Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 18:24:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234142.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_SRR6234142 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234142.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 18:24:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234142.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,136,084
Mapped reads	849,383 / 74.76%
Unmapped reads	286,701 / 25.24%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,948 / 0.52%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	40,625 / 3.58%
Duplication rate	3.89%
Clipped reads	406,753 / 35.8%

2.2. ACGT Content

Number/percentage of A's	15,679,680 / 28.13%
Number/percentage of C's	9,623,455 / 17.27%
Number/percentage of T's	18,362,074 / 32.94%
Number/percentage of G's	12,064,174 / 21.64%
Number/percentage of N's	8,653 / 0.02%
GC Percentage	38.91%

2.3. Coverage

Mean	0.018

Standard Deviation	0.2374

2.4. Mapping Quality

Mean Mapping Quality	46.69

2.5. Mismatches and indels

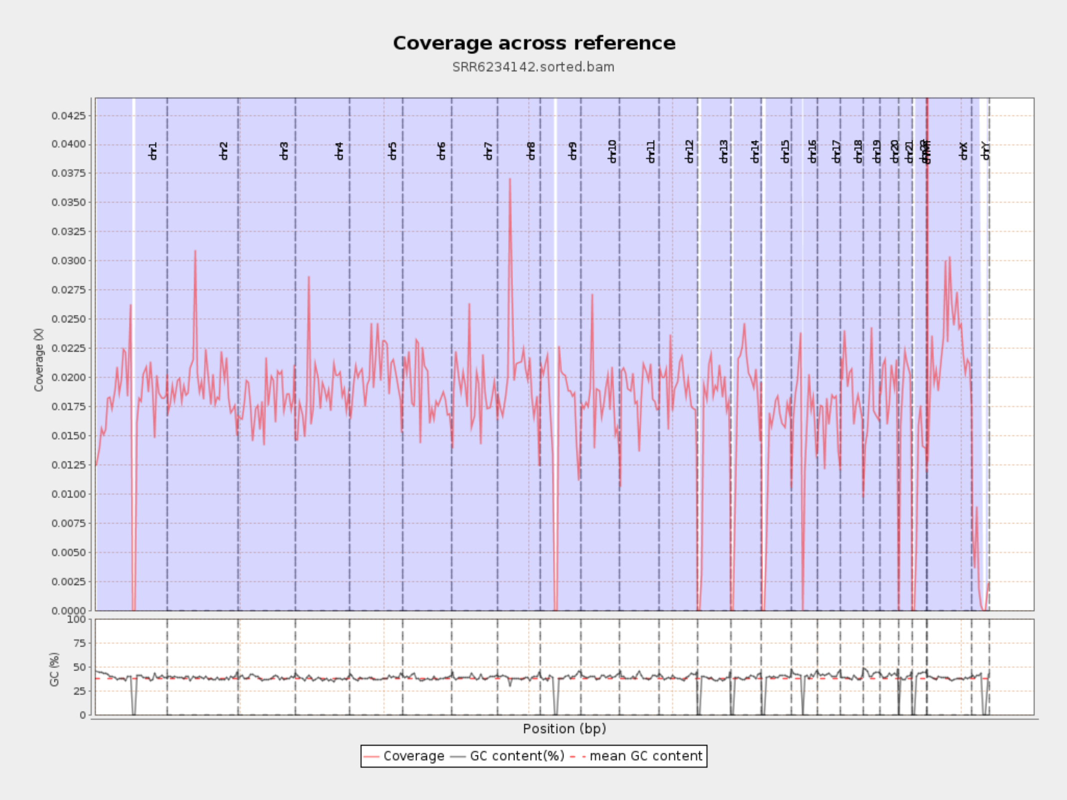
General error rate	0.88%
Mismatches	483,295
Insertions	4,862
Mapped reads with at least one insertion	0.57%
Deletions	16,730
Mapped reads with at least one deletion	1.94%
Homopolymer indels	46.39%

2.6. Chromosome stats

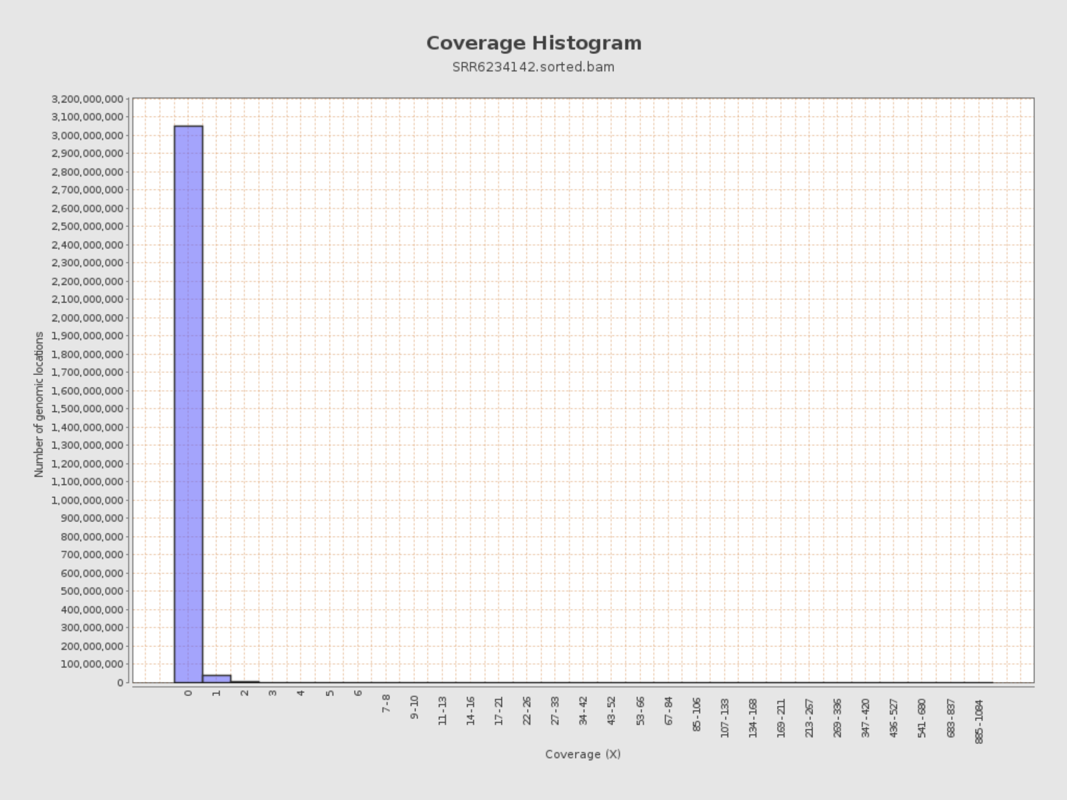
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4330438	0.0174	0.285
chr2	243199373	4724452	0.0194	0.2272
chr3	198022430	3575742	0.0181	0.1558
chr4	191154276	3563976	0.0186	0.1696
chr5	180915260	3707398	0.0205	0.1667
chr6	171115067	3231491	0.0189	0.1684
chr7	159138663	3012017	0.0189	0.211

chr8	146364022	3006045	0.0205	0.6792
chr9	141213431	2350117	0.0166	0.178
chr10	135534747	2454209	0.0181	0.1879
chr11	135006516	2544012	0.0188	0.1901
chr12	133851895	2579844	0.0193	0.1638
chr13	115169878	1846491	0.016	0.1477
chr14	107349540	1834843	0.0171	0.1554
chr15	102531392	1405467	0.0137	0.1356
chr16	90354753	1419665	0.0157	0.1535
chr17	81195210	1328533	0.0164	0.1535
chr18	78077248	1501727	0.0192	0.2871
chr19	59128983	1019617	0.0172	0.2017
chr20	63025520	1209814	0.0192	0.1623
chr21	48129895	838663	0.0174	0.1585
chr22	51304566	542410	0.0106	0.1167
chrMT	16571	39864	2.4056	2.2239
chrX	155270560	3533649	0.0228	0.1828
chrY	59373566	167026	0.0028	0.0765

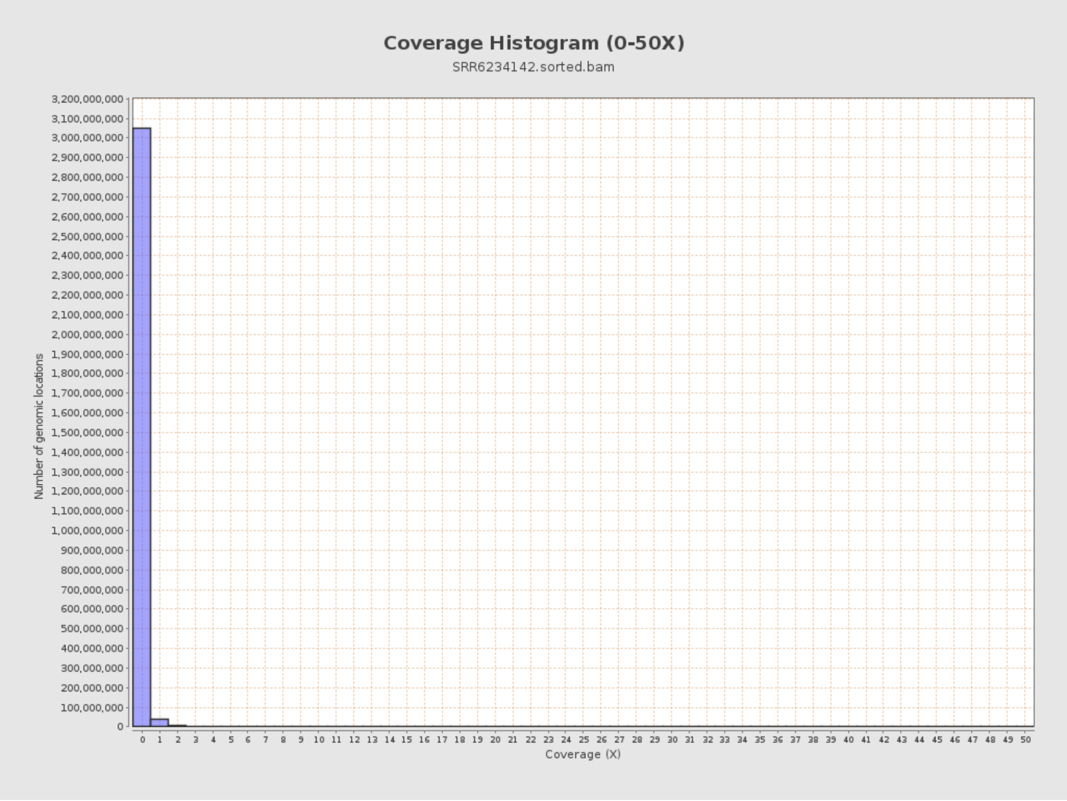
3. Results : Coverage across reference



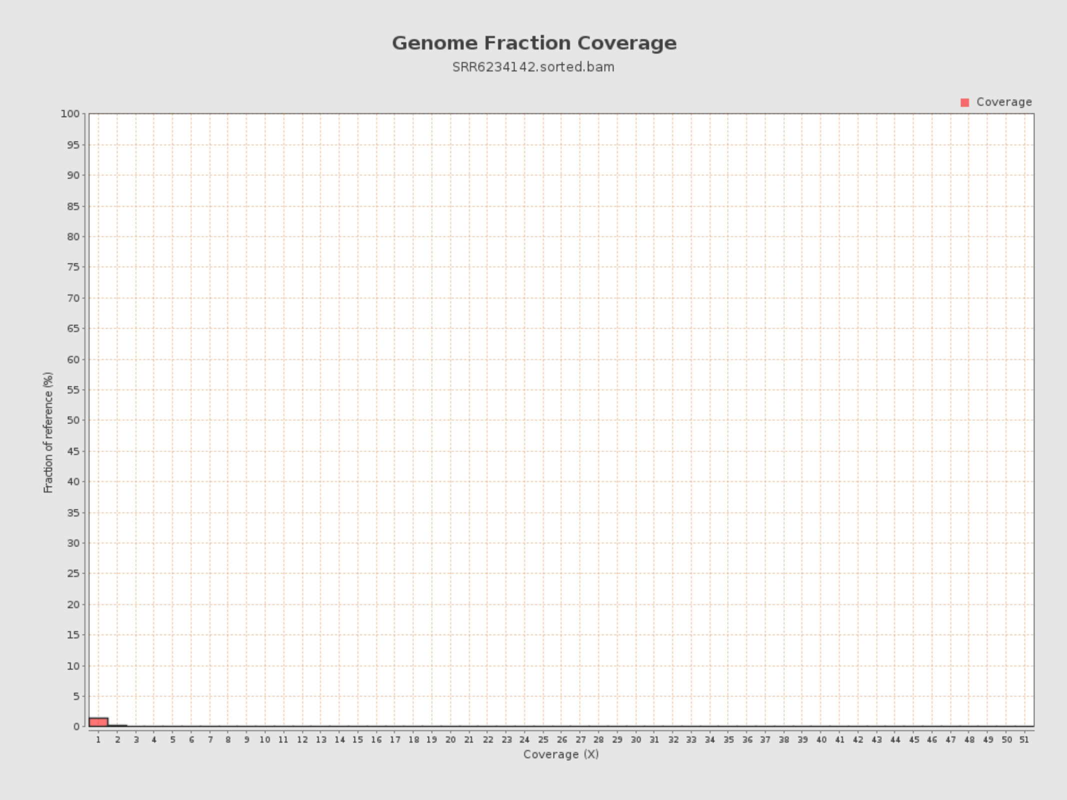
4. Results : Coverage Histogram



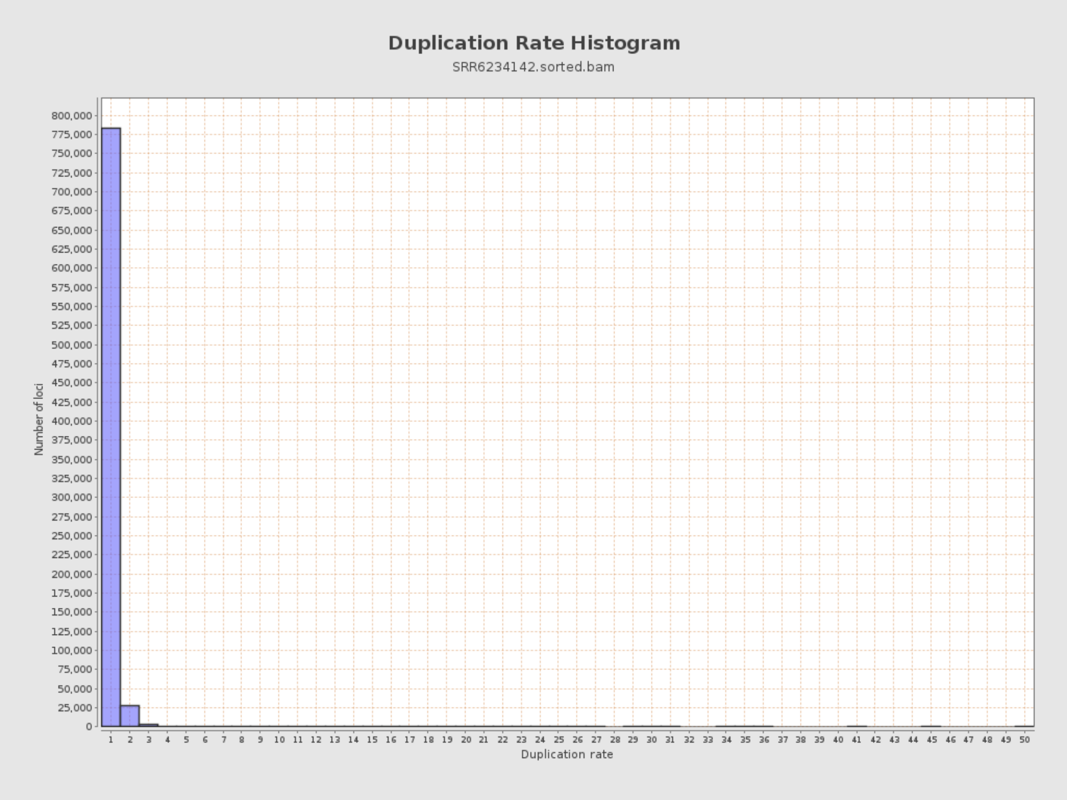
5. Results : Coverage Histogram (0-50X)



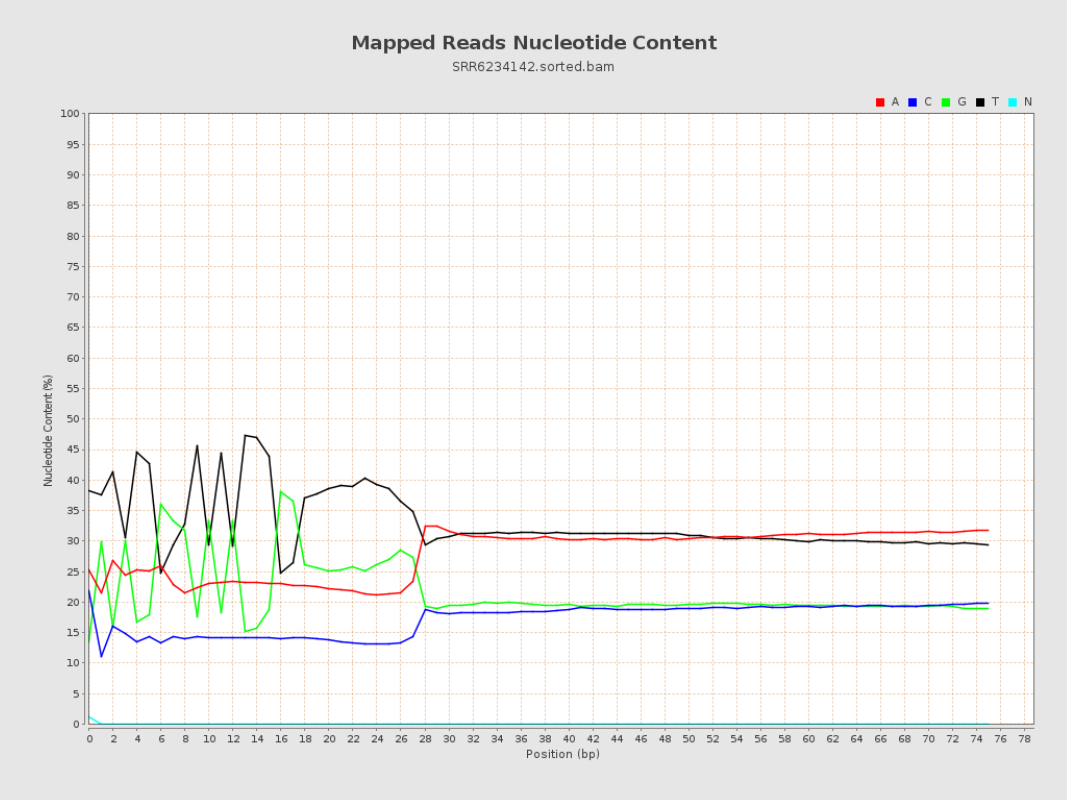
6. Results : Genome Fraction Coverage



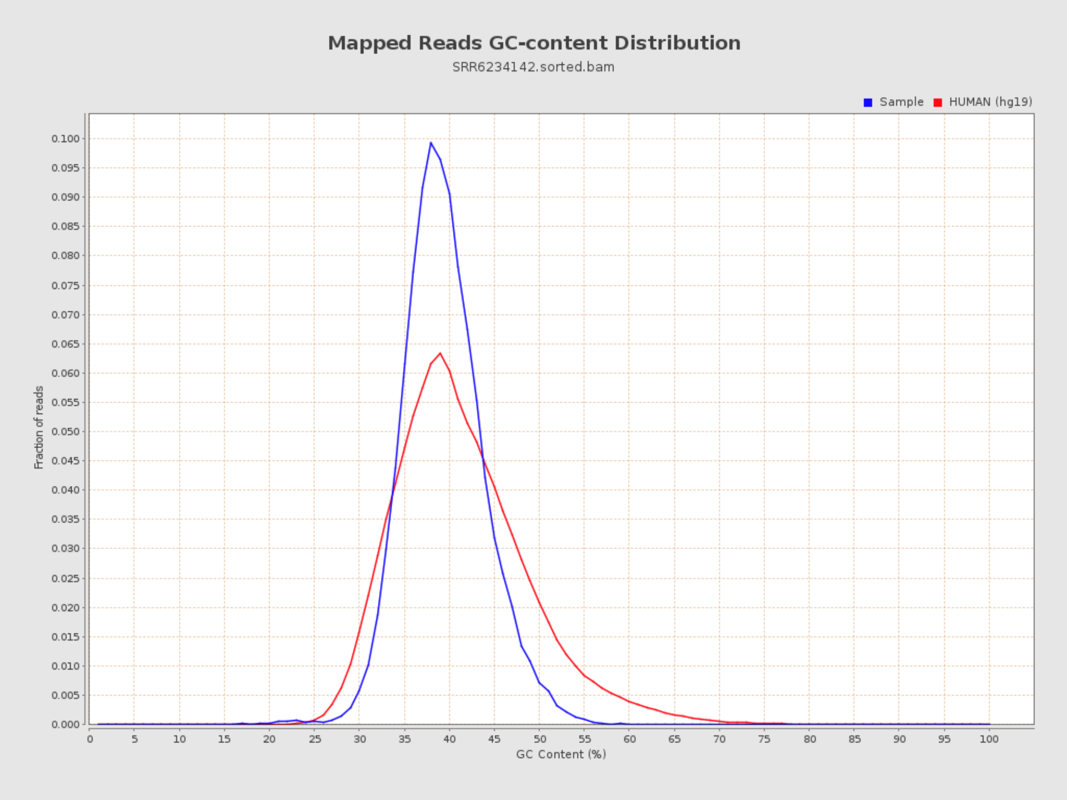
7. Results : Duplication Rate Histogram



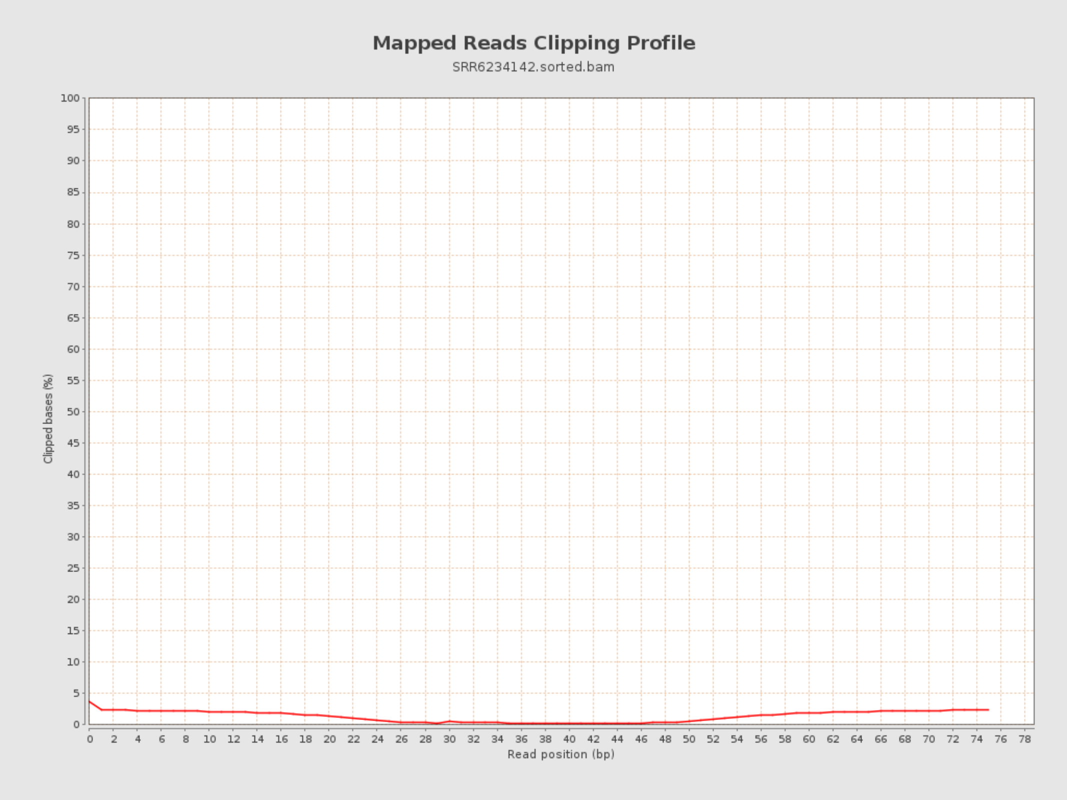
8. Results : Mapped Reads Nucleotide Content



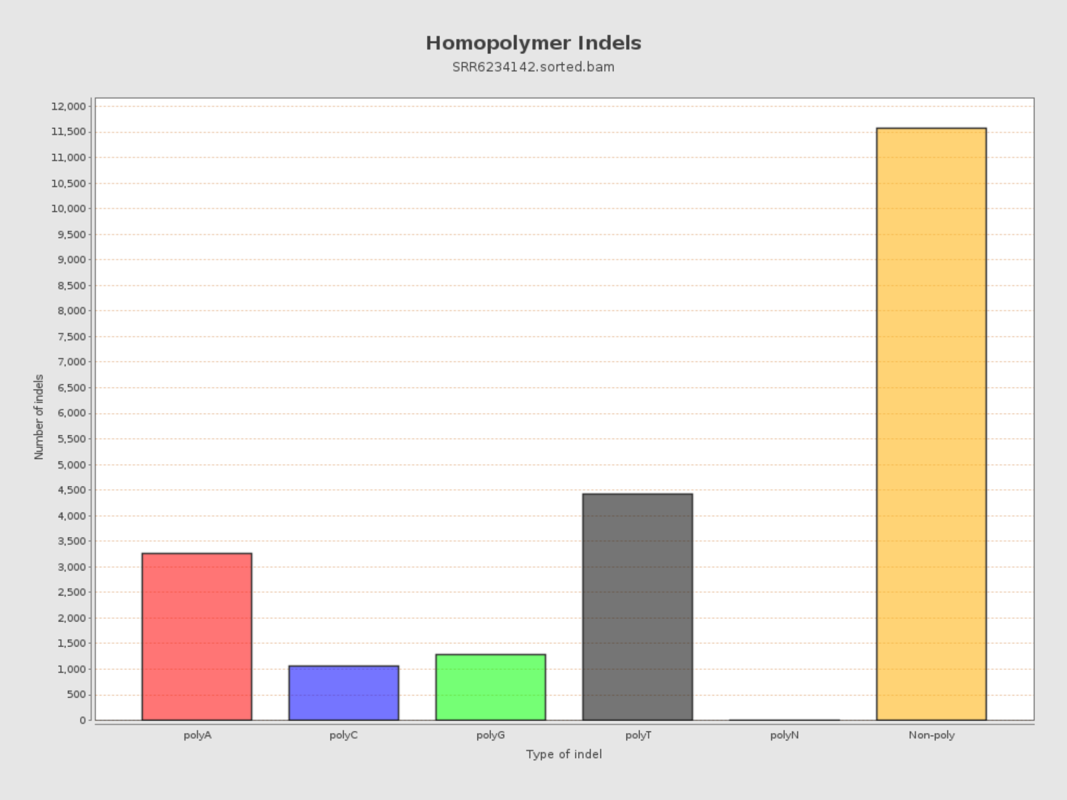
9. Results : Mapped Reads GC-content Distribution



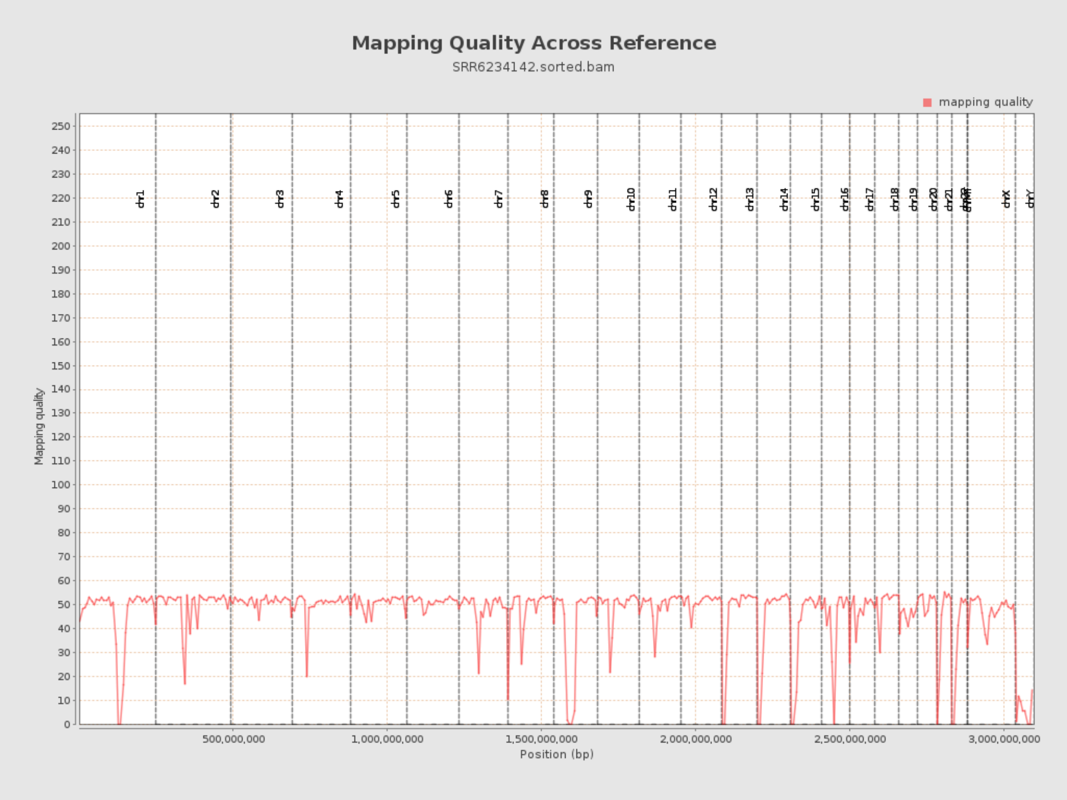
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram