Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 23:11:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013358.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_SRR6013358 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013358.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 23:11:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013358.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,504,906
Mapped reads	965,238 / 21.43%
Unmapped reads	3,539,668 / 78.57%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,352 / 0.07%
Read min/max/mean length	30 / 76 / 76.03
Duplicated reads (estimated)	132,598 / 2.94%
Duplication rate	11.16%
Clipped reads	826,593 / 18.35%

2.2. ACGT Content

Number/percentage of A's	14,681,798 / 28.03%
Number/percentage of C's	9,591,963 / 18.32%
Number/percentage of T's	16,136,505 / 30.81%
Number/percentage of G's	11,944,957 / 22.81%
Number/percentage of N's	16,050 / 0.03%
GC Percentage	41.12%

2.3. Coverage

Mean	0.0169

Standard Deviation	0.2058

2.4. Mapping Quality

Mean Mapping Quality	42.37

2.5. Mismatches and indels

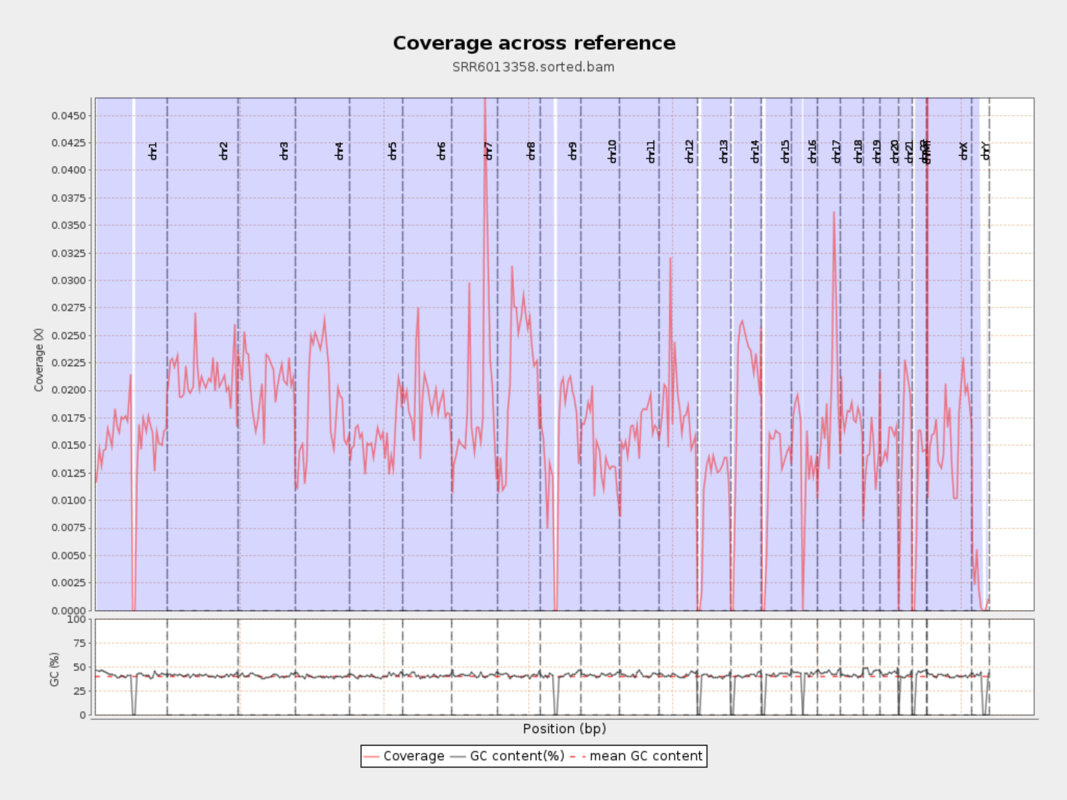
General error rate	0.94%
Mismatches	489,100
Insertions	3,256
Mapped reads with at least one insertion	0.34%
Deletions	12,562
Mapped reads with at least one deletion	1.29%
Homopolymer indels	46.18%

