Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 17:10:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013231.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_SRR6013231 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013231.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 17:10:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013231.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,405,869
Mapped reads	1,273,475 / 90.58%
Unmapped reads	132,394 / 9.42%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,970 / 0.42%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	42,240 / 3%
Duplication rate	2.69%
Clipped reads	435,672 / 30.99%

2.2. ACGT Content

Number/percentage of A's	25,163,771 / 28.58%
Number/percentage of C's	16,165,628 / 18.36%
Number/percentage of T's	28,322,045 / 32.17%
Number/percentage of G's	18,375,252 / 20.87%
Number/percentage of N's	19,334 / 0.02%
GC Percentage	39.23%

2.3. Coverage

Mean	0.0285

Standard Deviation	0.2631

2.4. Mapping Quality

Mean Mapping Quality	46.97

2.5. Mismatches and indels

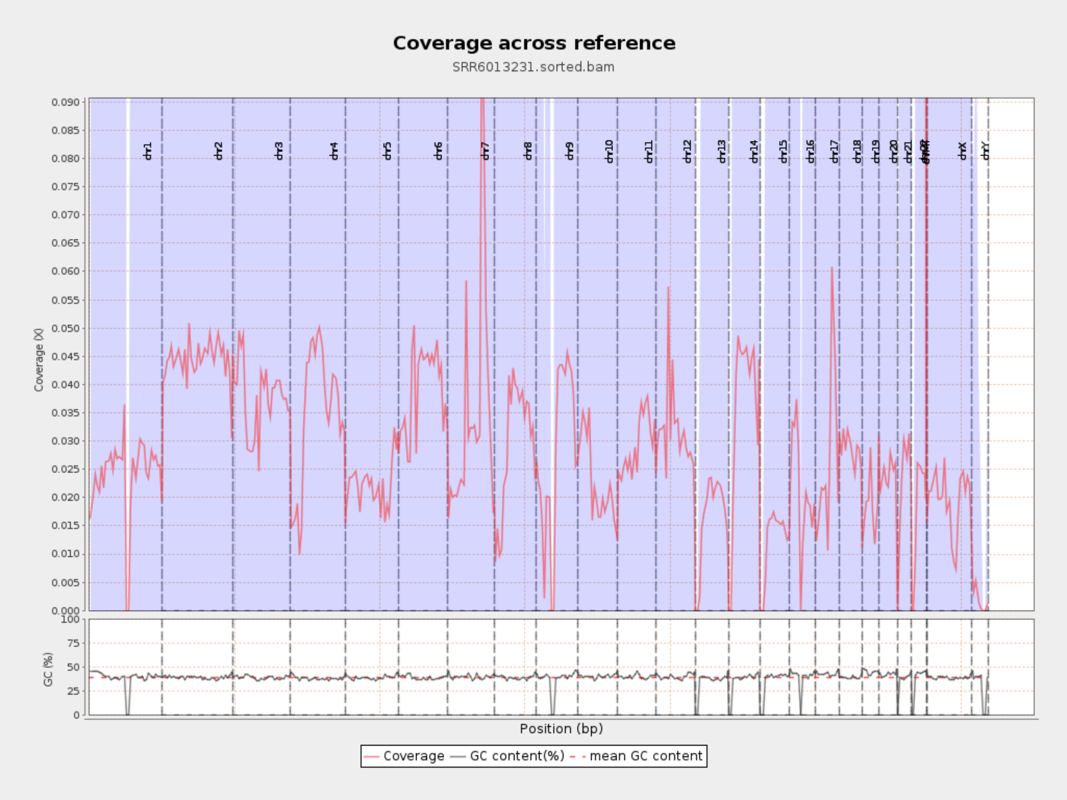
General error rate	0.79%
Mismatches	681,164
Insertions	6,676
Mapped reads with at least one insertion	0.52%
Deletions	21,824
Mapped reads with at least one deletion	1.7%
Homopolymer indels	47.42%

2.6. Chromosome stats

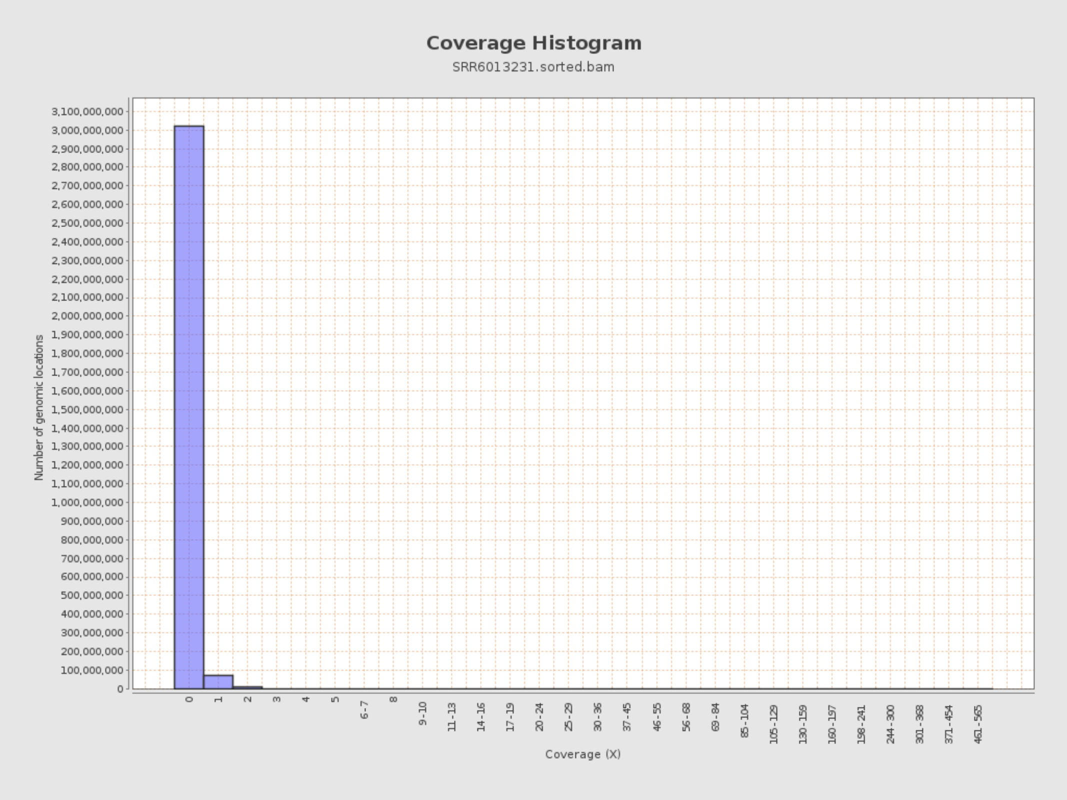
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5991819	0.024	0.3177
chr2	243199373	10833627	0.0445	0.3496
chr3	198022430	7487492	0.0378	0.2165
chr4	191154276	6604351	0.0345	0.2095
chr5	180915260	4029882	0.0223	0.1656
chr6	171115067	6704189	0.0392	0.2525
chr7	159138663	5773358	0.0363	0.5244

chr8	146364022	4327799	0.0296	0.3405
chr9	141213431	3906235	0.0277	0.2278
chr10	135534747	3140064	0.0232	0.2439
chr11	135006516	3937077	0.0292	0.2064
chr12	133851895	4273442	0.0319	0.2001
chr13	115169878	1884976	0.0164	0.1429
chr14	107349540	3855237	0.0359	0.2214
chr15	102531392	1272043	0.0124	0.1235
chr16	90354753	1933889	0.0214	0.1749
chr17	81195210	2129265	0.0262	0.182
chr18	78077248	2234644	0.0286	0.3843
chr19	59128983	1116736	0.0189	0.2384
chr20	63025520	1491511	0.0237	0.1725
chr21	48129895	1084244	0.0225	0.1704
chr22	51304566	887397	0.0173	0.1441
chrMT	16571	47542	2.869	2.4005
chrX	155270560	3018865	0.0194	0.1616
chrY	59373566	117598	0.002	0.0556

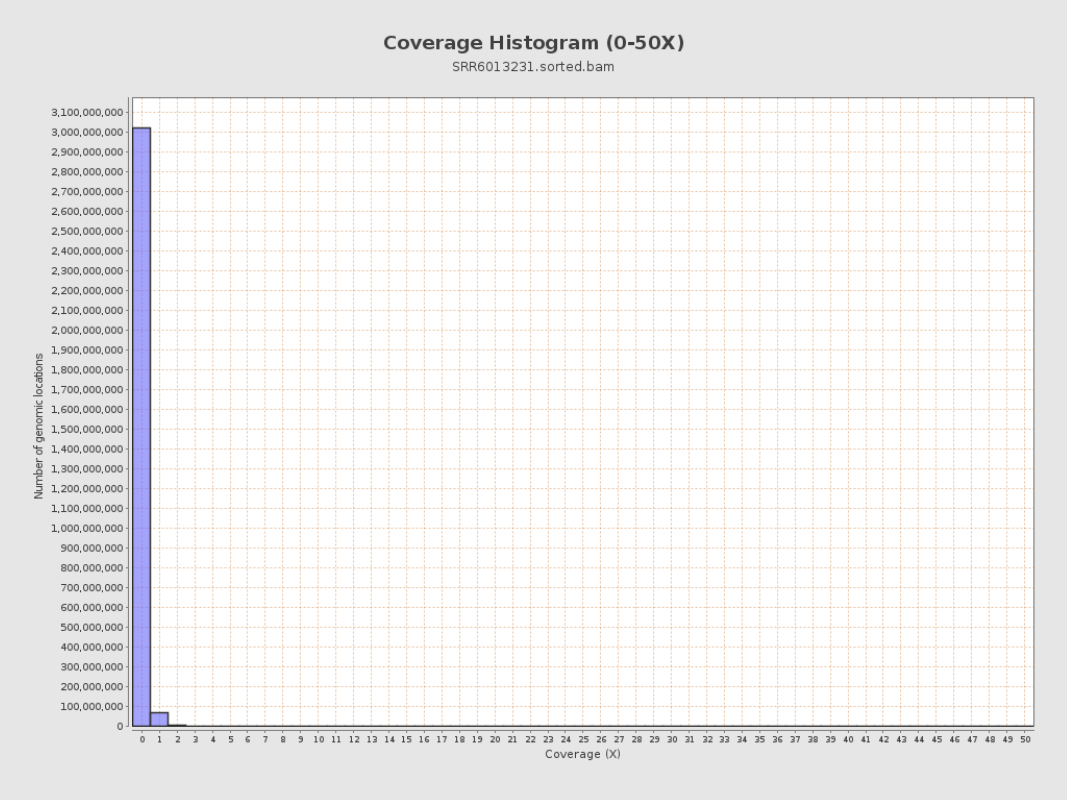
3. Results : Coverage across reference



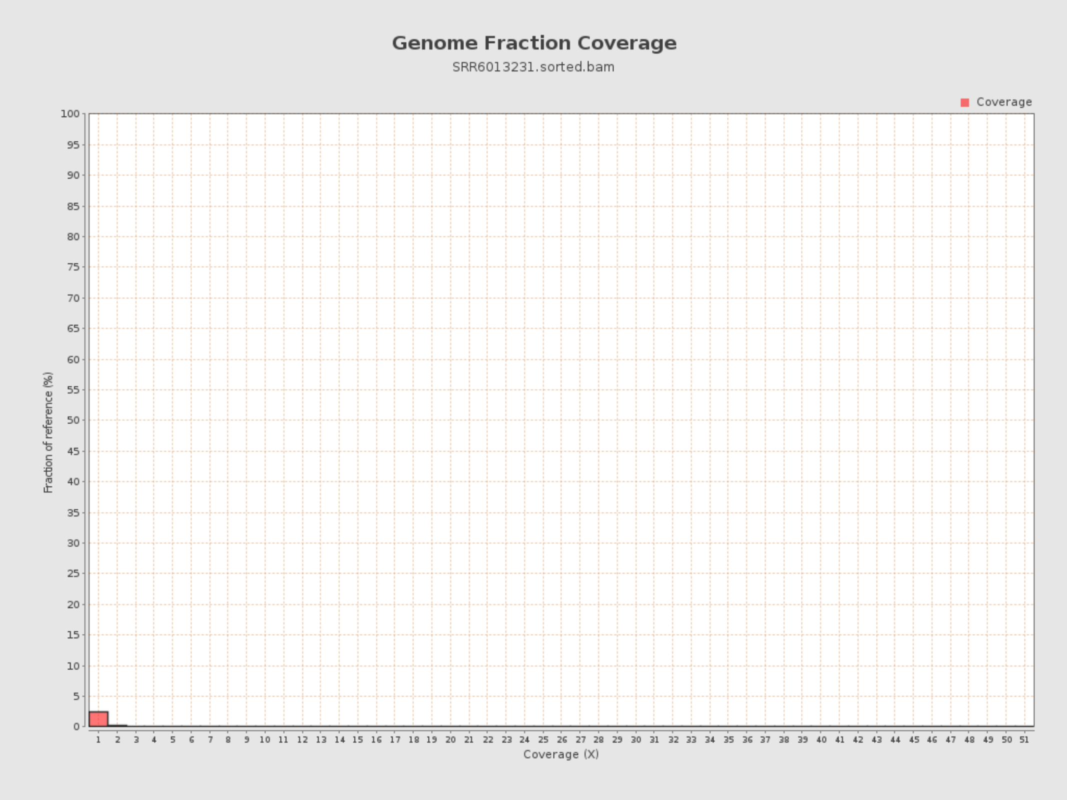
4. Results : Coverage Histogram



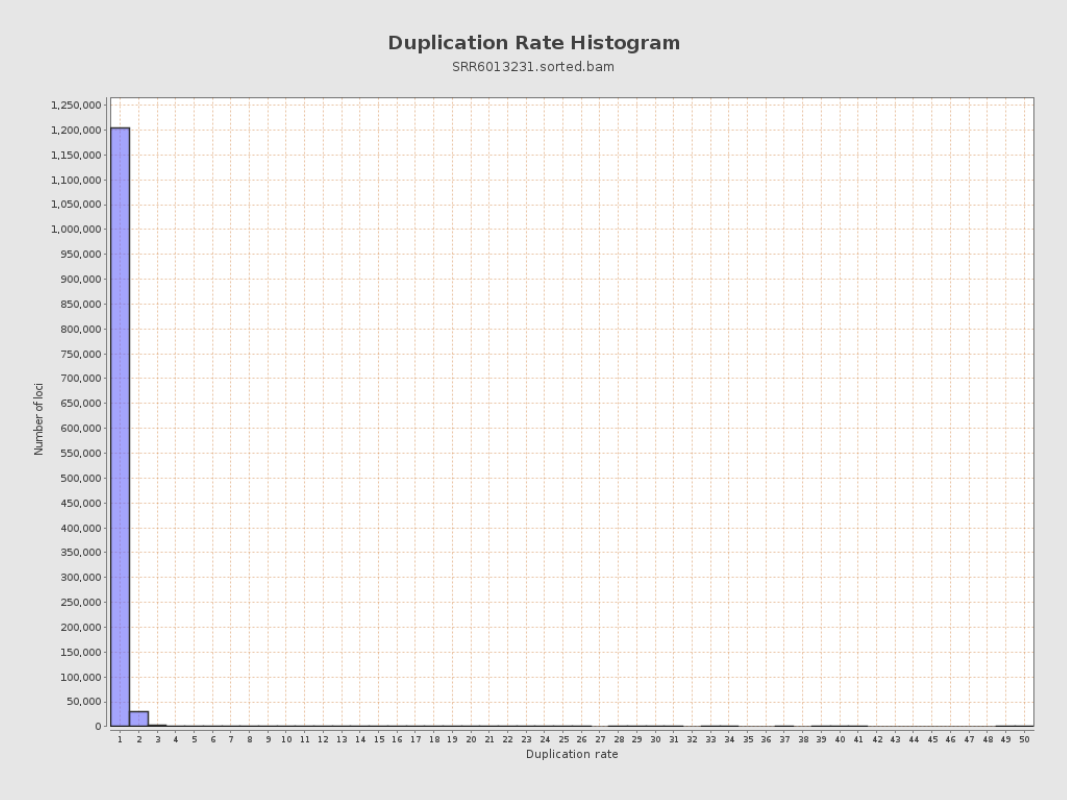
5. Results : Coverage Histogram (0-50X)



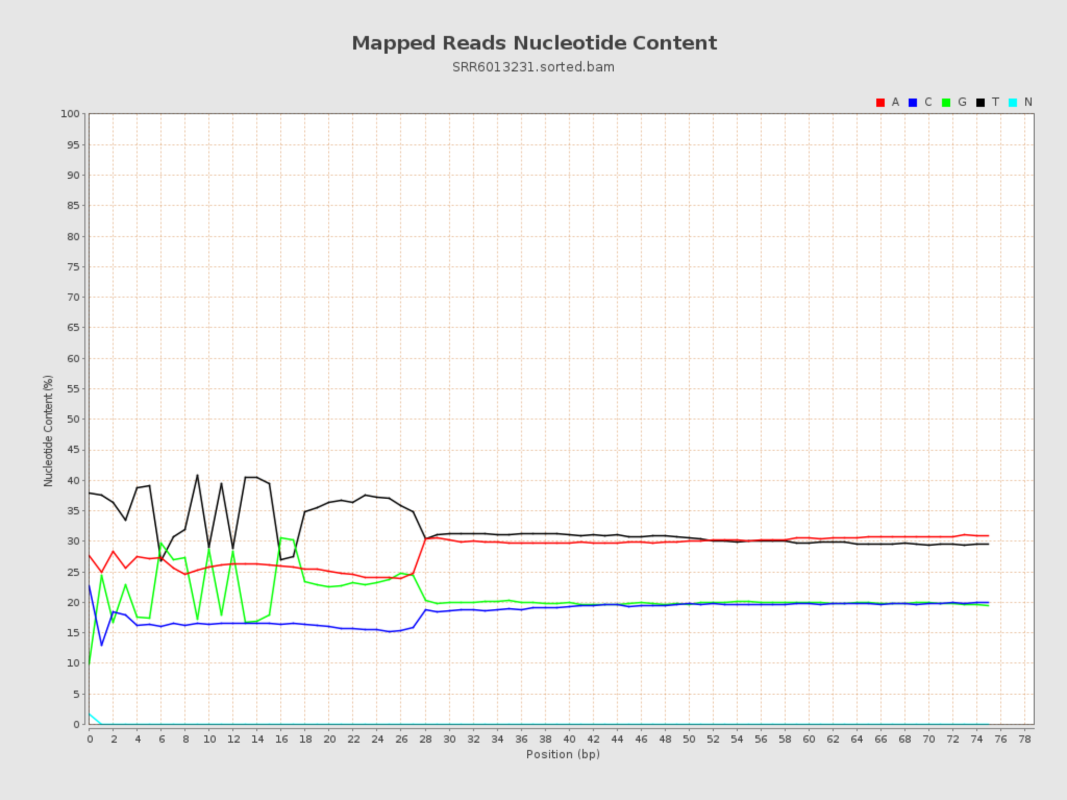
6. Results : Genome Fraction Coverage



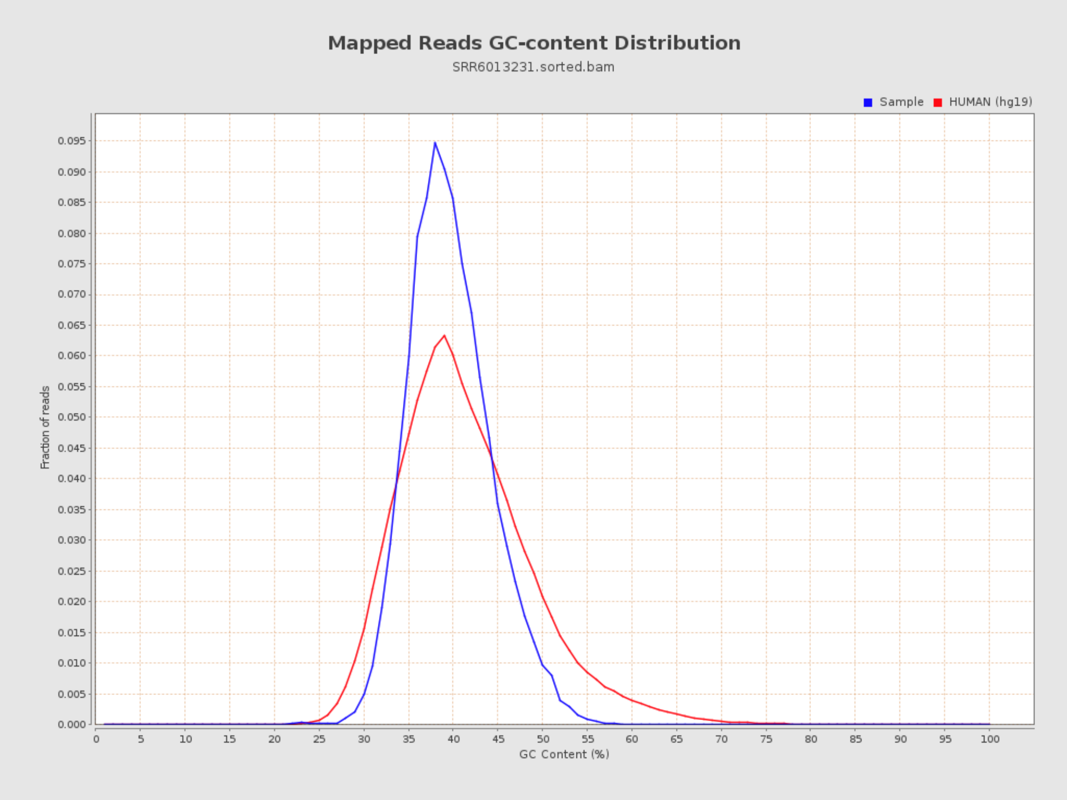
7. Results : Duplication Rate Histogram



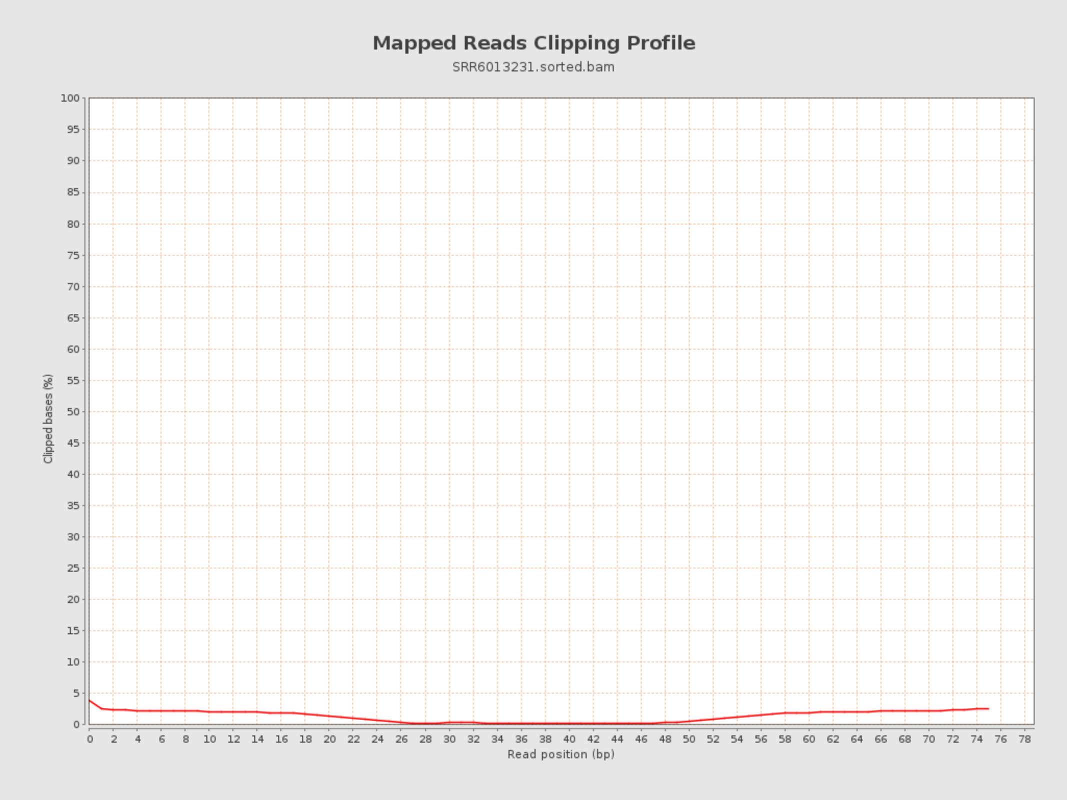
8. Results : Mapped Reads Nucleotide Content



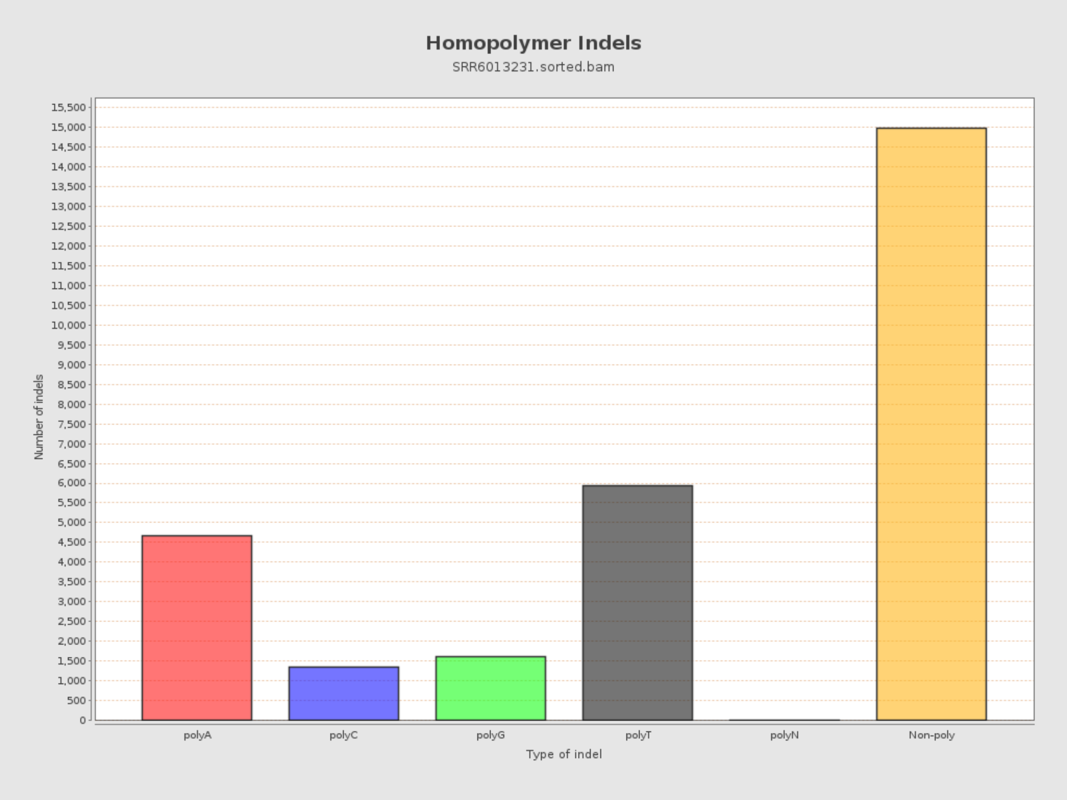
9. Results : Mapped Reads GC-content Distribution



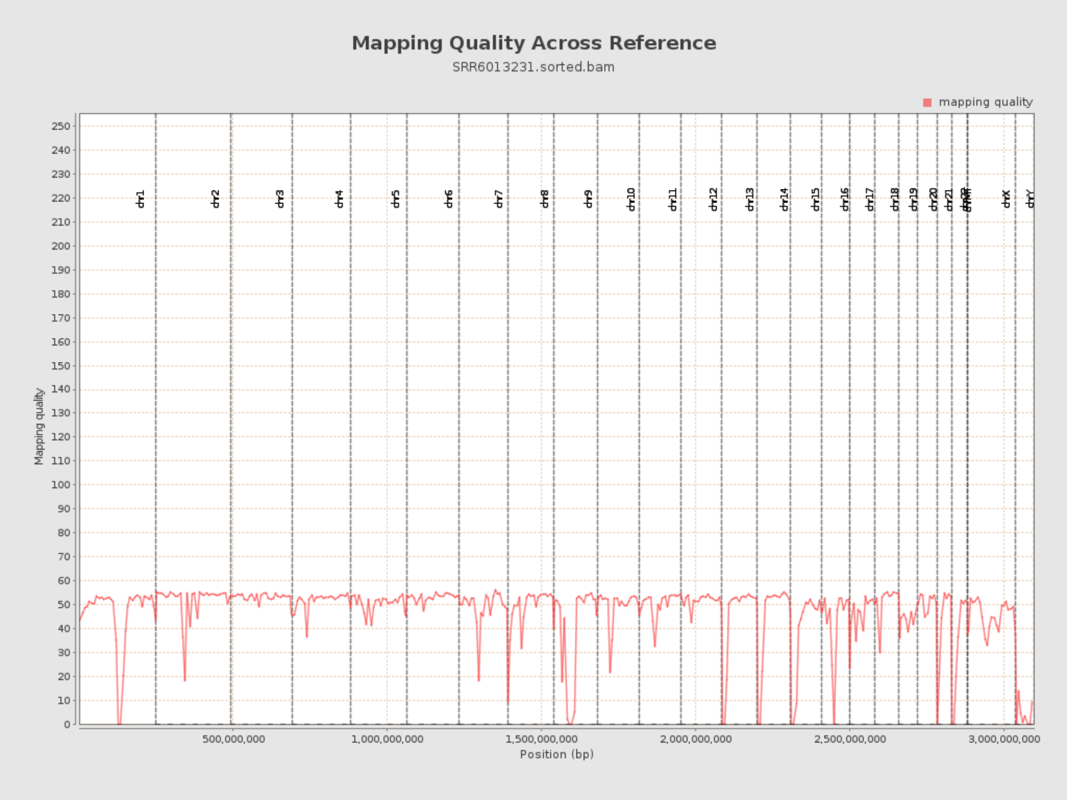
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram