Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 22:43:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013349.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_SRR6013349 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013349.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 22:43:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013349.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,018,630
Mapped reads	754,277 / 37.37%
Unmapped reads	1,264,353 / 62.63%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,955 / 0.39%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	136,212 / 6.75%
Duplication rate	12.65%
Clipped reads	445,840 / 22.09%

2.2. ACGT Content

Number/percentage of A's	12,779,207 / 26.89%
Number/percentage of C's	8,981,368 / 18.9%
Number/percentage of T's	14,834,291 / 31.21%
Number/percentage of G's	10,925,018 / 22.99%
Number/percentage of N's	5,146 / 0.01%
GC Percentage	41.89%

2.3. Coverage

Mean	0.0154

Standard Deviation	0.2548

2.4. Mapping Quality

Mean Mapping Quality	43.18

2.5. Mismatches and indels

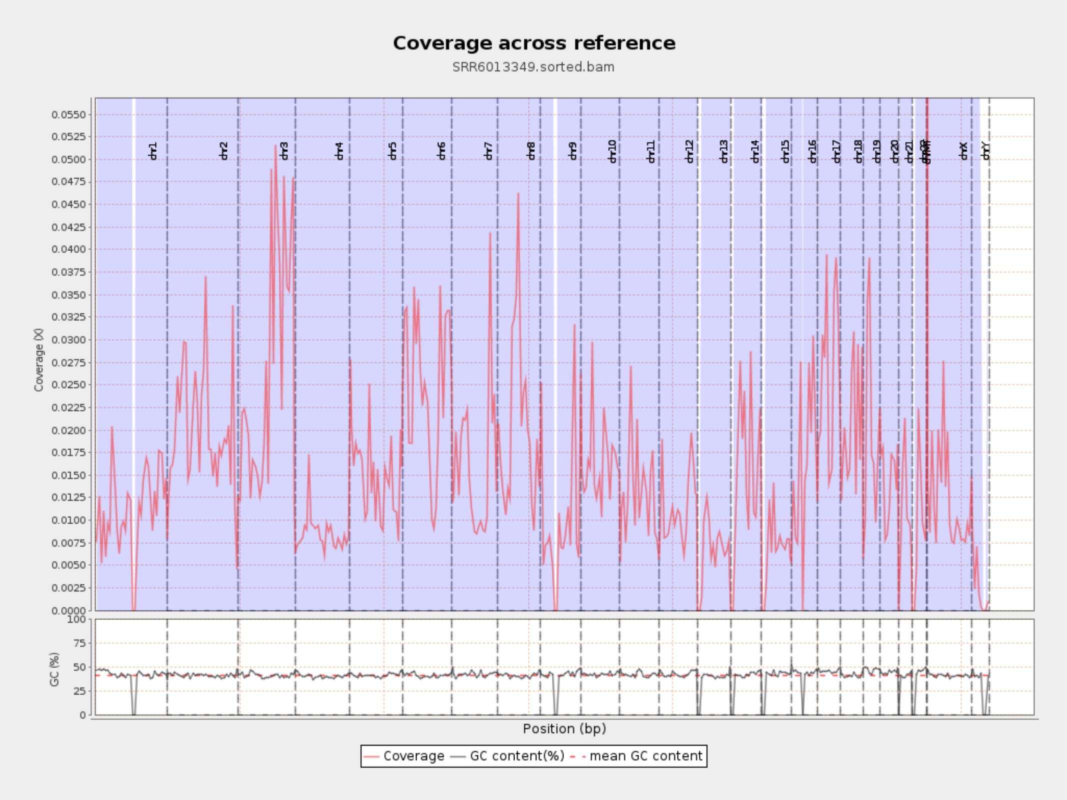
General error rate	0.87%
Mismatches	407,164
Insertions	3,510
Mapped reads with at least one insertion	0.46%
Deletions	13,995
Mapped reads with at least one deletion	1.84%
Homopolymer indels	45.19%

2.6. Chromosome stats

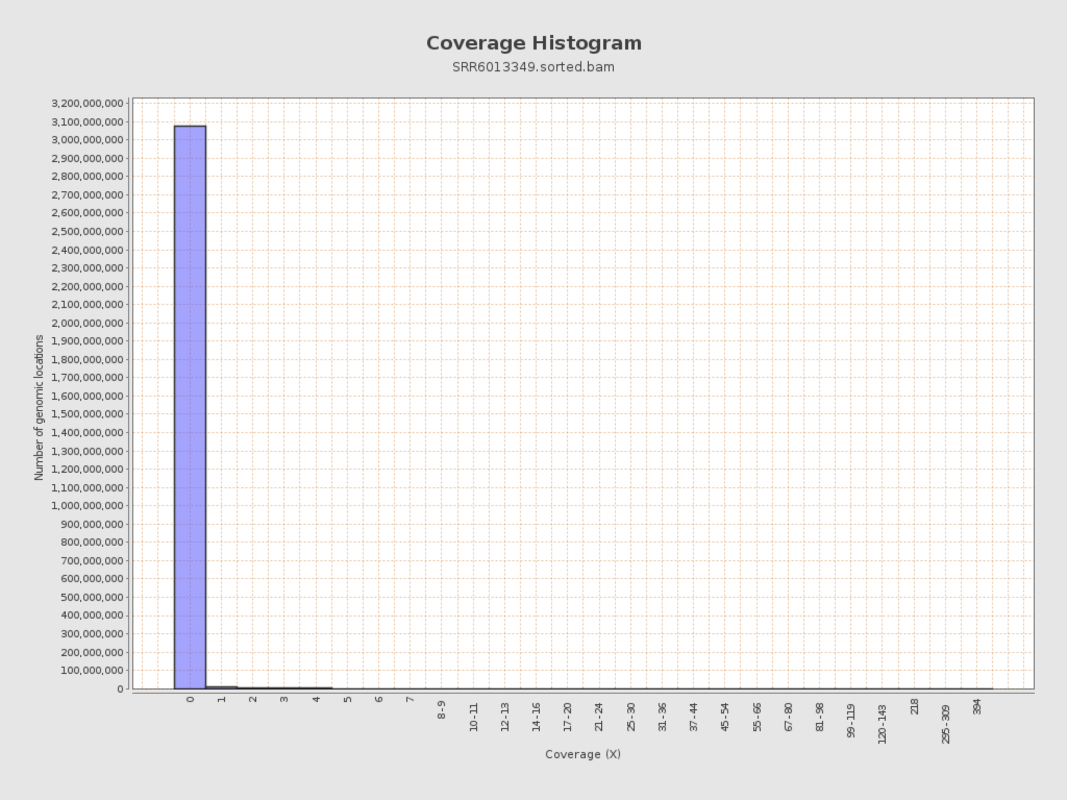
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2704102	0.0108	0.2247
chr2	243199373	4913804	0.0202	0.3277
chr3	198022430	5370646	0.0271	0.3225
chr4	191154276	1627093	0.0085	0.1758
chr5	180915260	2687246	0.0149	0.2338
chr6	171115067	4268488	0.0249	0.3334
chr7	159138663	2527460	0.0159	0.2541

chr8	146364022	3043193	0.0208	0.2891
chr9	141213431	1396243	0.0099	0.195
chr10	135534747	2224819	0.0164	0.2631
chr11	135006516	1770036	0.0131	0.2332
chr12	133851895	1513689	0.0113	0.2119
chr13	115169878	750965	0.0065	0.1563
chr14	107349540	1642394	0.0153	0.2466
chr15	102531392	697010	0.0068	0.1563
chr16	90354753	1441361	0.016	0.2456
chr17	81195210	2192474	0.027	0.3292
chr18	78077248	1599580	0.0205	0.3492
chr19	59128983	1202159	0.0203	0.2949
chr20	63025520	874540	0.0139	0.2416
chr21	48129895	532513	0.0111	0.2025
chr22	51304566	510879	0.01	0.1948
chrMT	16571	32981	1.9903	3.4453
chrX	155270560	1883003	0.0121	0.2112
chrY	59373566	142381	0.0024	0.0926

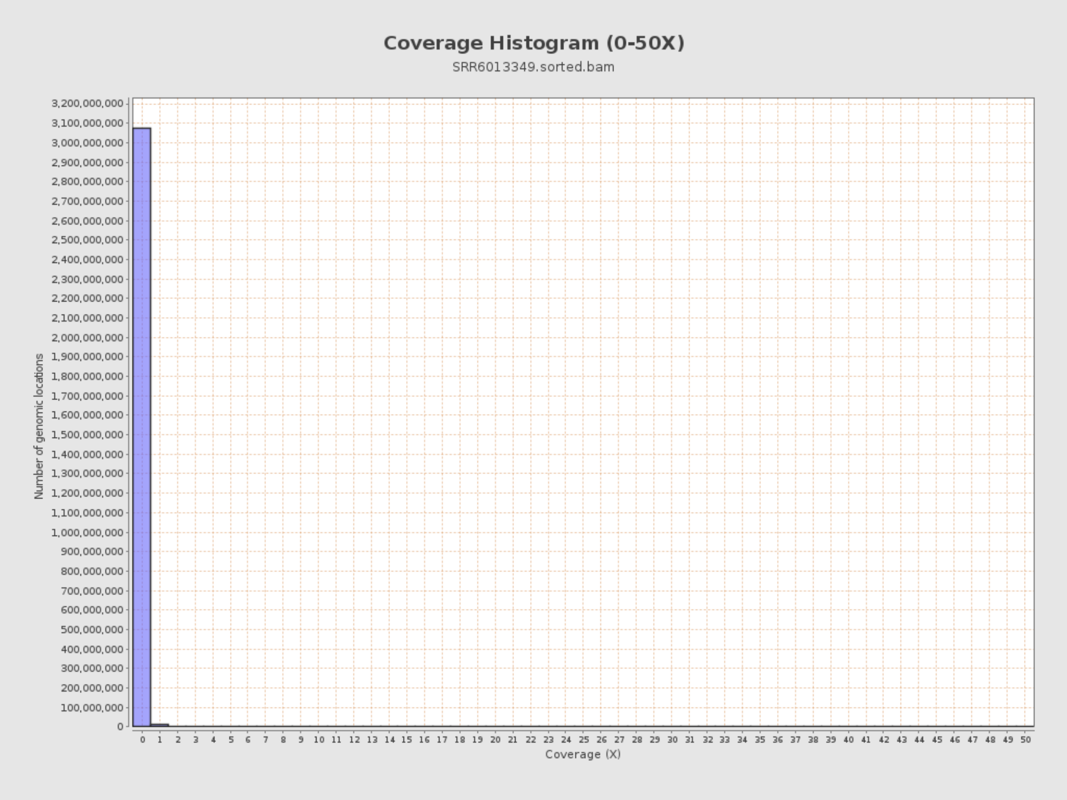
3. Results : Coverage across reference



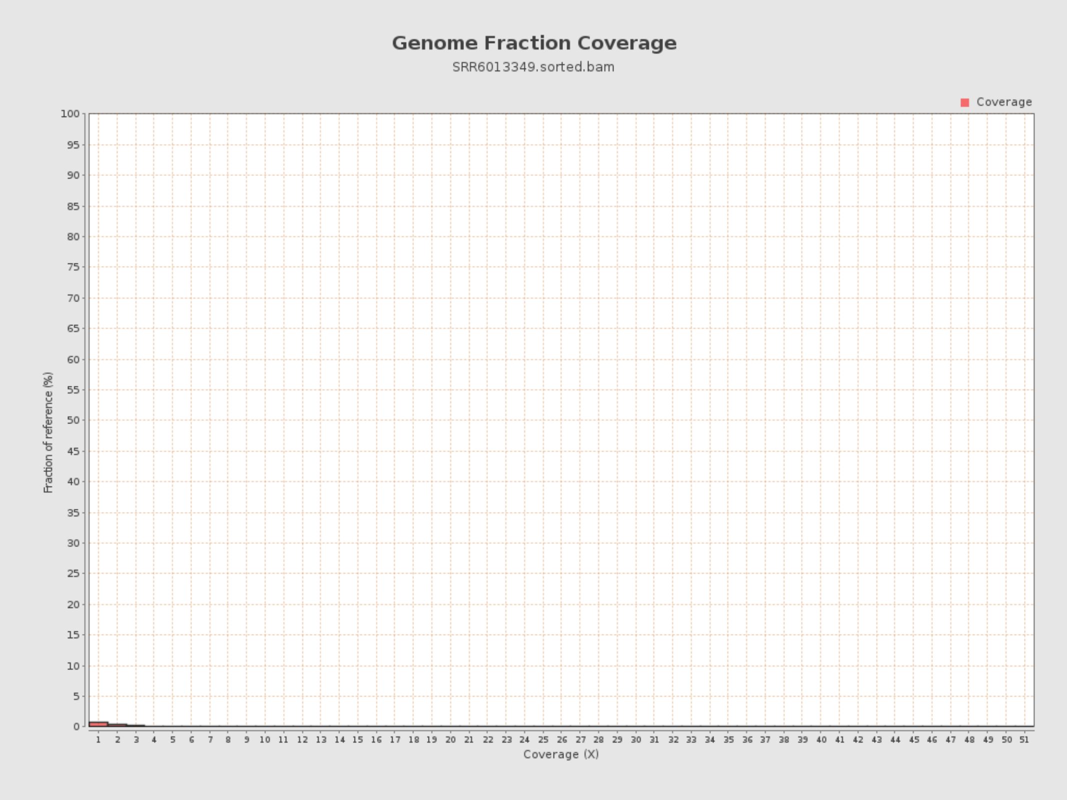
4. Results : Coverage Histogram



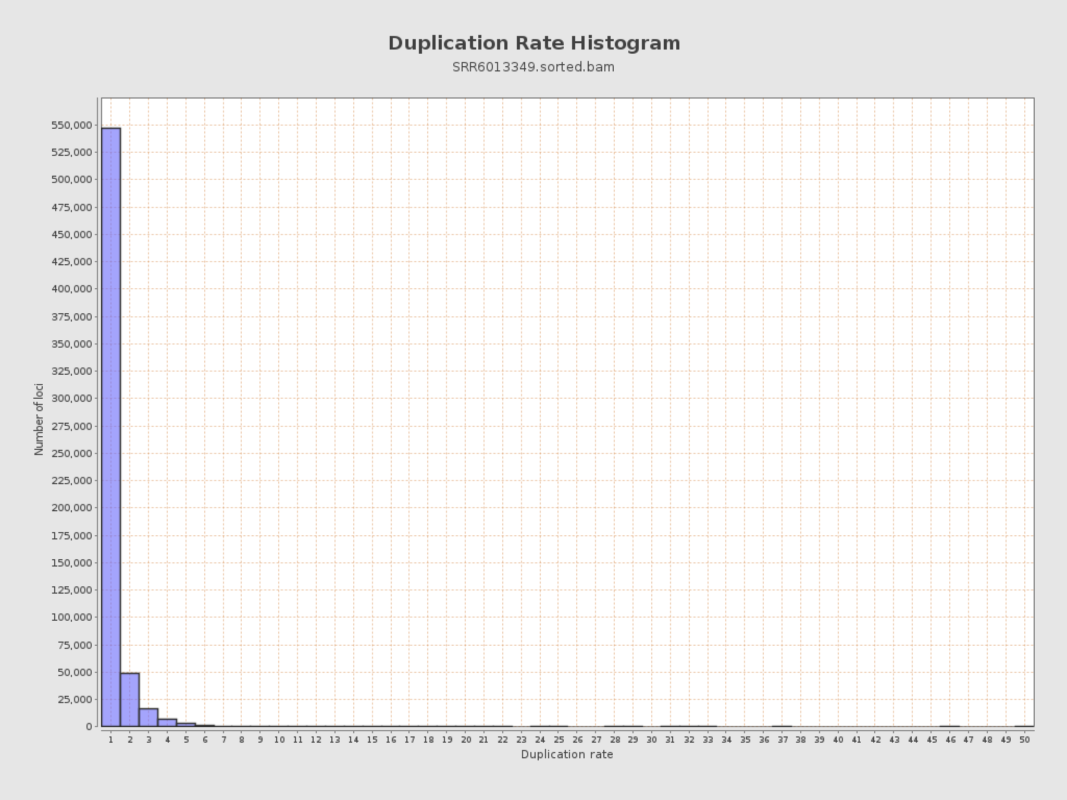
5. Results : Coverage Histogram (0-50X)



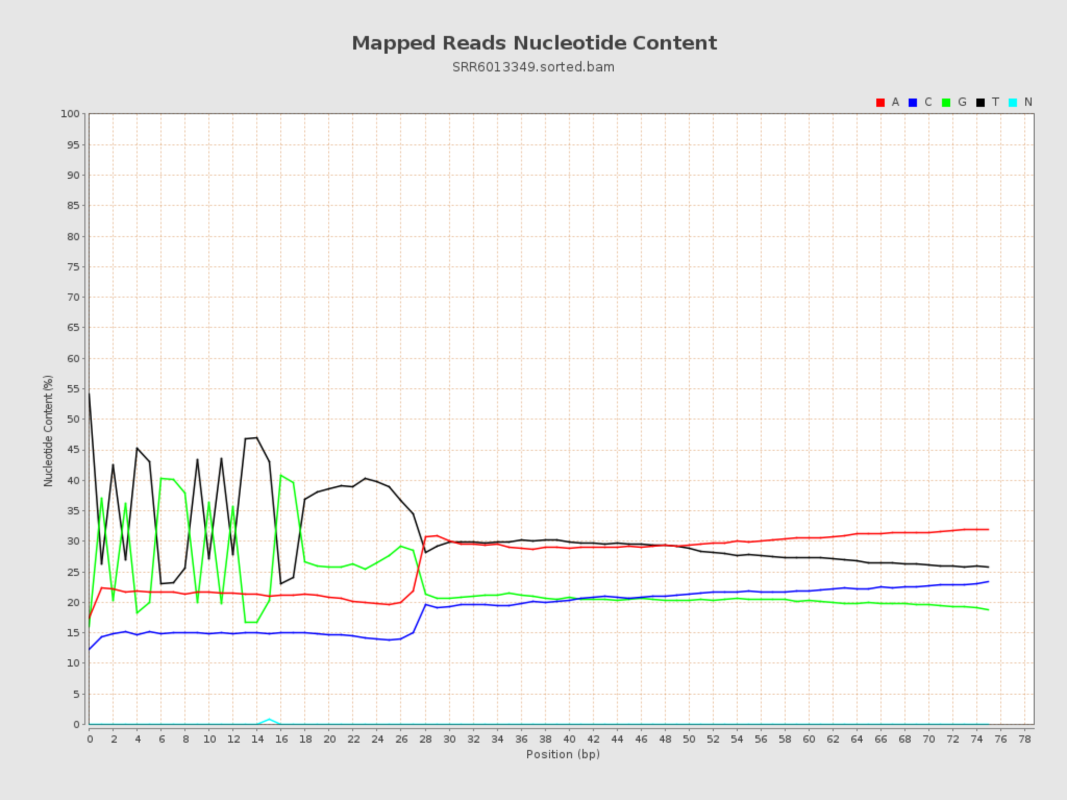
6. Results : Genome Fraction Coverage



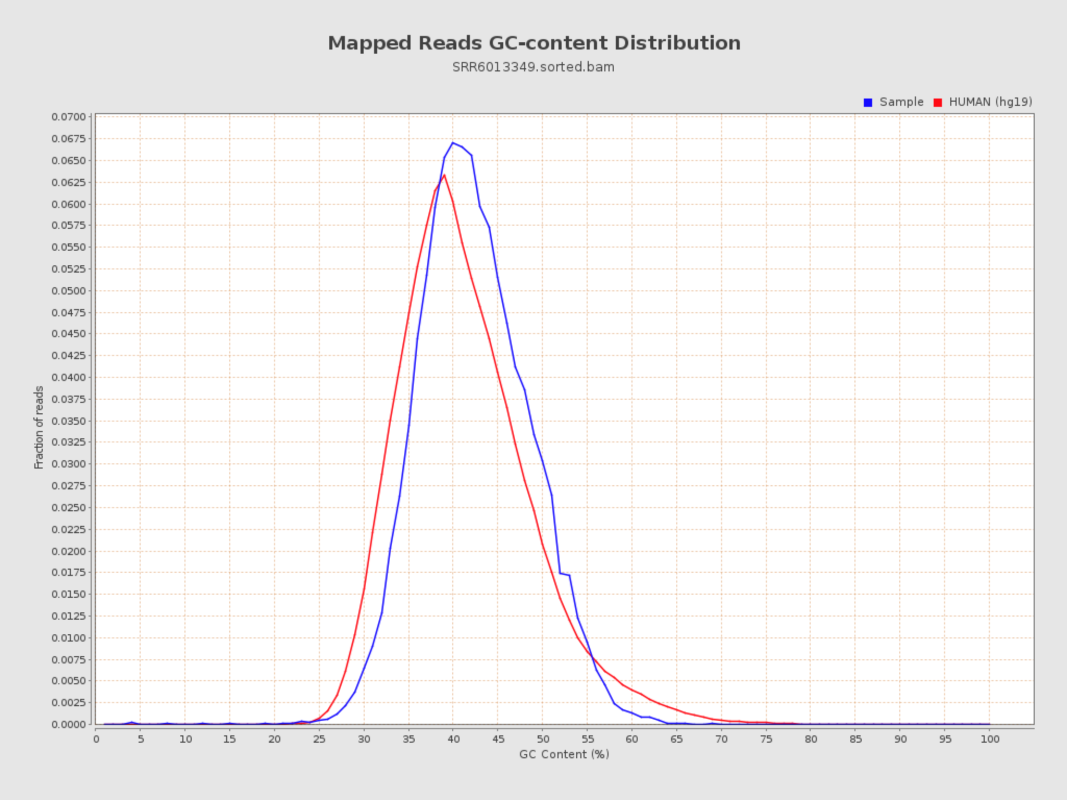
7. Results : Duplication Rate Histogram



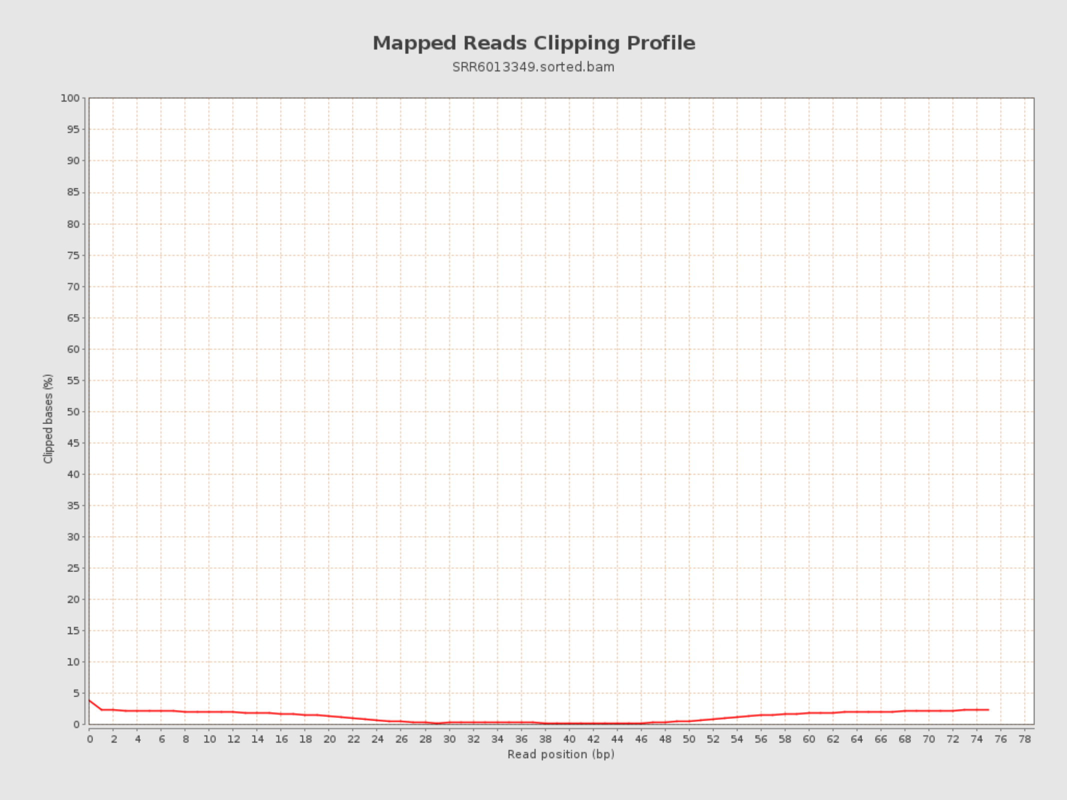
8. Results : Mapped Reads Nucleotide Content



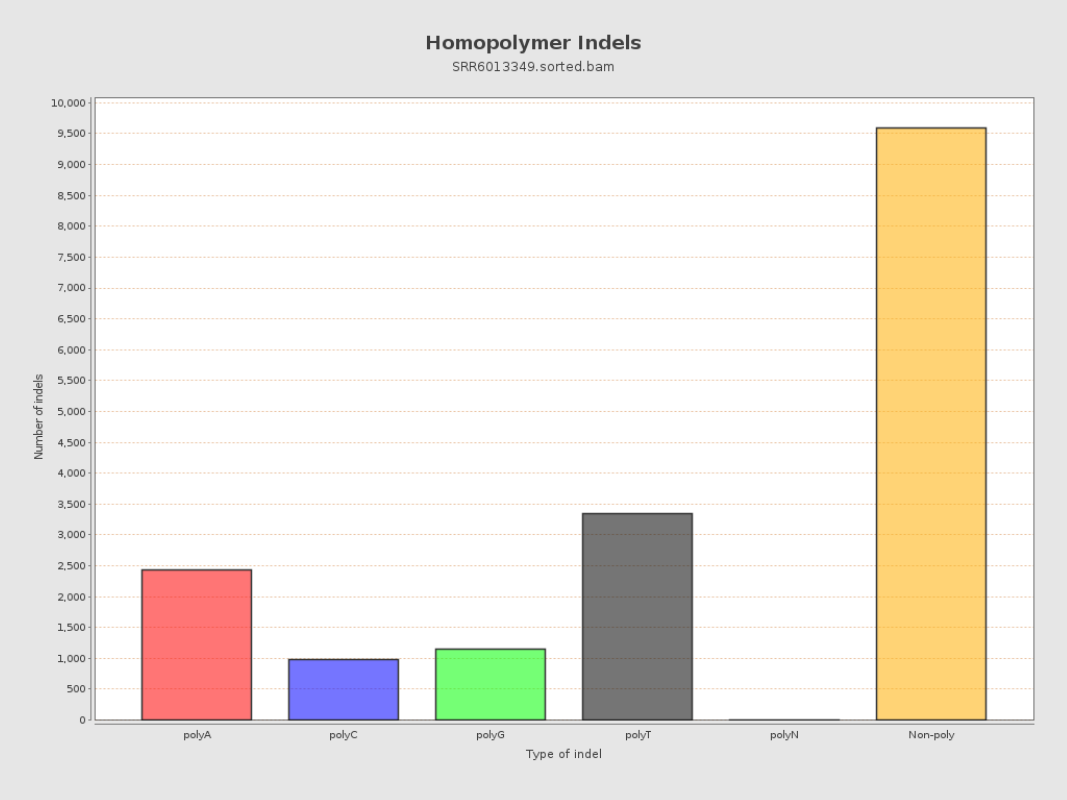
9. Results : Mapped Reads GC-content Distribution



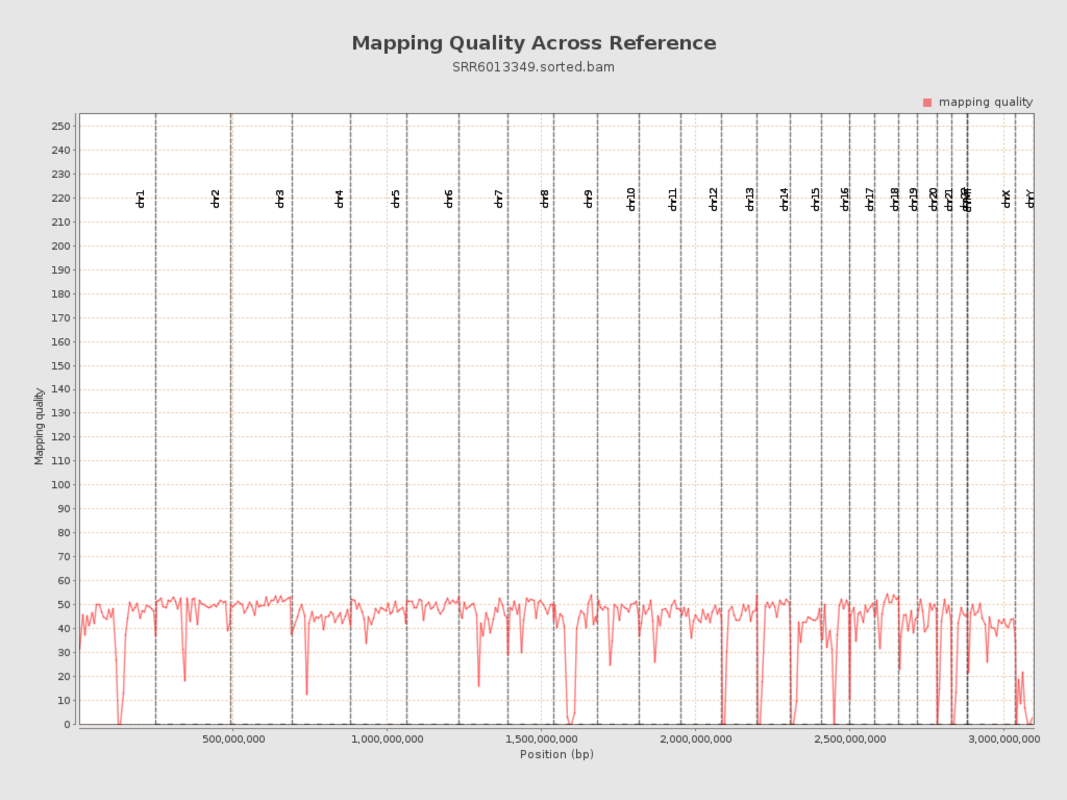
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram