogram



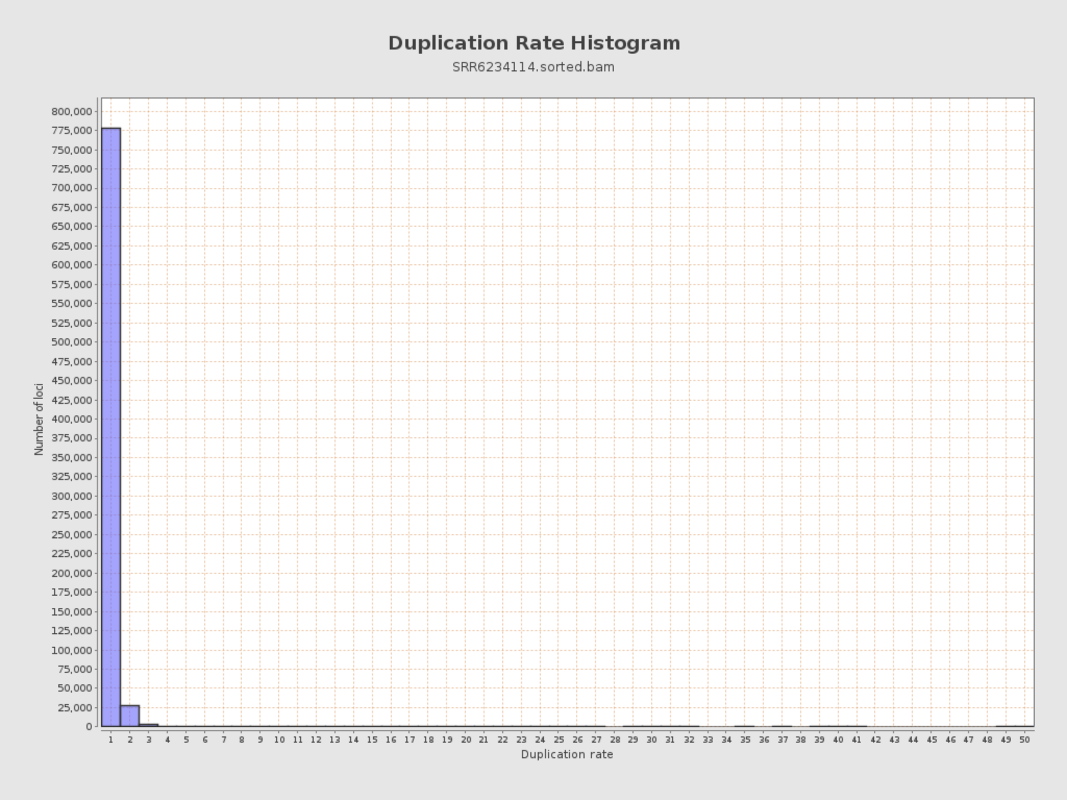
5. Results : Coverage Histogram (0-50X)



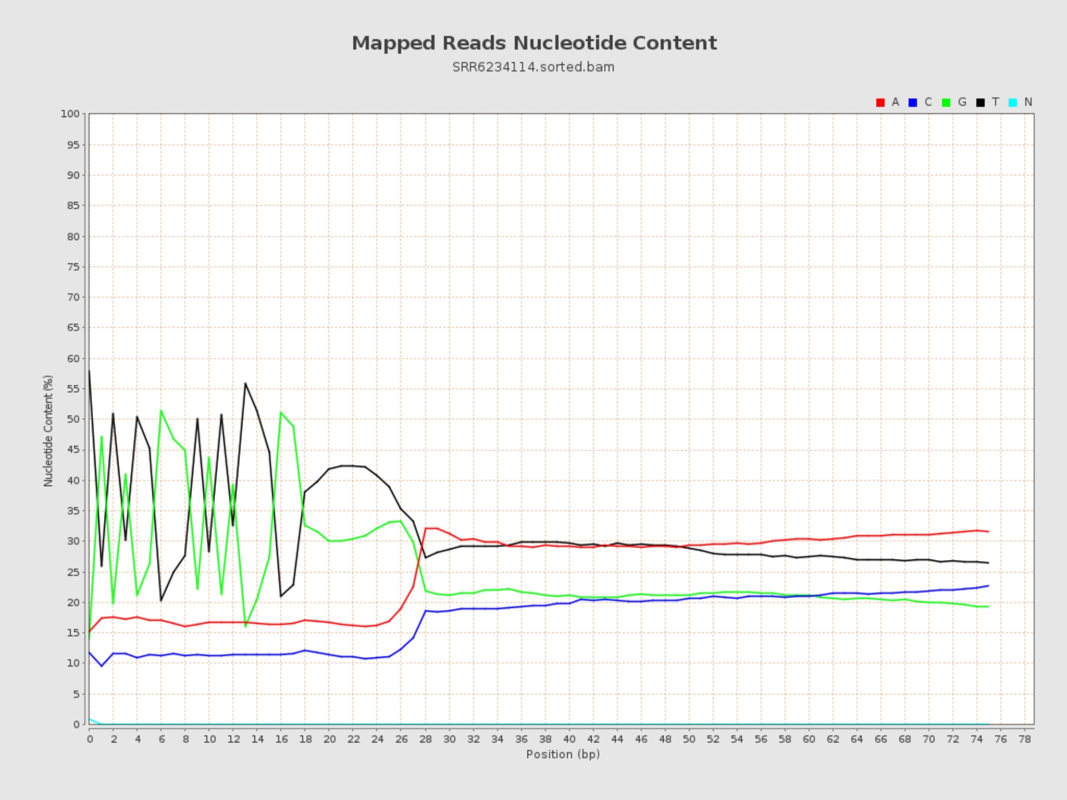
6. Results : Genome Fraction Coverage



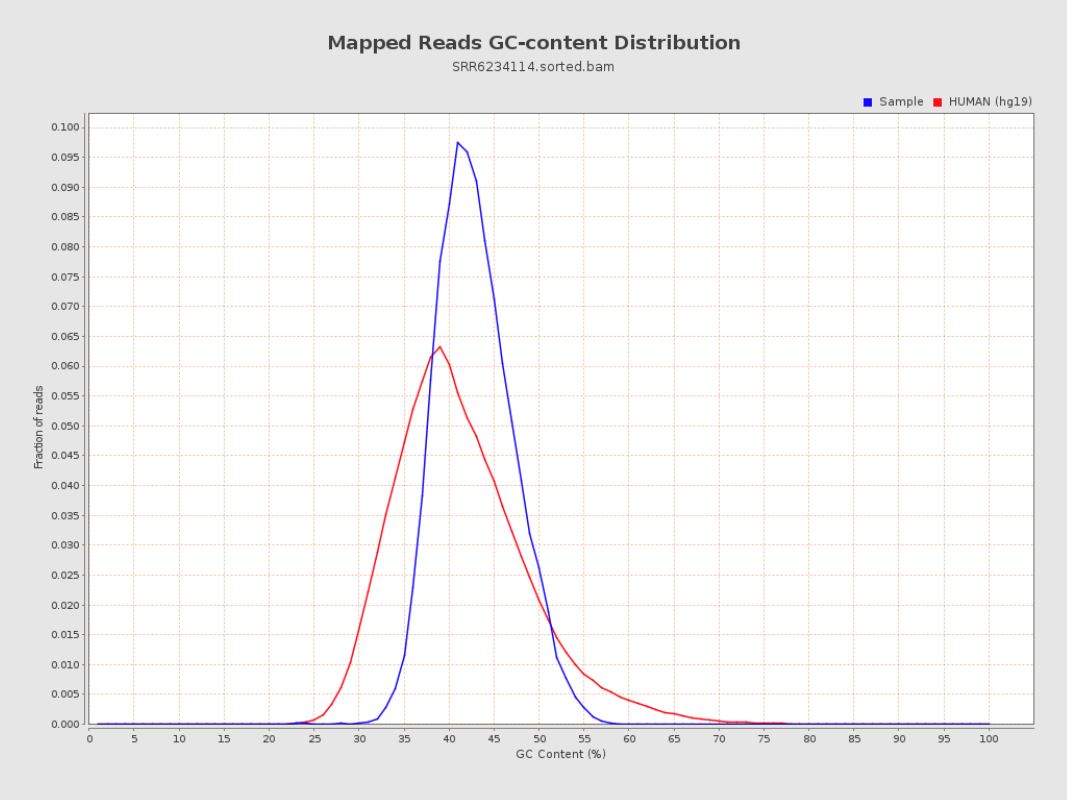
7. Results : Duplication Rate Histogram



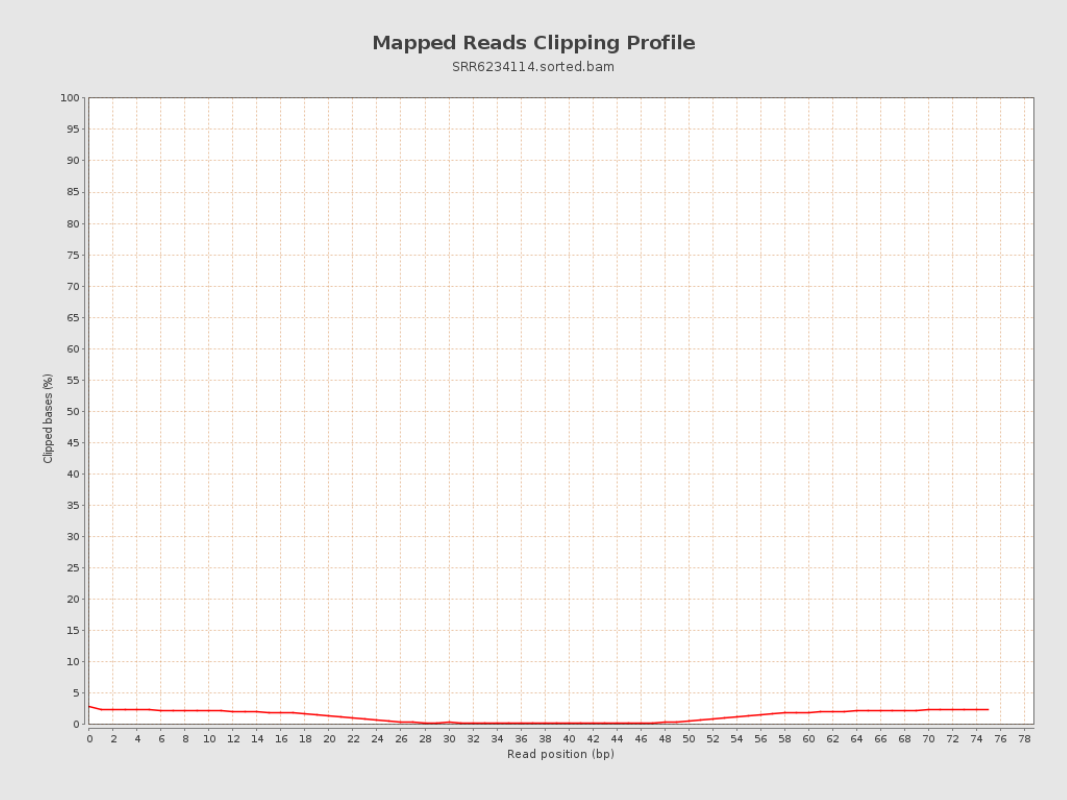
8. Results : Mapped Reads Nucleotide Content



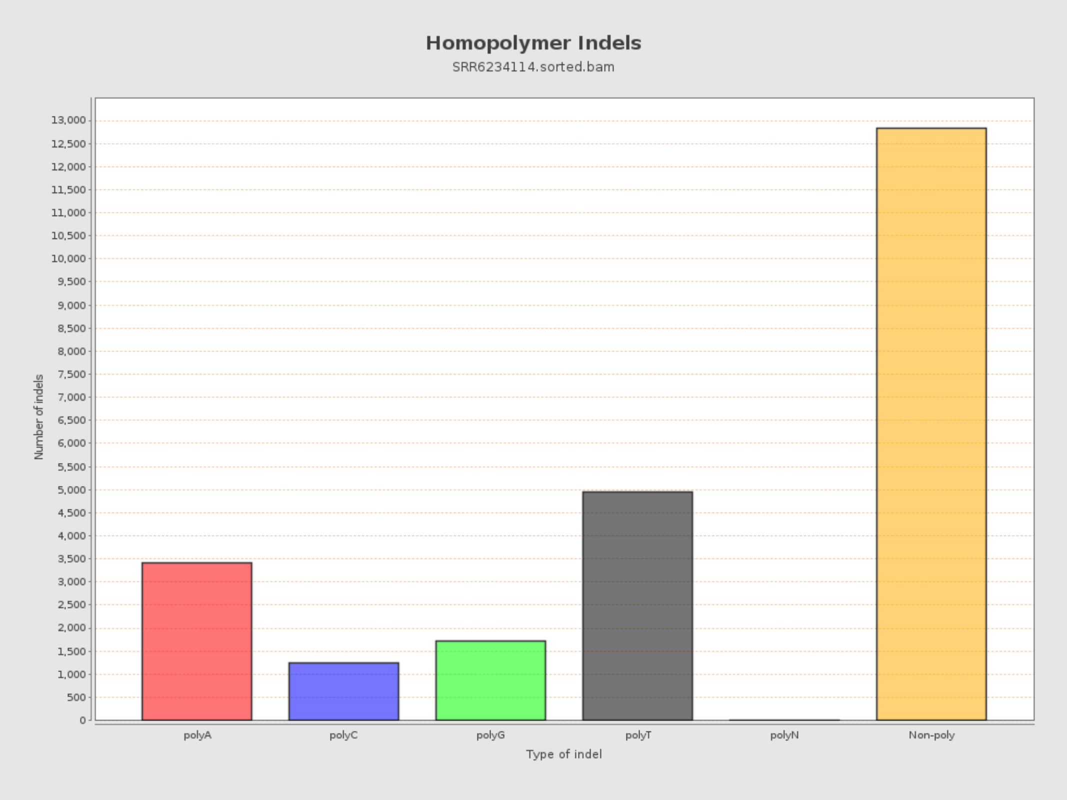
9. Results : Mapped Reads GC-content Distribution



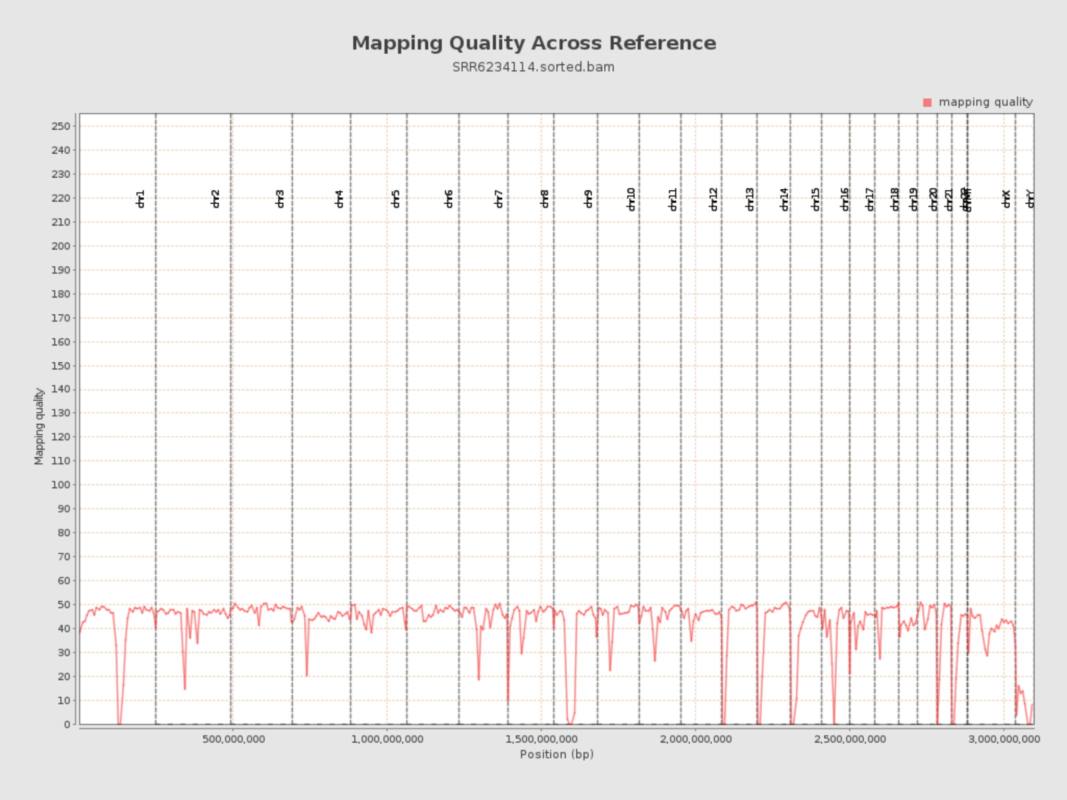
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram