Qualimap Analysis Results

BAM QC analysis
Generated by Qualimap v.2.2.2-dev
2024/09/14 14:14:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013174.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_SRR6013174 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013174.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 14:14:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013174.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,636,298
Mapped reads	2,384,344 / 90.44%
Unmapped reads	251,954 / 9.56%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,955 / 0.57%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	74,182 / 2.81%
Duplication rate	2.23%
Clipped reads	1,201,203 / 45.56%

2.2. ACGT Content

Number/percentage of A's	42,462,337 / 27.31%
Number/percentage of C's	29,958,207 / 19.27%
Number/percentage of T's	47,139,212 / 30.32%
Number/percentage of G's	35,893,966 / 23.08%
Number/percentage of N's	36,907 / 0.02%
GC Percentage	42.35%

2.3. Coverage

Mean	0.0502

Standard Deviation	0.4048

2.4. Mapping Quality

Mean Mapping Quality	44.12

2.5. Mismatches and indels

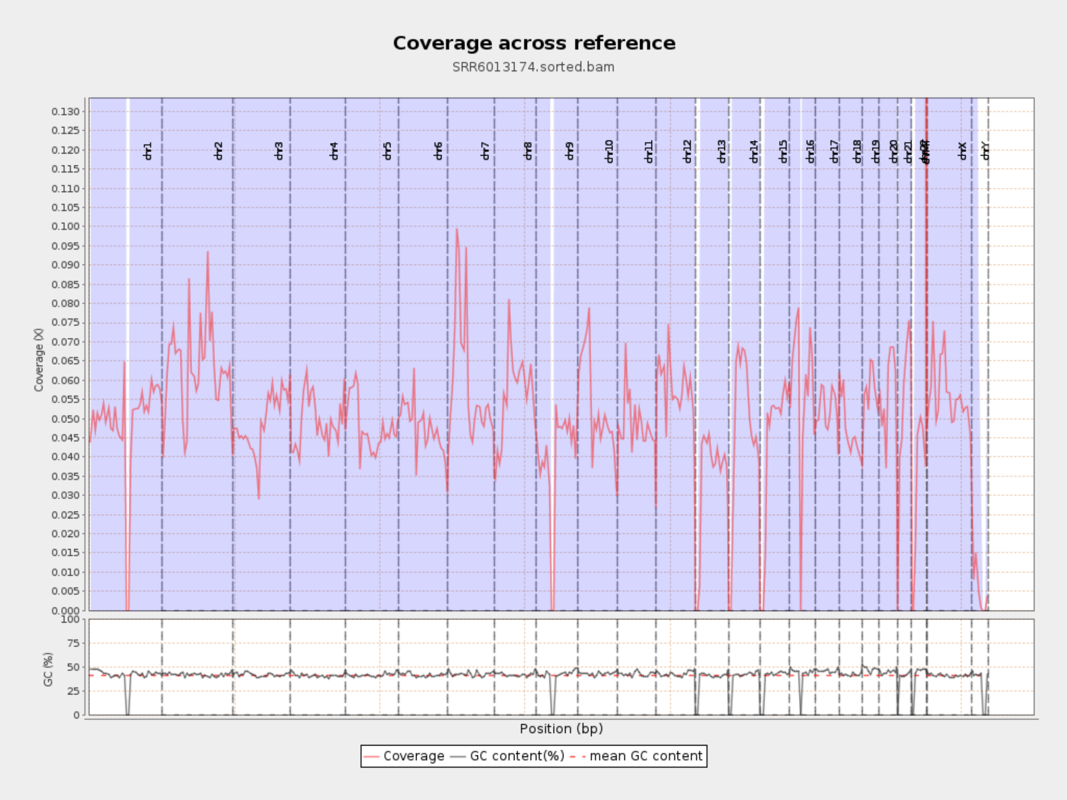
General error rate	0.81%
Mismatches	1,246,900
Insertions	10,867
Mapped reads with at least one insertion	0.45%
Deletions	39,198
Mapped reads with at least one deletion	1.63%
Homopolymer indels	44.68%

2.6. Chromosome stats

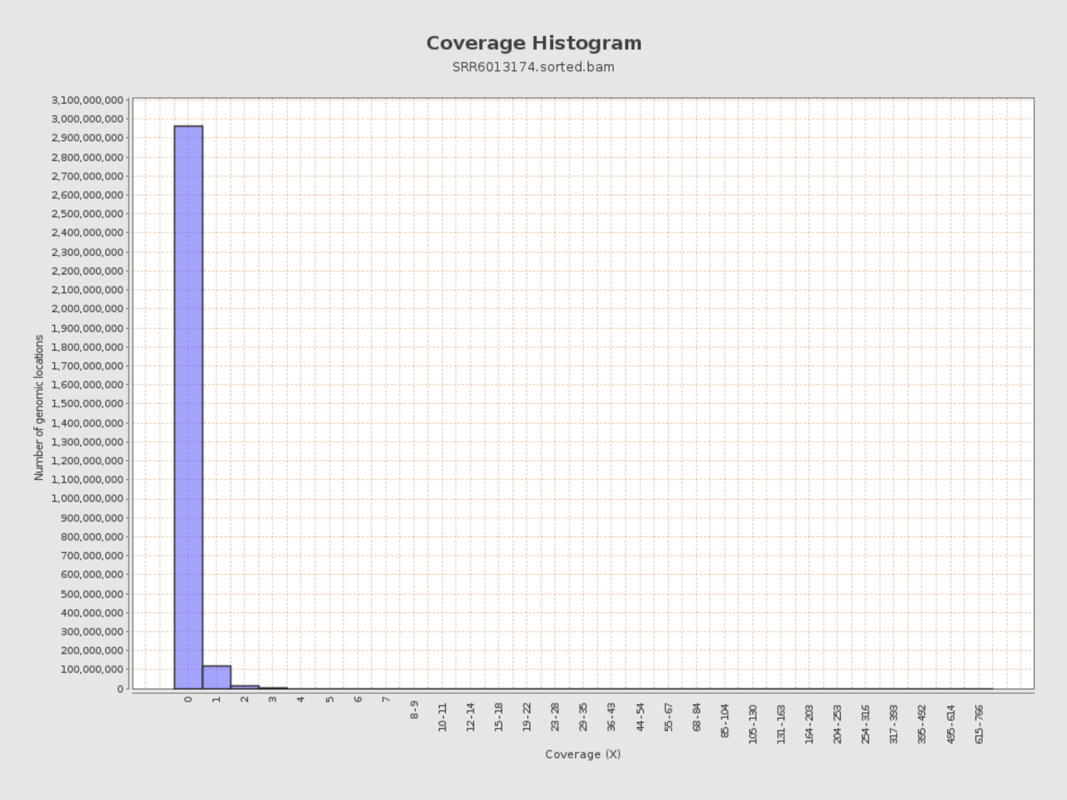
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12146586	0.0487	0.6154
chr2	243199373	15367115	0.0632	0.5198
chr3	198022430	9668469	0.0488	0.245
chr4	191154276	9371782	0.049	0.2545
chr5	180915260	8649053	0.0478	0.2452
chr6	171115067	8158799	0.0477	0.3064
chr7	159138663	9542816	0.06	0.7509

chr8	146364022	8253197	0.0564	0.3806
chr9	141213431	5530784	0.0392	0.3436
chr10	135534747	7292145	0.0538	0.409
chr11	135006516	6543068	0.0485	0.3149
chr12	133851895	7836484	0.0585	0.2723
chr13	115169878	3901078	0.0339	0.2094
chr14	107349540	5068660	0.0472	0.2635
chr15	102531392	4421168	0.0431	0.2375
chr16	90354753	5226389	0.0578	0.3075
chr17	81195210	4228889	0.0521	0.2814
chr18	78077248	3683145	0.0472	0.6184
chr19	59128983	3378720	0.0571	0.5289
chr20	63025520	3555673	0.0564	0.2688
chr21	48129895	2574617	0.0535	0.2747
chr22	51304566	1633877	0.0318	0.1972
chrMT	16571	437418	26.3966	19.2568
chrX	155270560	8730919	0.0562	0.2972
chrY	59373566	357579	0.006	0.1181

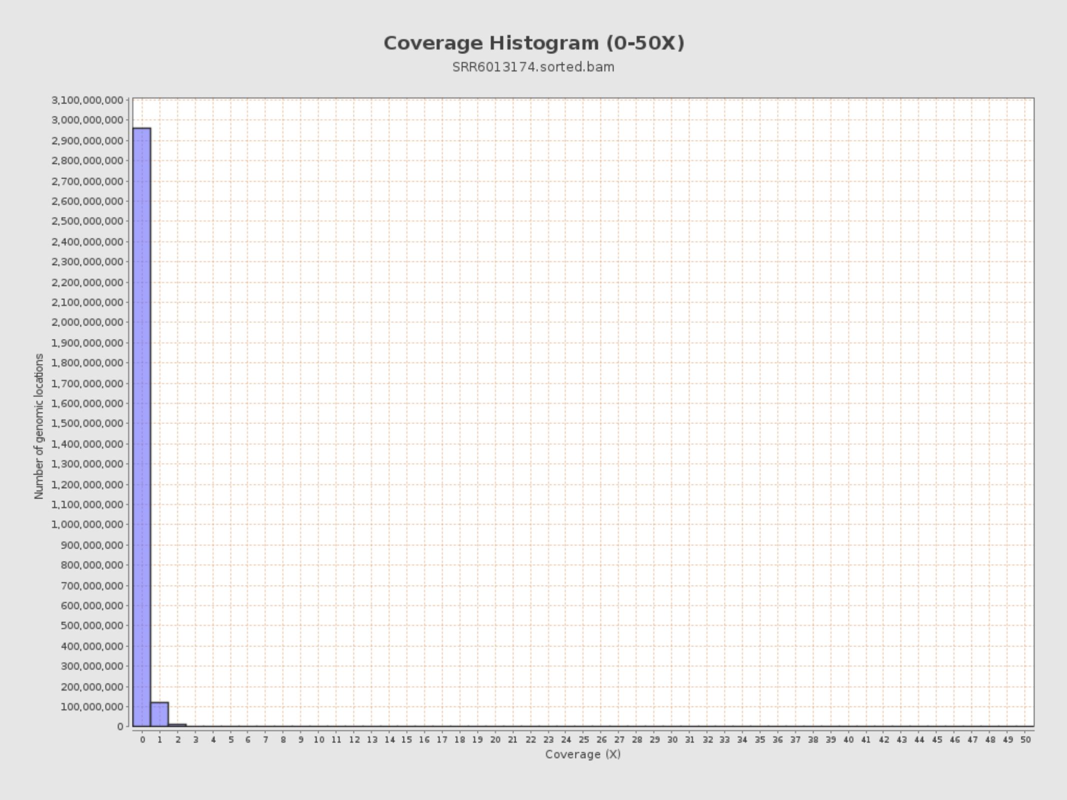
3. Results : Coverage across reference



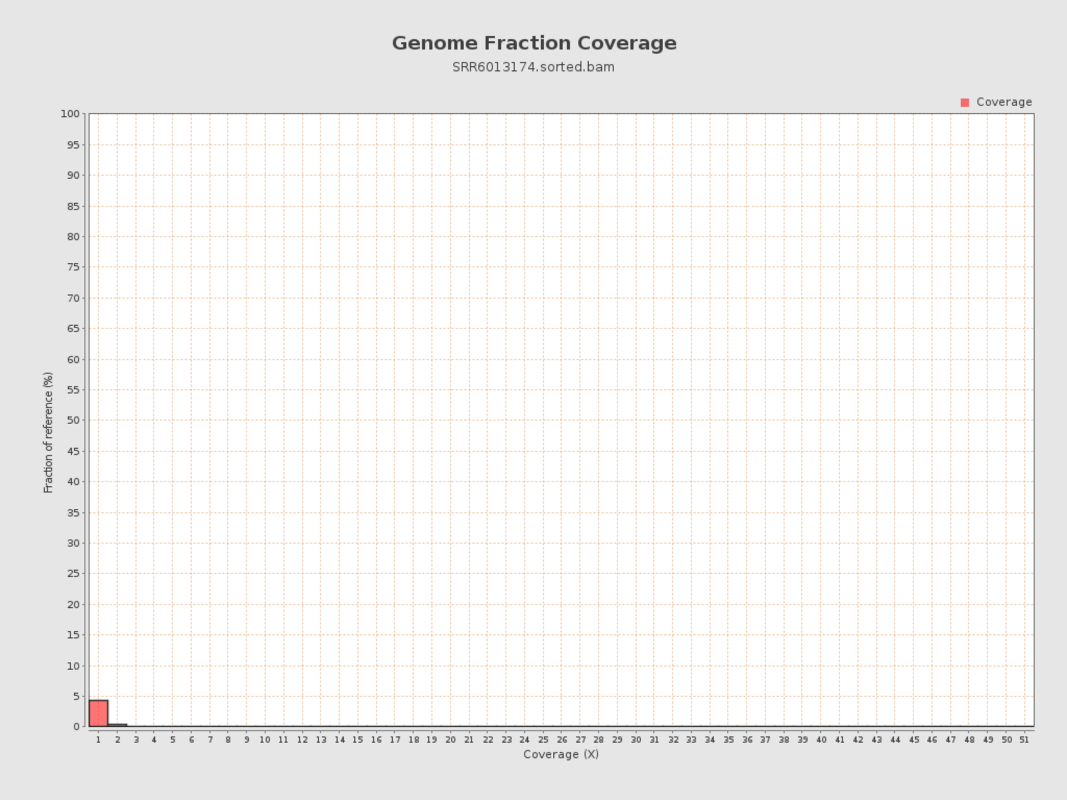
4. Results : Coverage Histogram



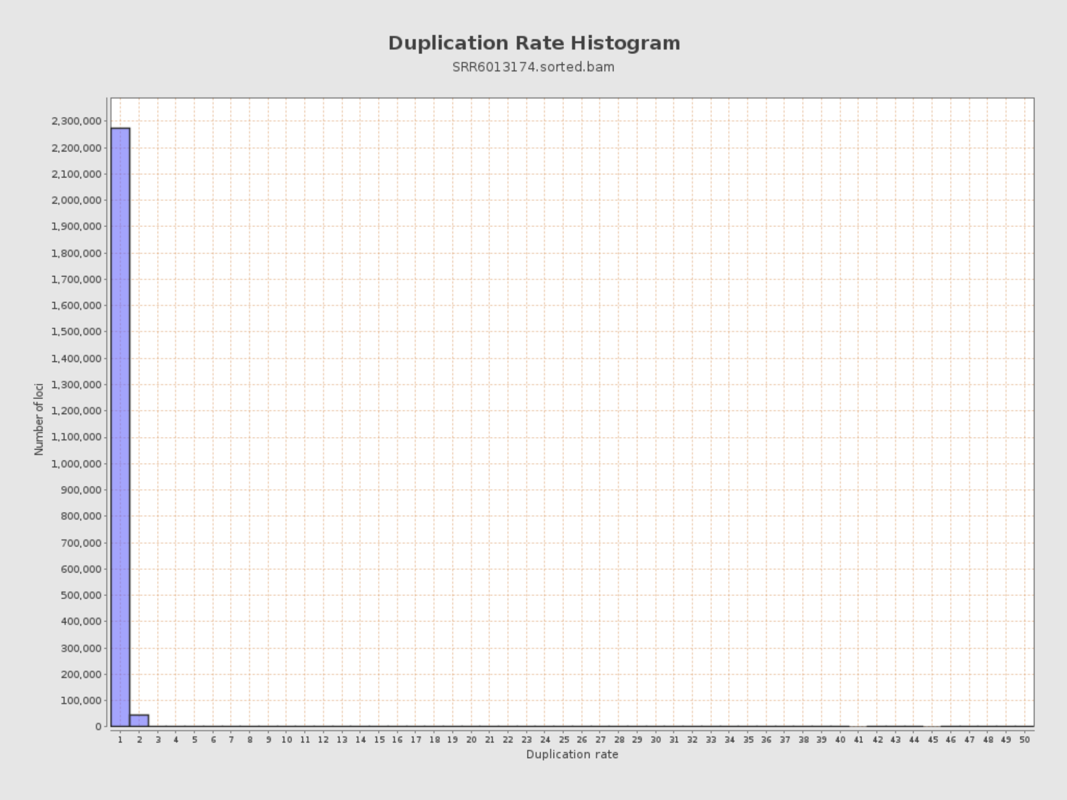
5. Results : Coverage Histogram (0-50X)



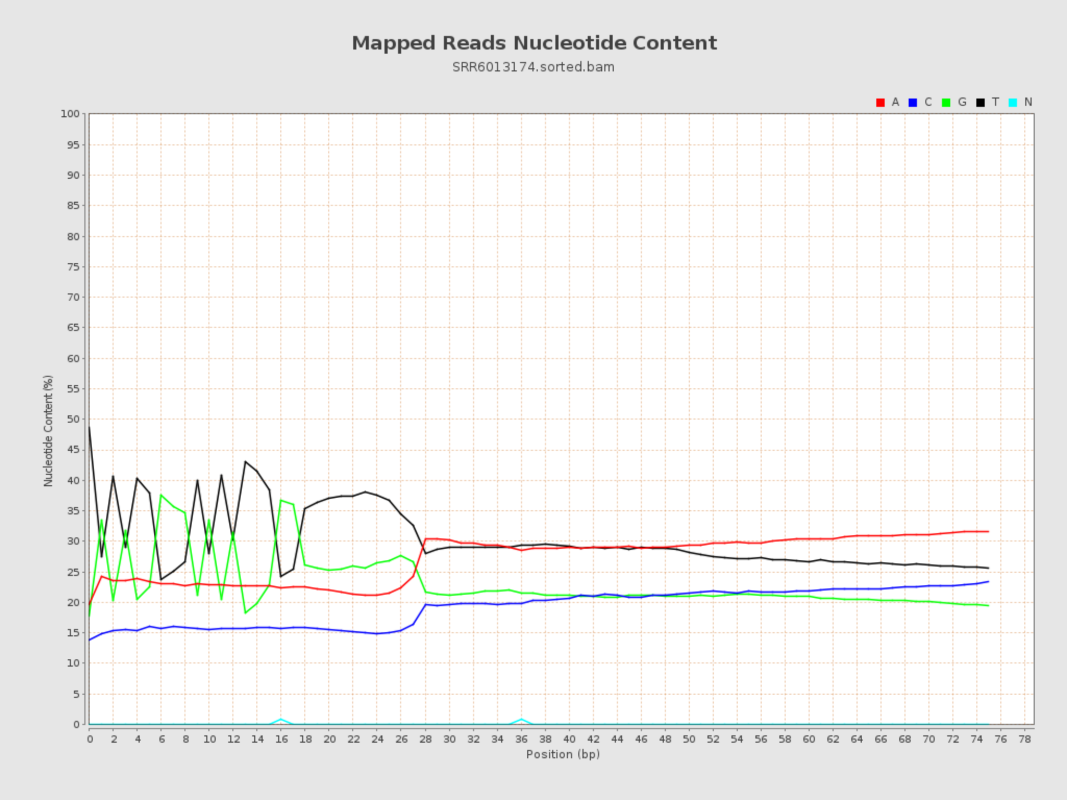
6. Results : Genome Fraction Coverage



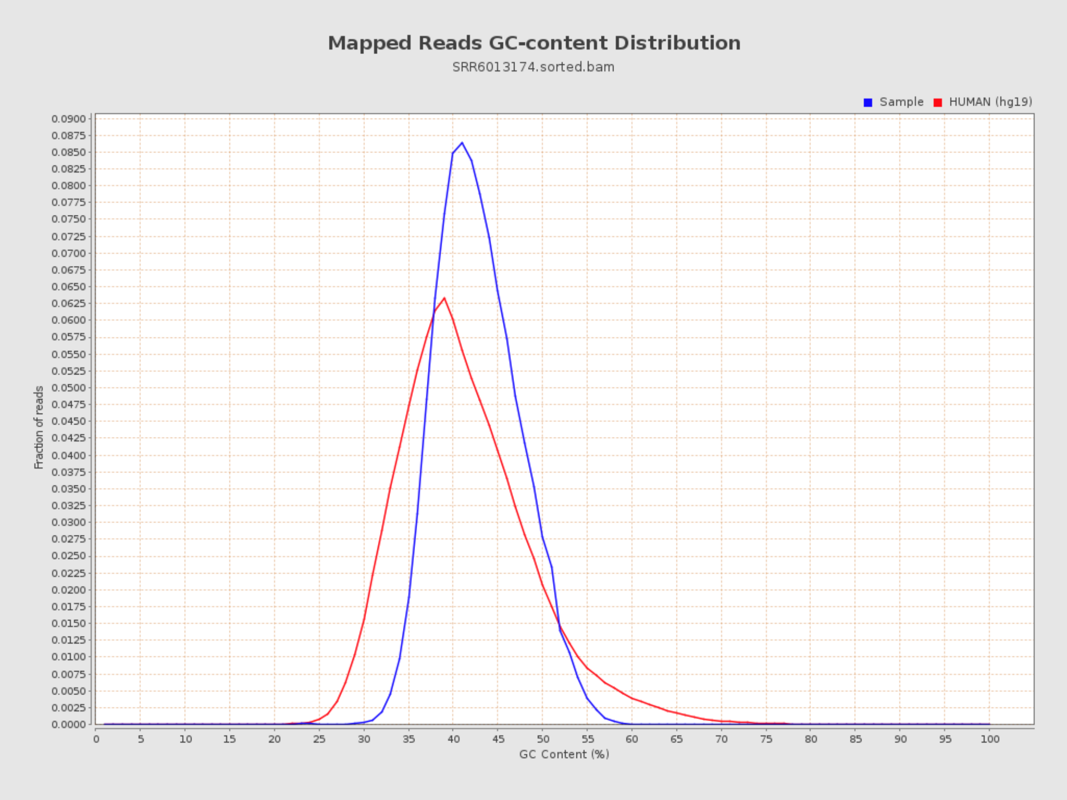
7. Results : Duplication Rate Histogram



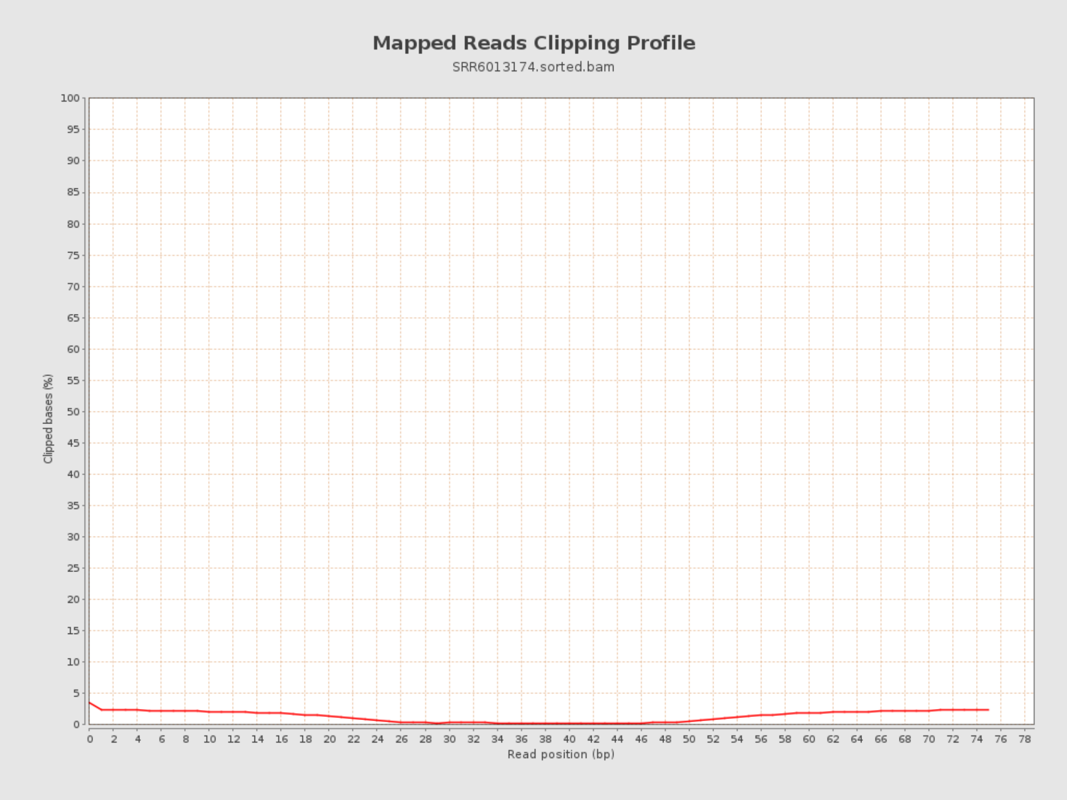
8. Results : Mapped Reads Nucleotide Content



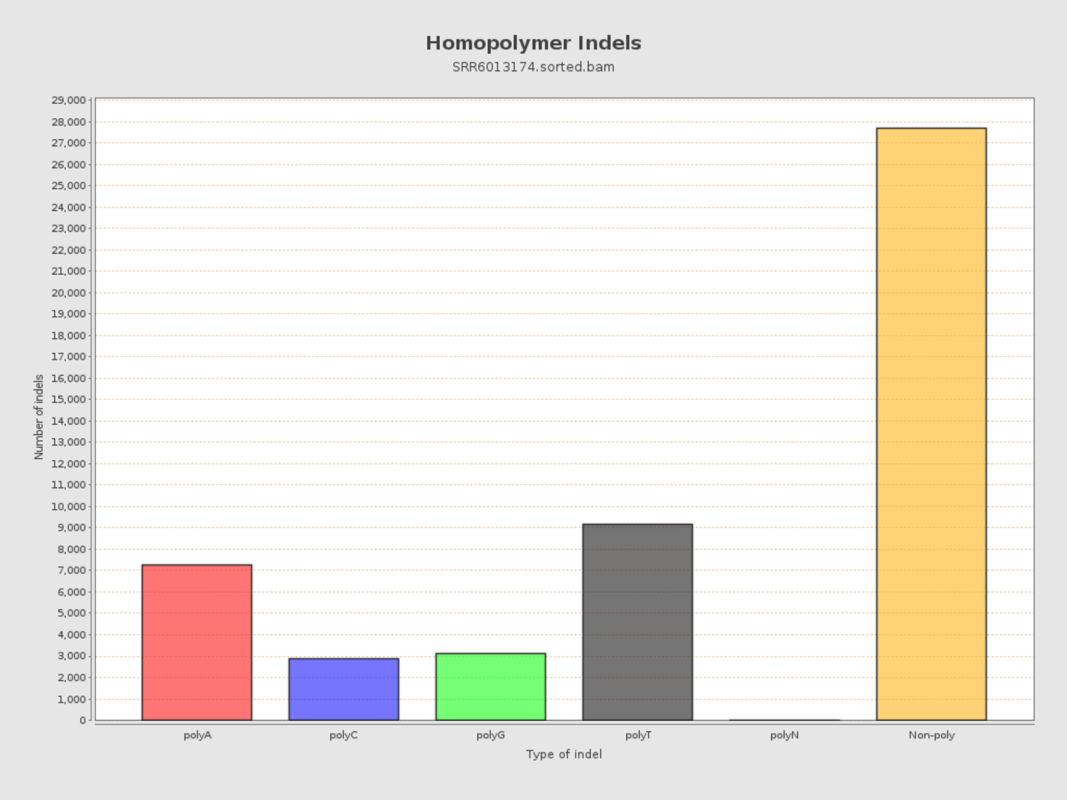
9. Results : Mapped Reads GC-content Distribution



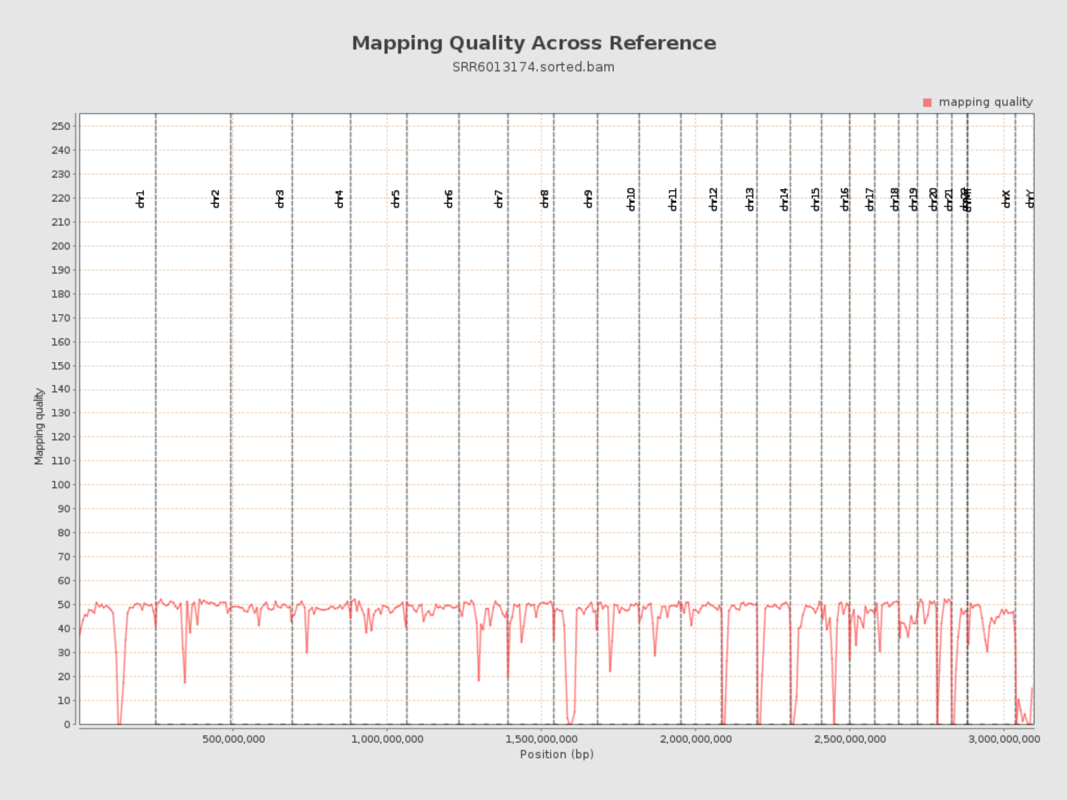
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram