

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 23:29:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013364.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_SRR6013364 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013364.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 23:29:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013364.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,299,926
Mapped reads	1,890,580 / 82.2%
Unmapped reads	409,346 / 17.8%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	25,766 / 1.12%
Read min/max/mean length	30 / 76 / 76.39
Duplicated reads (estimated)	218,183 / 9.49%
Duplication rate	8.68%
Clipped reads	887,610 / 38.59%

2.2. ACGT Content

Number/percentage of A's	34,410,959 / 27.47%
Number/percentage of C's	23,693,117 / 18.92%
Number/percentage of T's	39,008,233 / 31.14%
Number/percentage of G's	28,132,426 / 22.46%
Number/percentage of N's	14,778 / 0.01%
GC Percentage	41.37%

2.3. Coverage

Mean	0.0405

Standard Deviation	0.4379
--------------------	--------

2.4. Mapping Quality

Mean Mapping Quality	45.65
----------------------	-------

2.5. Mismatches and indels

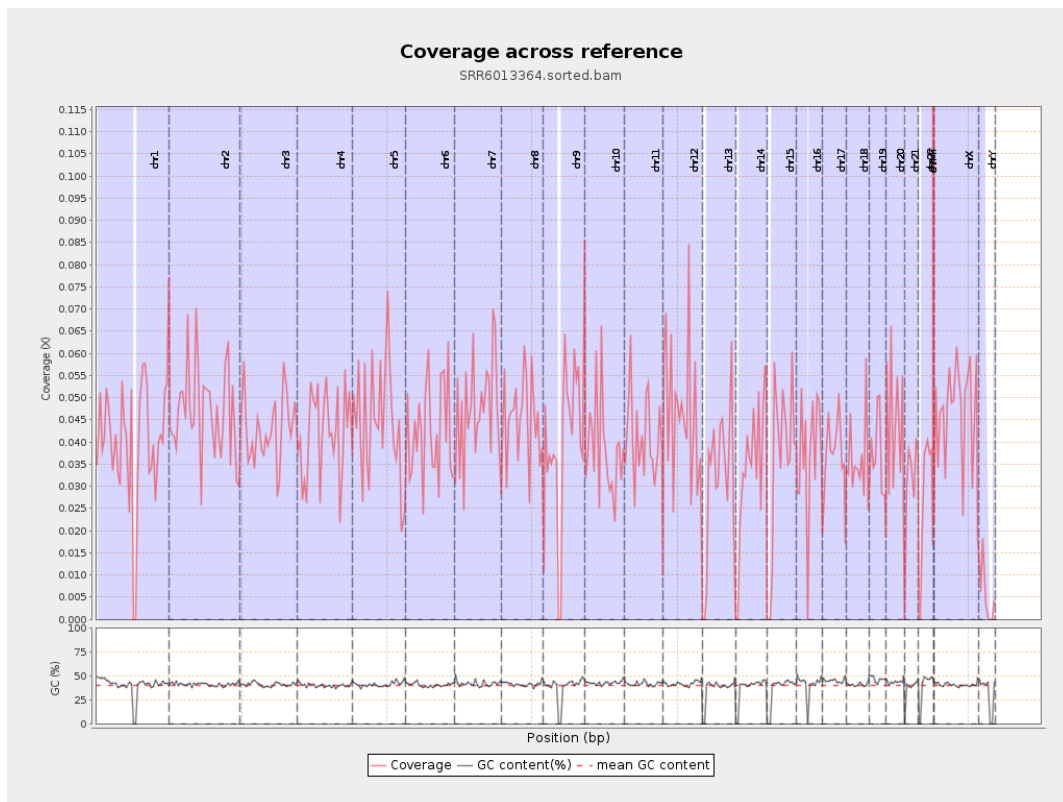
General error rate	0.76%
Mismatches	930,229
Insertions	8,804
Mapped reads with at least one insertion	0.46%
Deletions	28,502
Mapped reads with at least one deletion	1.49%
Homopolymer indels	46.88%

2.6. Chromosome stats

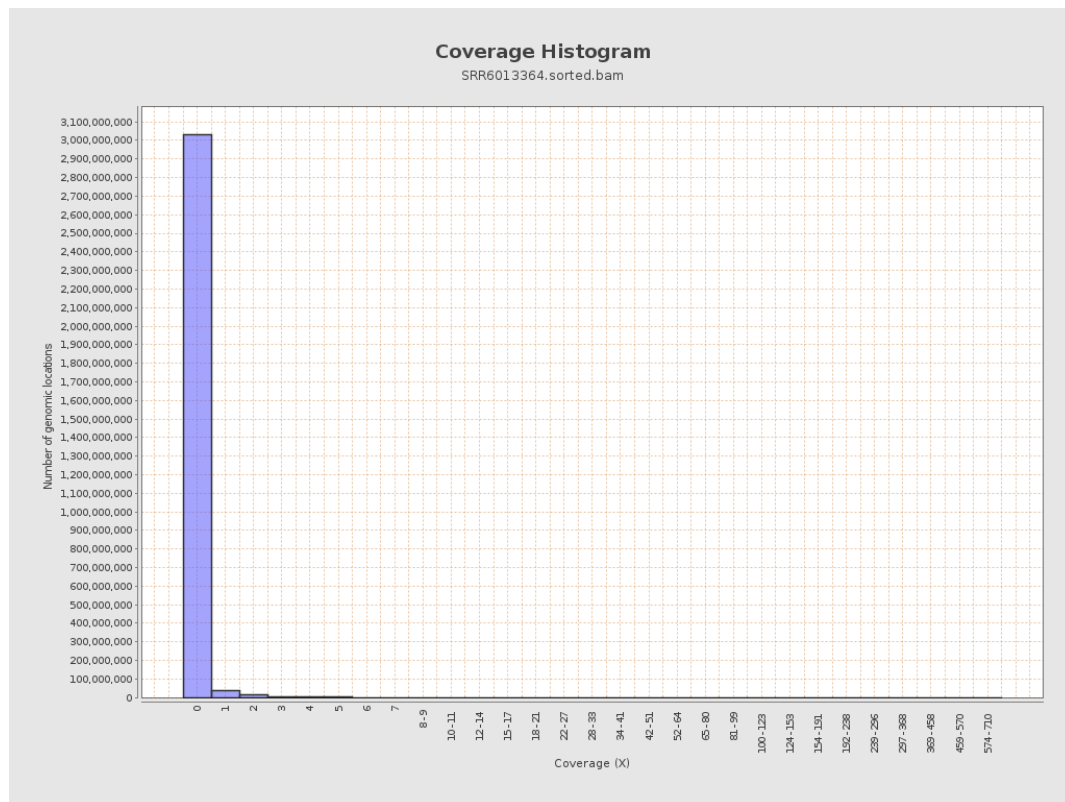
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	9968260	0.04	0.6871
chr2	243199373	11384620	0.0468	0.5183
chr3	198022430	8429365	0.0426	0.3527
chr4	191154276	8019722	0.042	0.3614
chr5	180915260	8061233	0.0446	0.36
chr6	171115067	7127774	0.0417	0.3868
chr7	159138663	7579517	0.0476	0.6166

chr8	146364022	6634324	0.0453	0.453
chr9	141213431	5715513	0.0405	0.4224
chr10	135534747	5183812	0.0382	0.4261
chr11	135006516	5529604	0.041	0.3681
chr12	133851895	6228590	0.0465	0.3763
chr13	115169878	3582312	0.0311	0.3086
chr14	107349540	3602671	0.0336	0.3364
chr15	102531392	3682194	0.0359	0.3507
chr16	90354753	3342395	0.037	0.3498
chr17	81195210	3015148	0.0371	0.3349
chr18	78077248	2822935	0.0362	0.5295
chr19	59128983	2192397	0.0371	0.4988
chr20	63025520	2796421	0.0444	0.3753
chr21	48129895	1515472	0.0315	0.3105
chr22	51304566	1380543	0.0269	0.2746
chrMT	16571	22194	1.3393	2.3057
chrX	155270560	7176975	0.0462	0.3809
chrY	59373566	314419	0.0053	0.1692

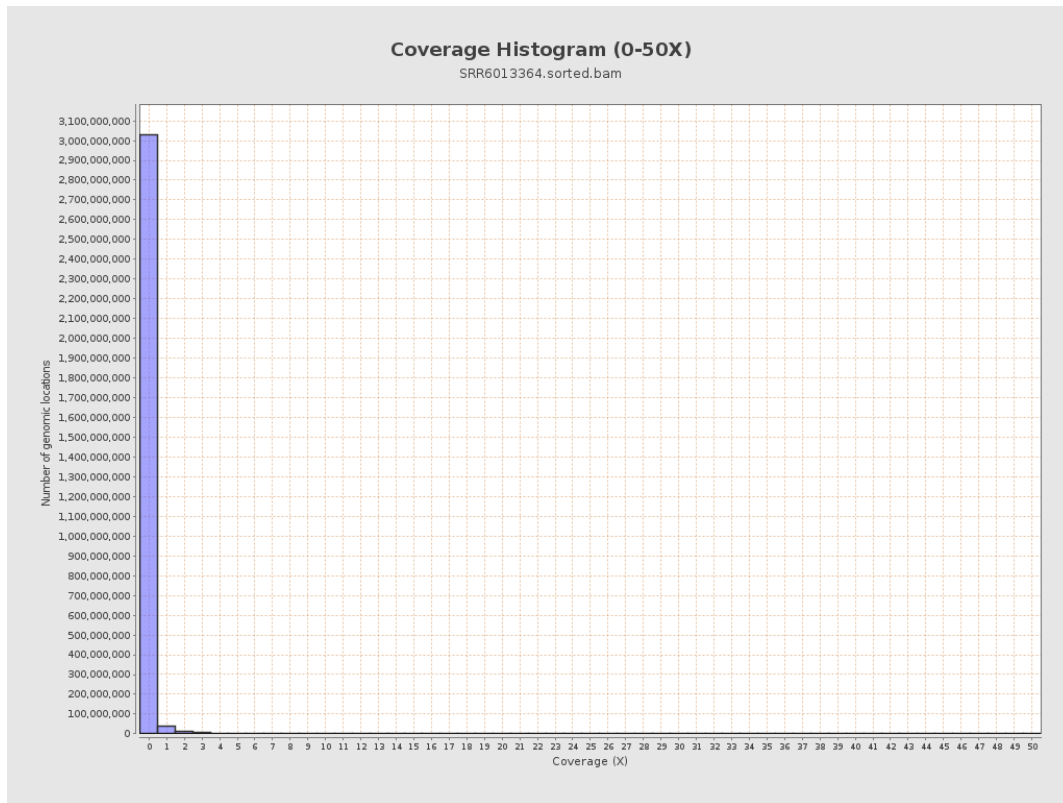
3. Results : Coverage across reference



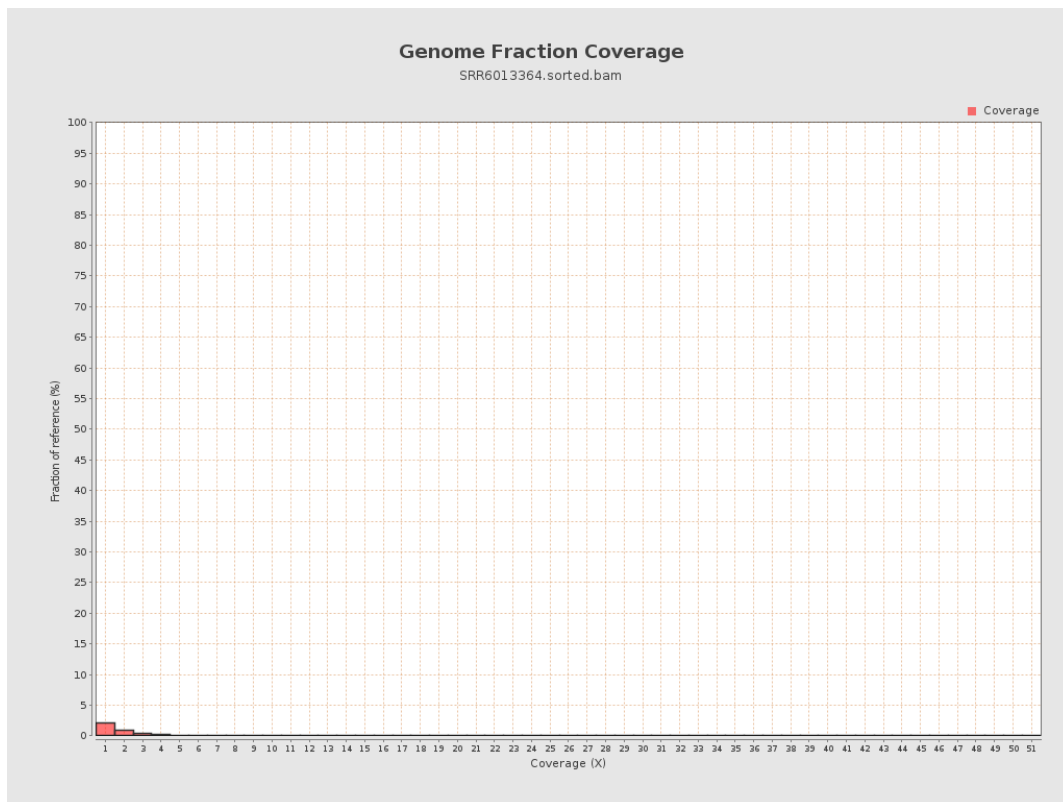
4. Results : Coverage Histogram



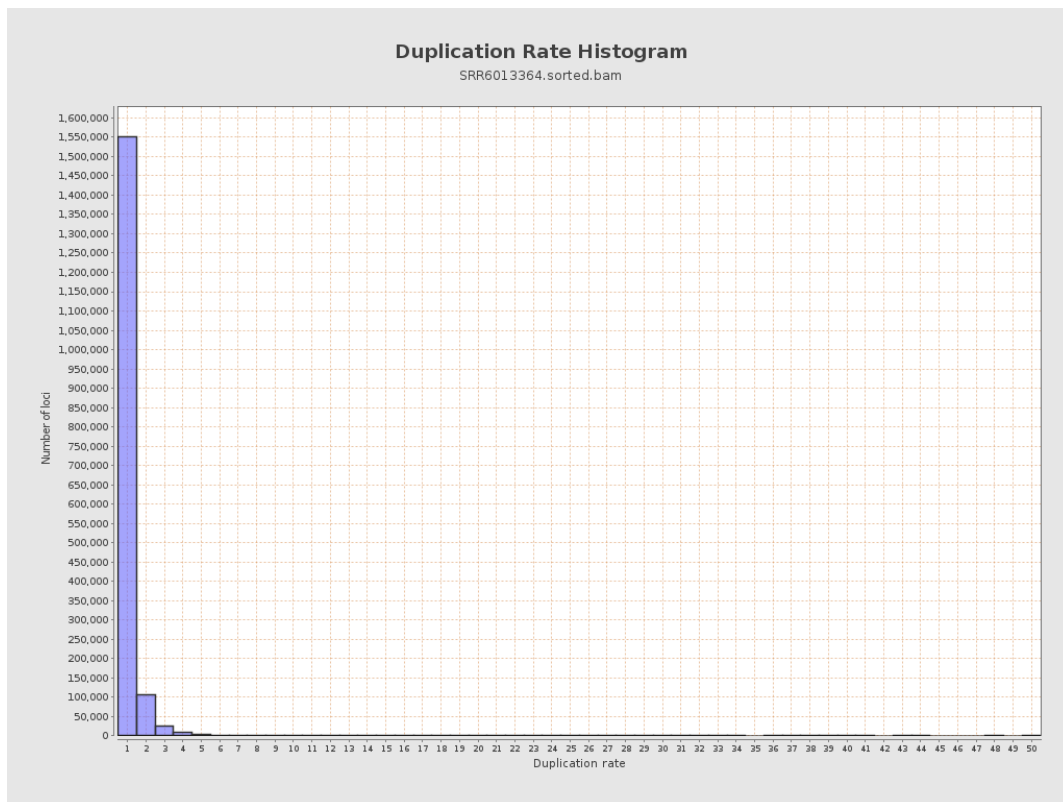
5. Results : Coverage Histogram (0-50X)



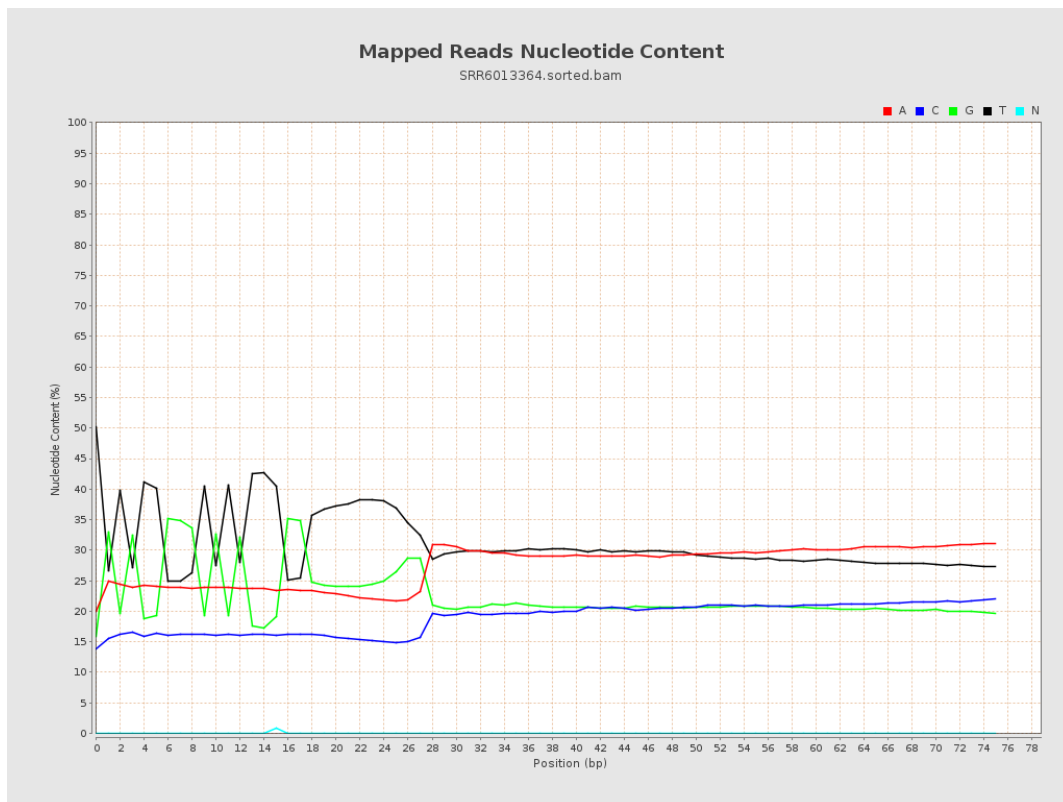
6. Results : Genome Fraction Coverage



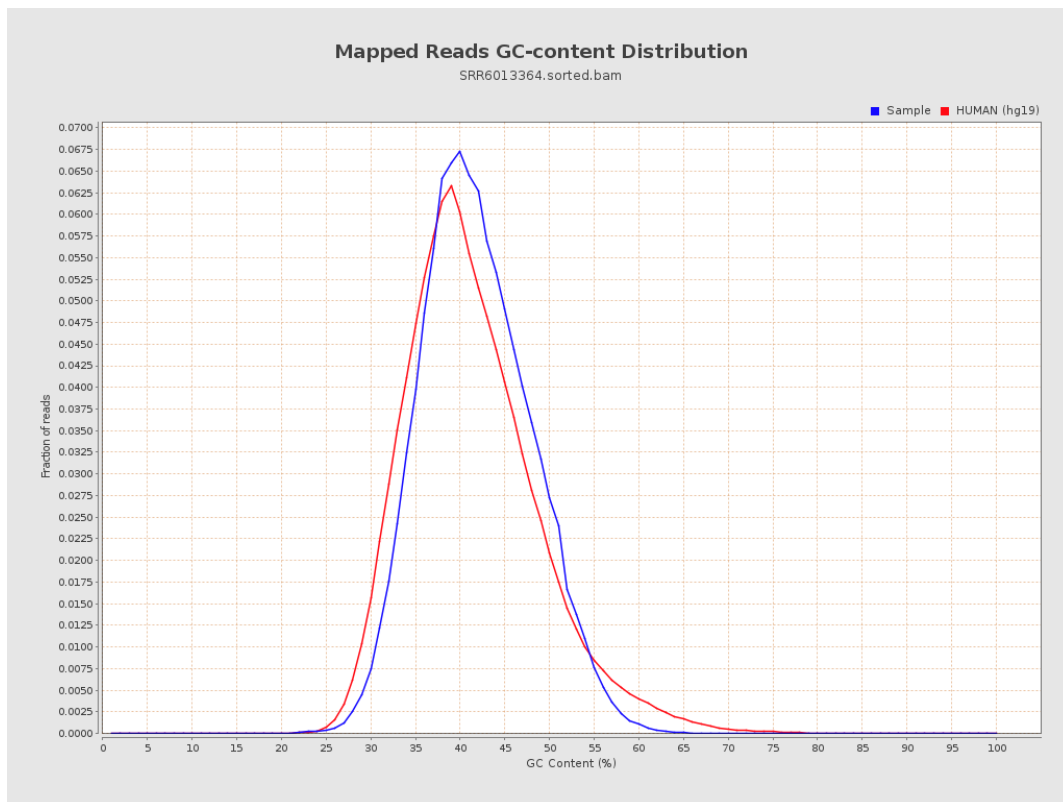
7. Results : Duplication Rate Histogram



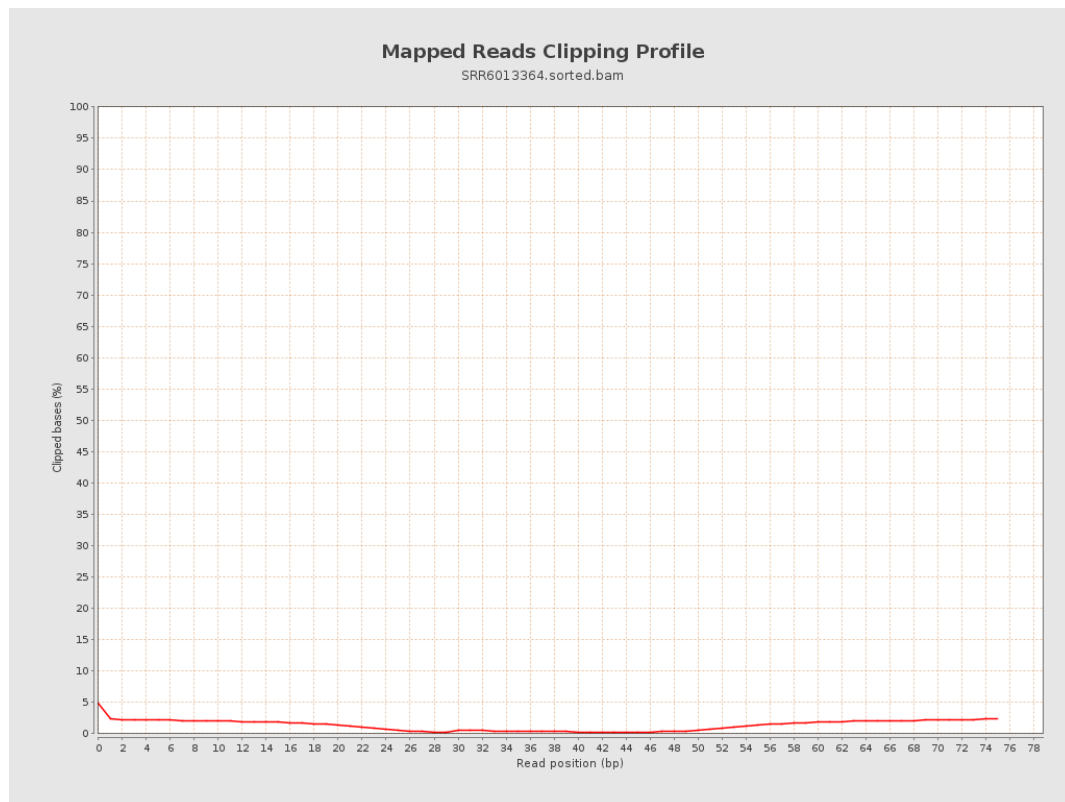
8. Results : Mapped Reads Nucleotide Content



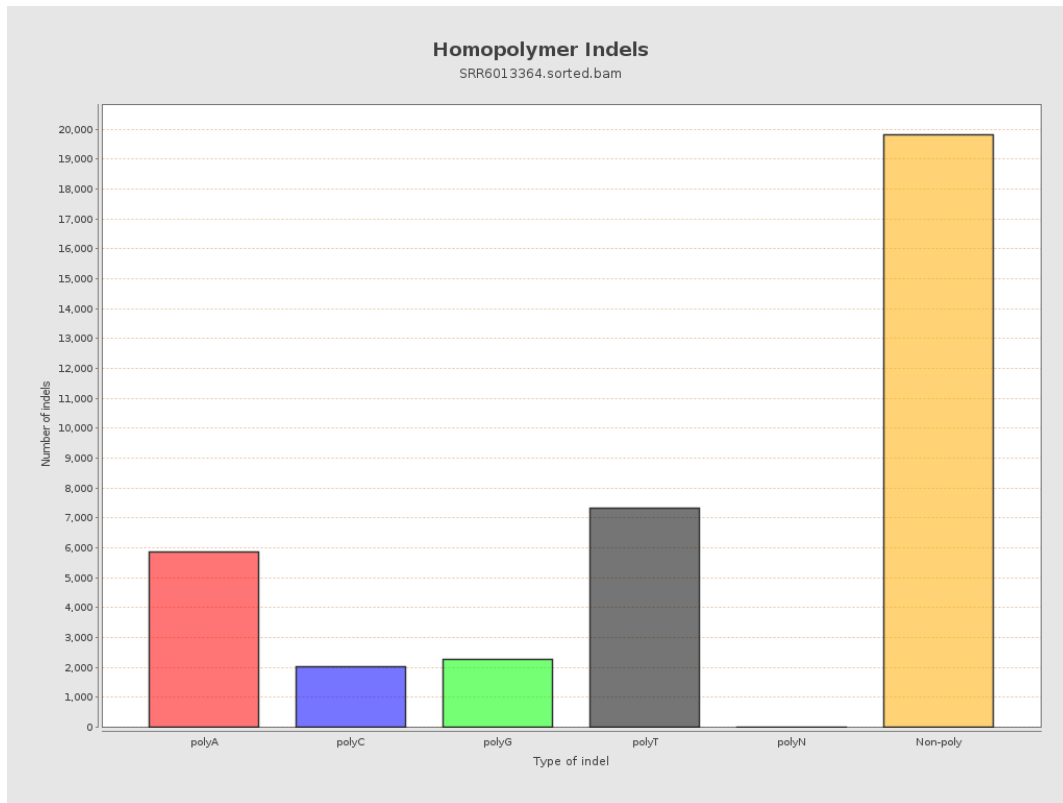
9. Results : Mapped Reads GC-content Distribution



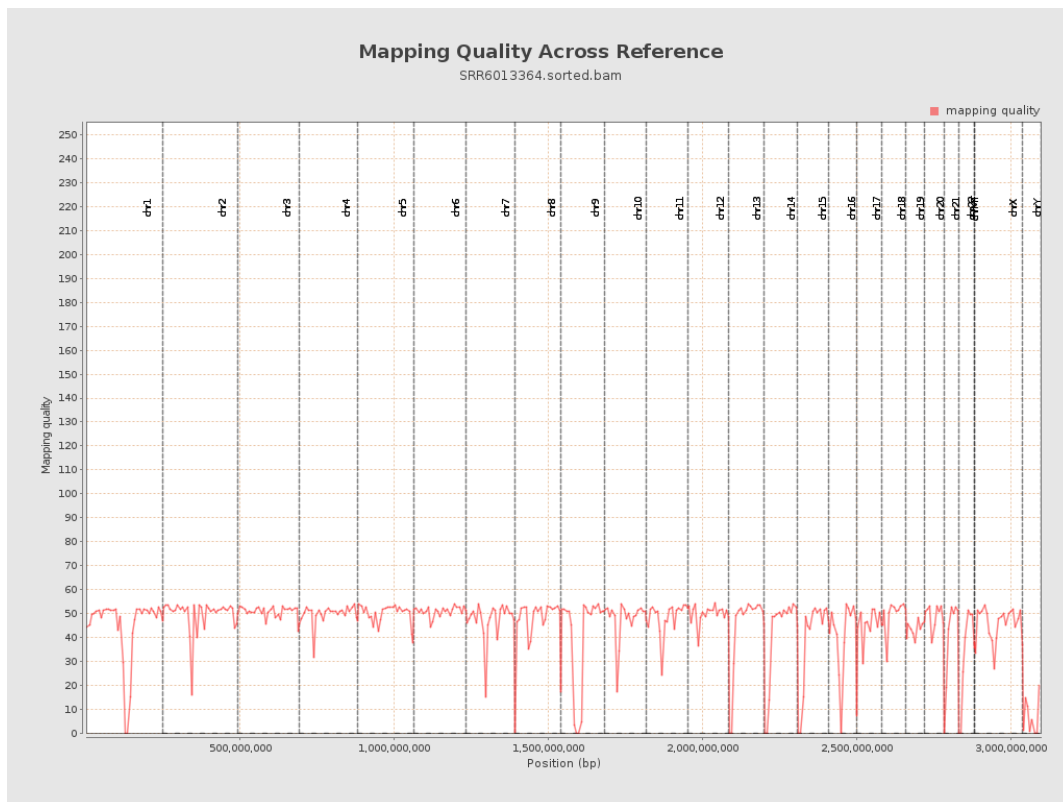
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