2.6. Chromosome stats

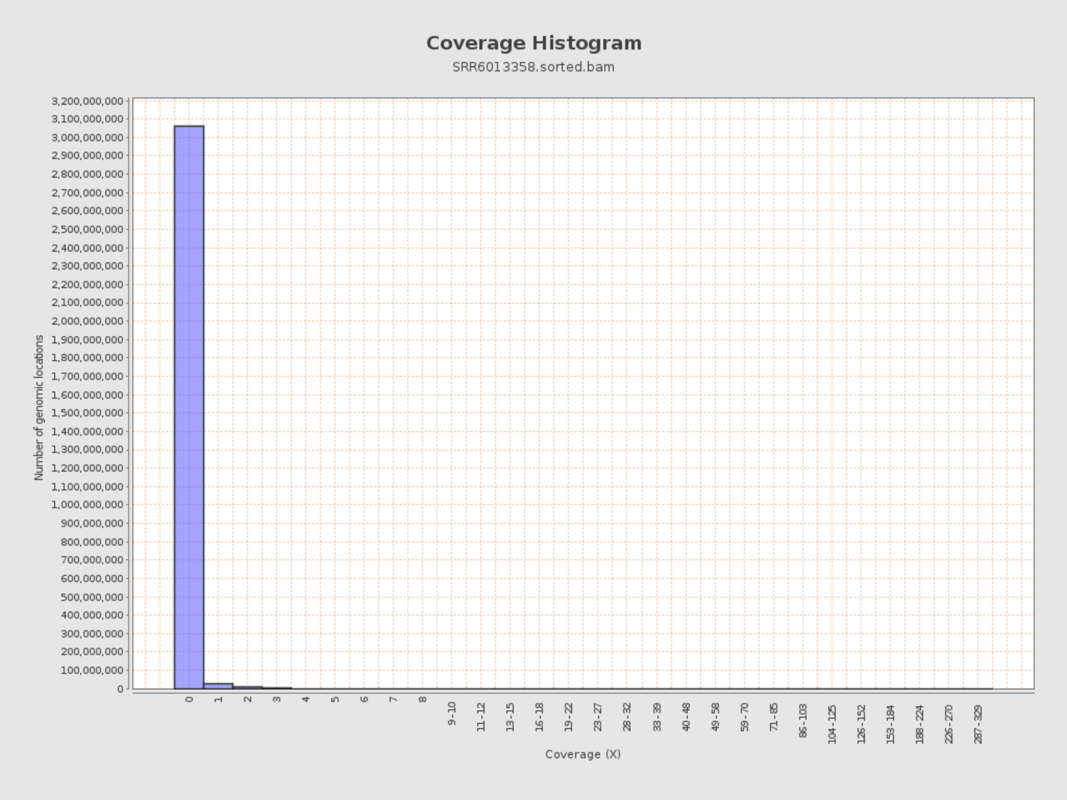
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3736766	0.015	0.2291
chr2	243199373	5160495	0.0212	0.2549
chr3	198022430	4136292	0.0209	0.2019
chr4	191154276	3631668	0.019	0.1995
chr5	180915260	2833442	0.0157	0.1736
chr6	171115067	3277966	0.0192	0.2095
chr7	159138663	3040552	0.0191	0.2828

chr8	146364022	3218456	0.022	0.2707
chr9	141213431	2110755	0.0149	0.185
chr10	135534747	1959107	0.0145	0.1849
chr11	135006516	2216340	0.0164	0.1859
chr12	133851895	2467592	0.0184	0.189
chr13	115169878	1239218	0.0108	0.1441
chr14	107349540	2110511	0.0197	0.1972
chr15	102531392	1248971	0.0122	0.1593
chr16	90354753	1229927	0.0136	0.1591
chr17	81195210	1582663	0.0195	0.1933
chr18	78077248	1393003	0.0178	0.2403
chr19	59128983	830162	0.014	0.1893
chr20	63025520	939185	0.0149	0.1723
chr21	48129895	780899	0.0162	0.1757
chr22	51304566	552156	0.0108	0.139
chrMT	16571	45455	2.743	3.3322
chrX	155270560	2537182	0.0163	0.1824
chrY	59373566	112542	0.0019	0.055

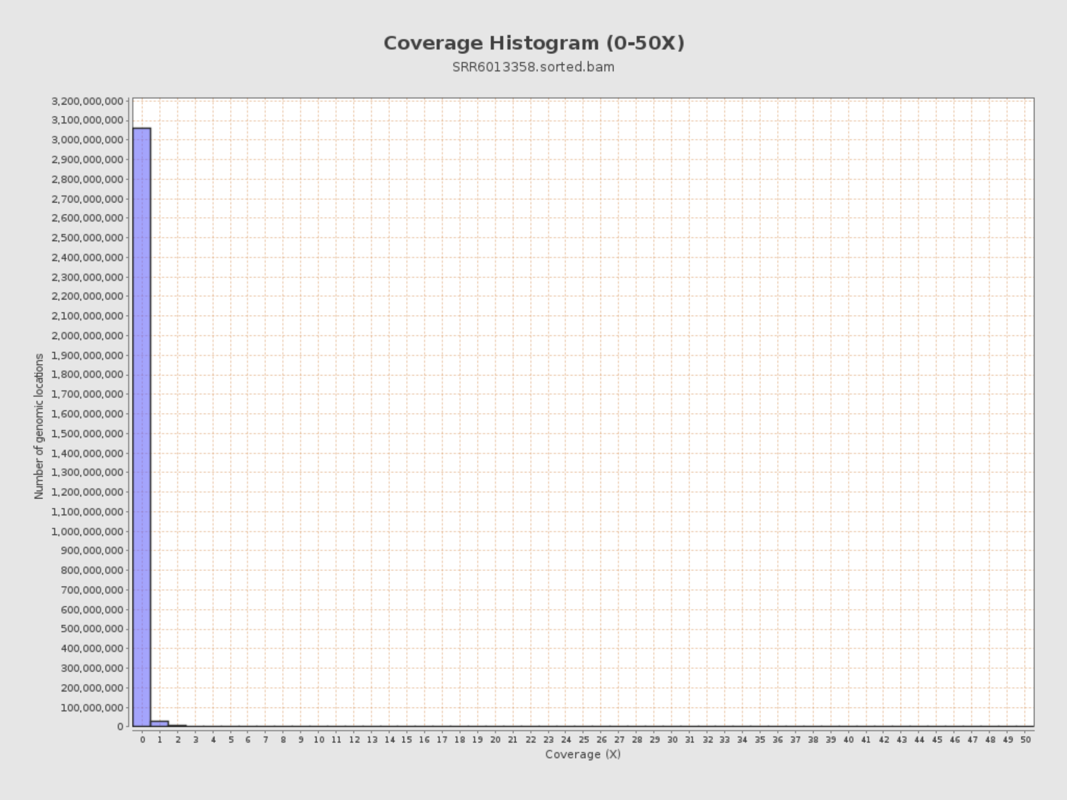
3. Results : Coverage across reference



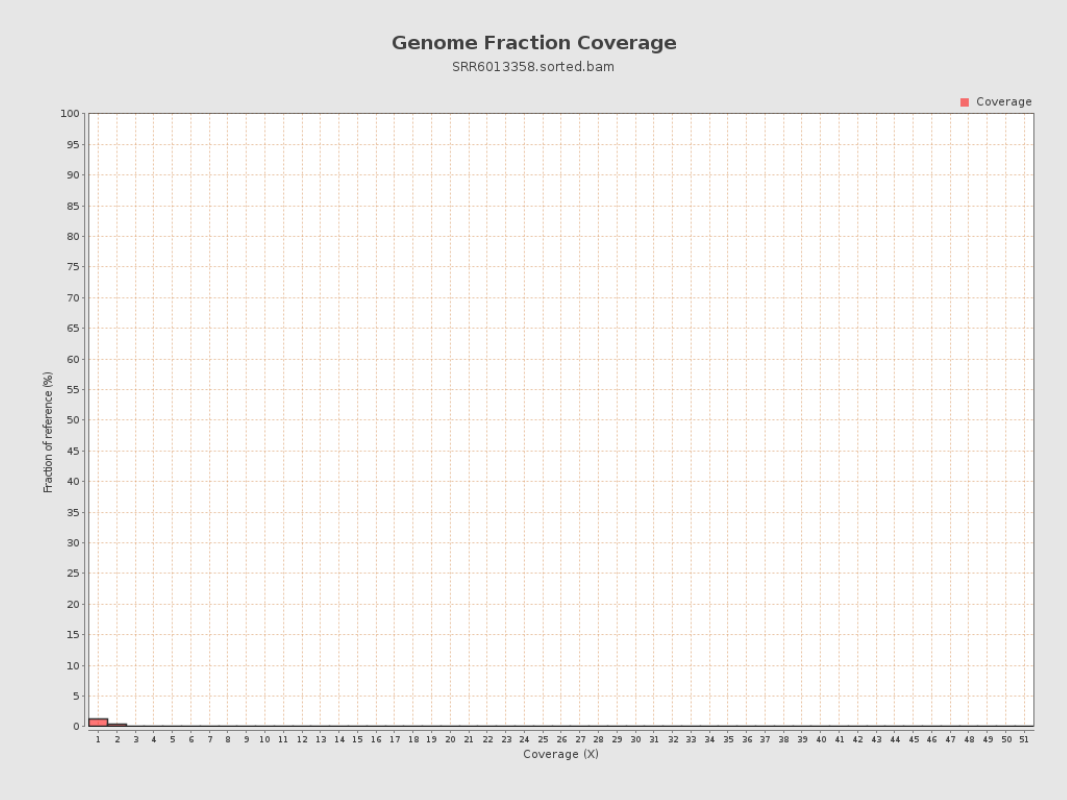
4. Results : Coverage Histogram



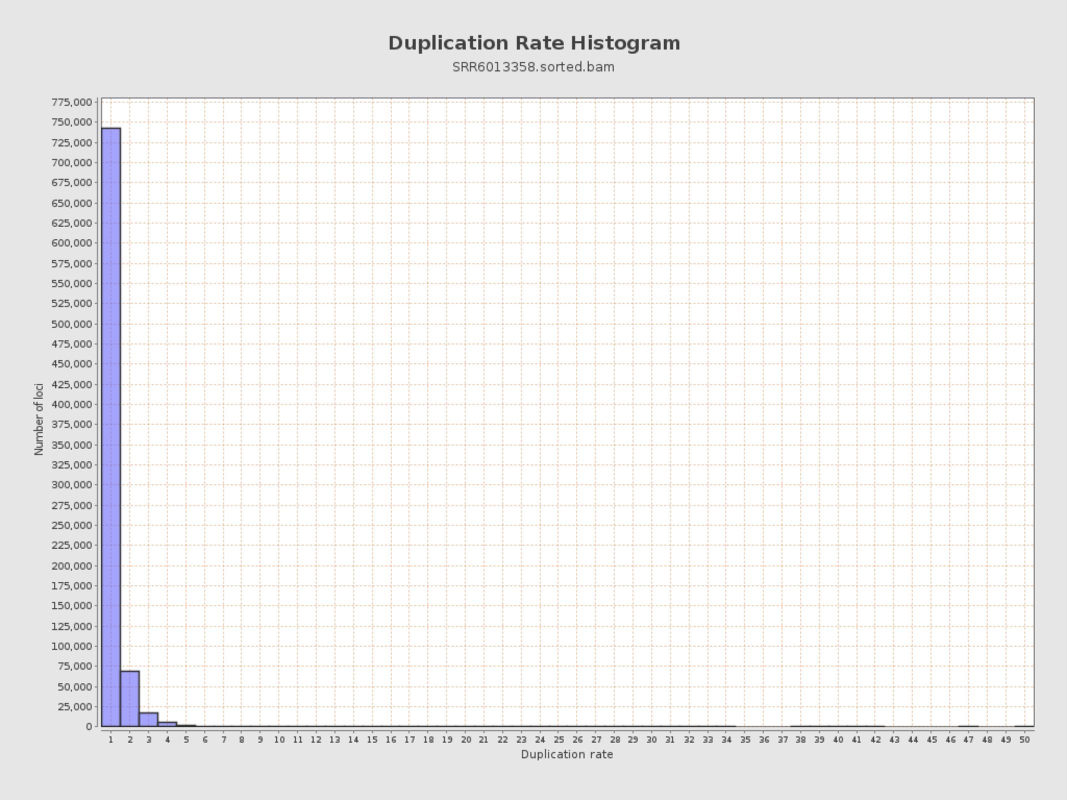
5. Results : Coverage Histogram (0-50X)



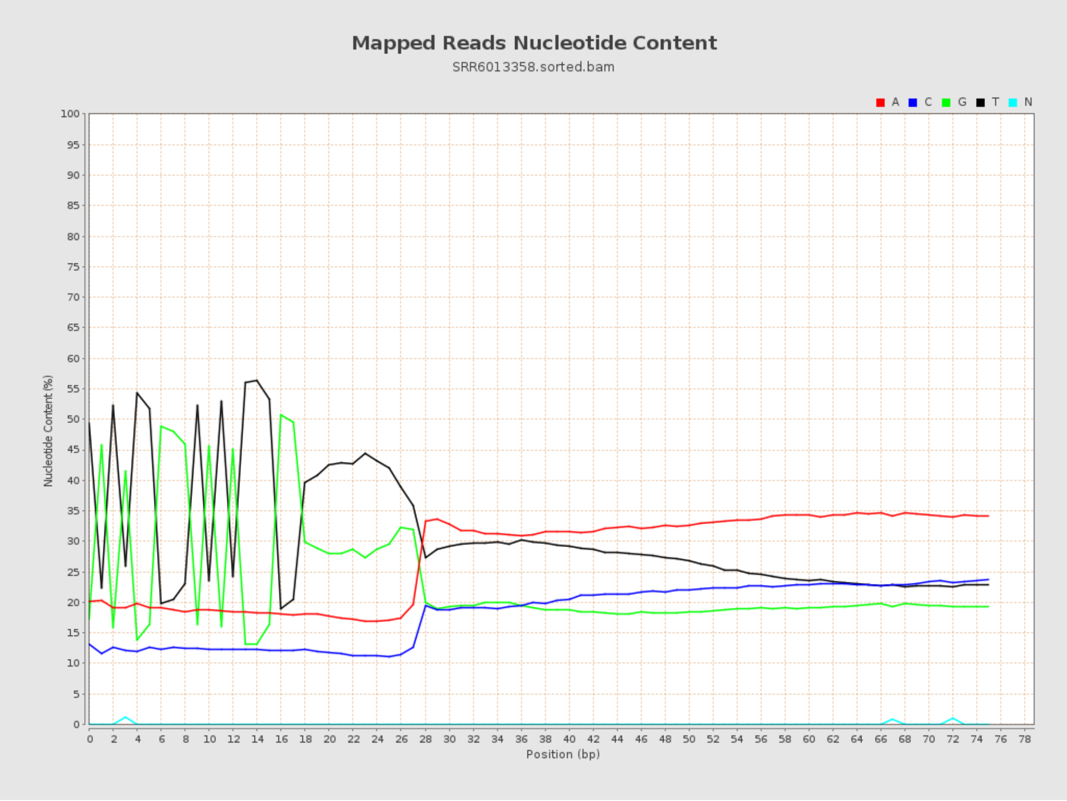
6. Results : Genome Fraction Coverage



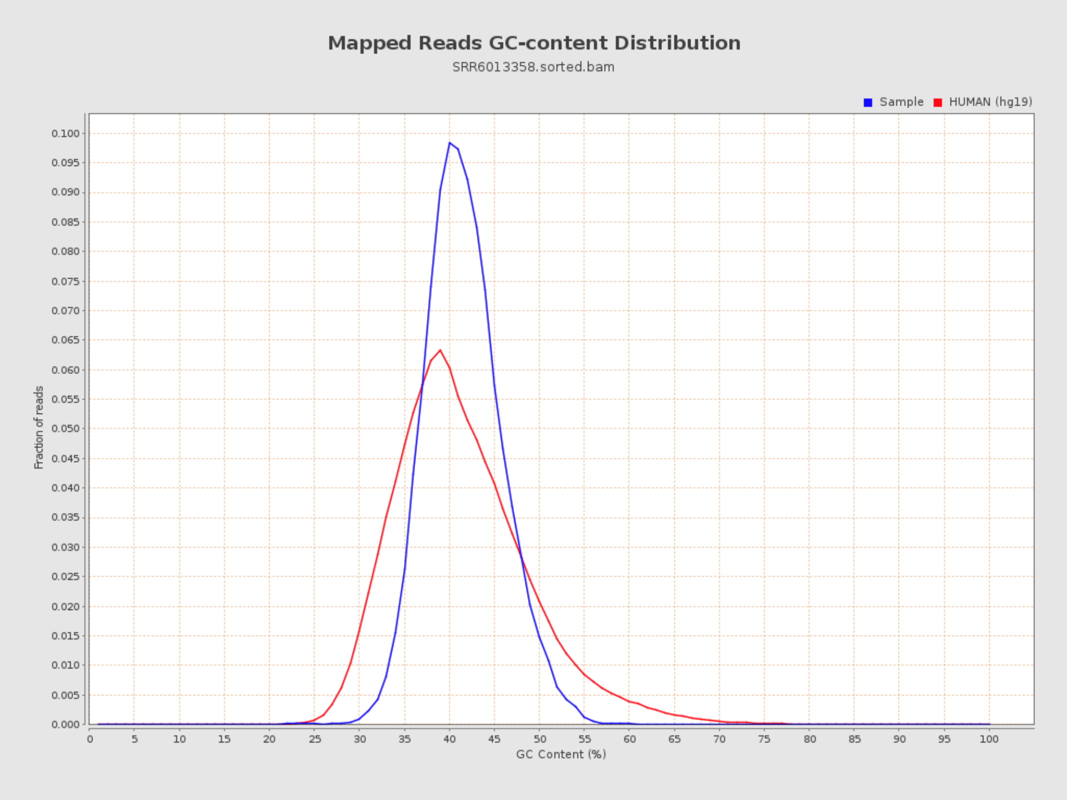
7. Results : Duplication Rate Histogram



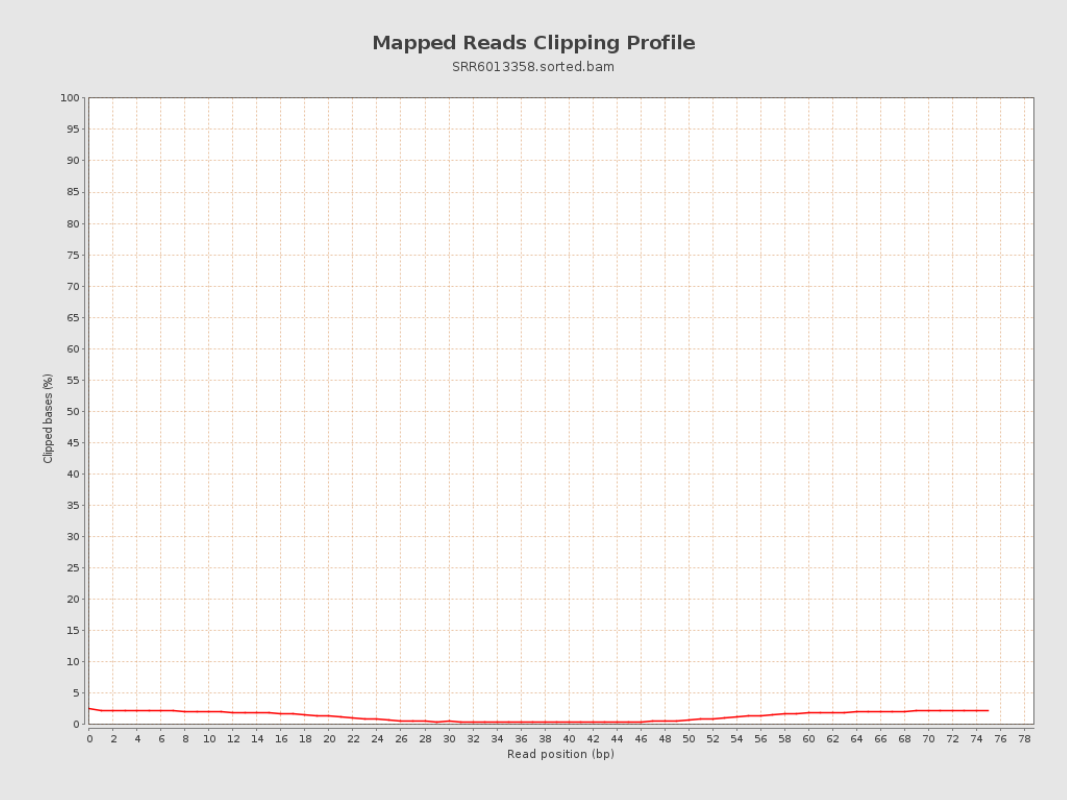
8. Results : Mapped Reads Nucleotide Content



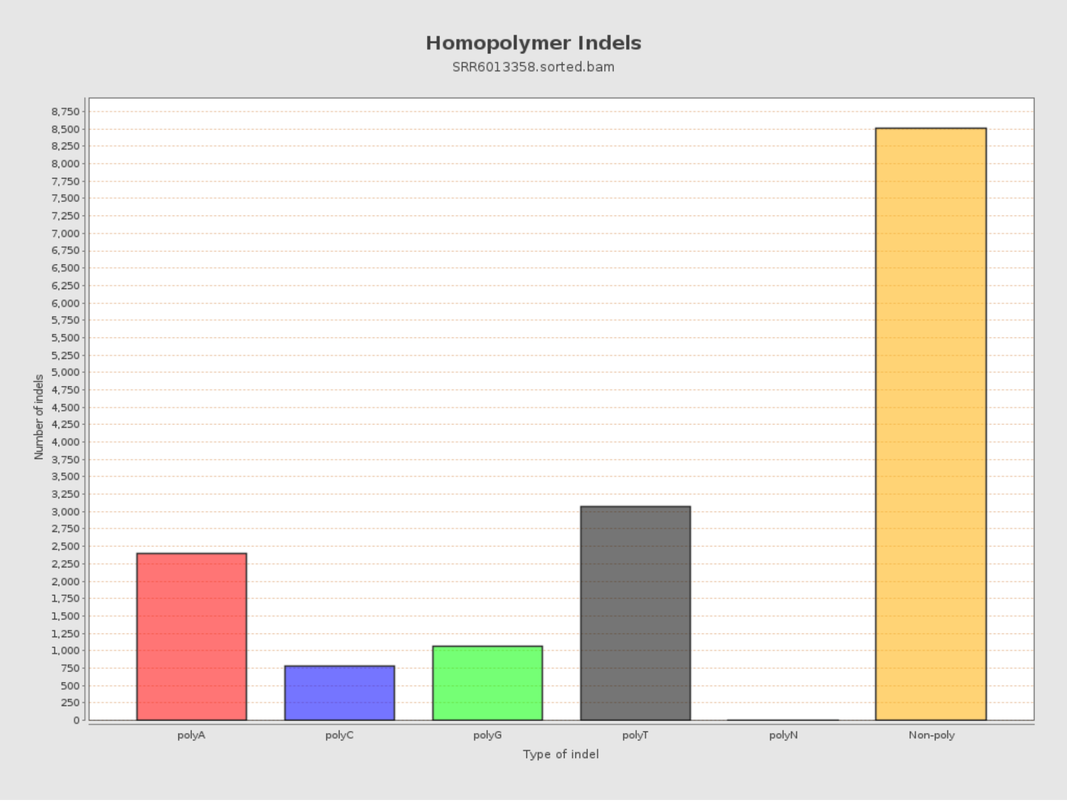
9. Results : Mapped Reads GC-content Distribution



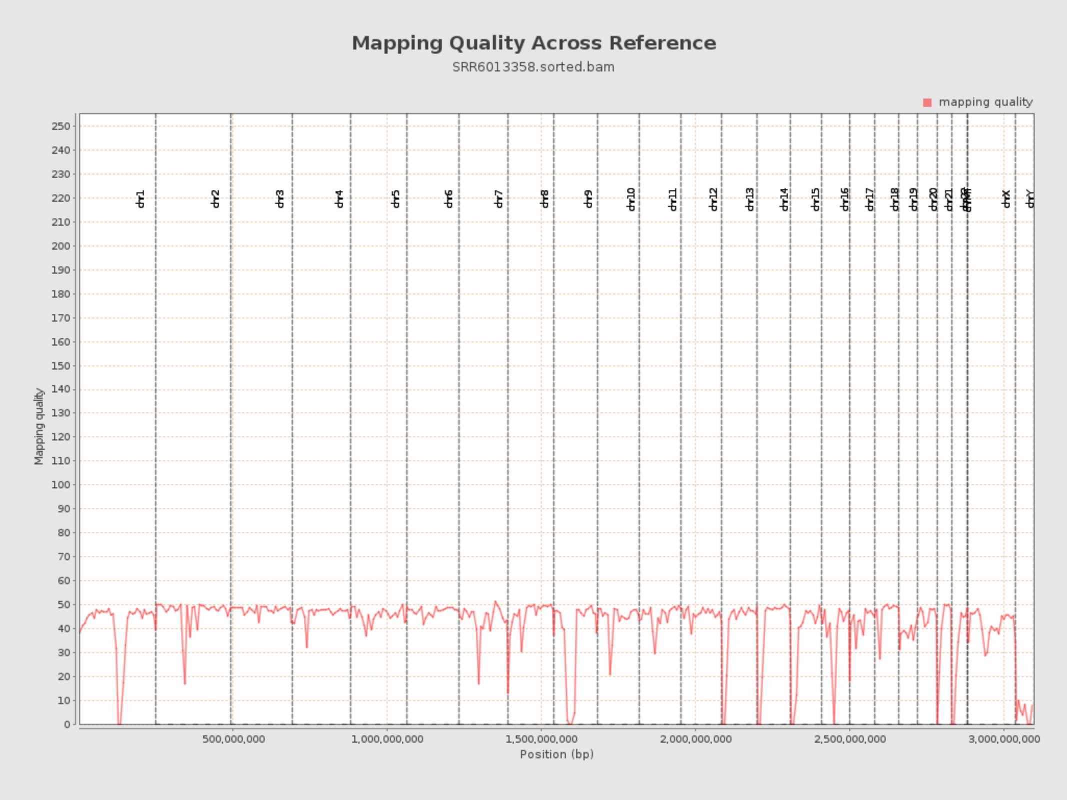
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram