

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 22:39:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013347.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_SRR6013347 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013347.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 22:39:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013347.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,832,344
Mapped reads	289,529 / 15.8%
Unmapped reads	1,542,815 / 84.2%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,706 / 0.2%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	71,489 / 3.9%
Duplication rate	14.66%
Clipped reads	169,977 / 9.28%

2.2. ACGT Content

Number/percentage of A's	4,956,968 / 27.13%
Number/percentage of C's	3,287,834 / 17.99%
Number/percentage of T's	5,908,300 / 32.33%
Number/percentage of G's	4,118,544 / 22.54%
Number/percentage of N's	2,098 / 0.01%
GC Percentage	40.53%

2.3. Coverage

Mean	0.0059

Standard Deviation	0.1918
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2.4. Mapping Quality

Mean Mapping Quality	43.09
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2.5. Mismatches and indels

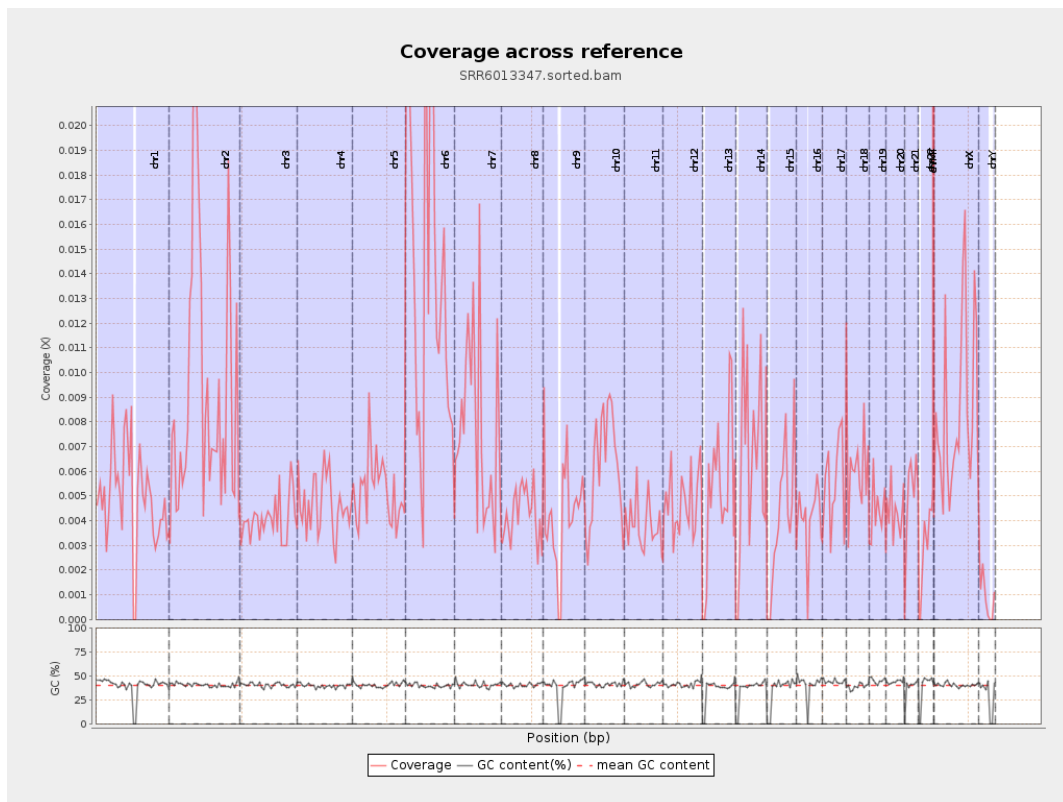
General error rate	0.85%
Mismatches	152,491
Insertions	1,426
Mapped reads with at least one insertion	0.48%
Deletions	5,392
Mapped reads with at least one deletion	1.84%
Homopolymer indels	45.23%

2.6. Chromosome stats

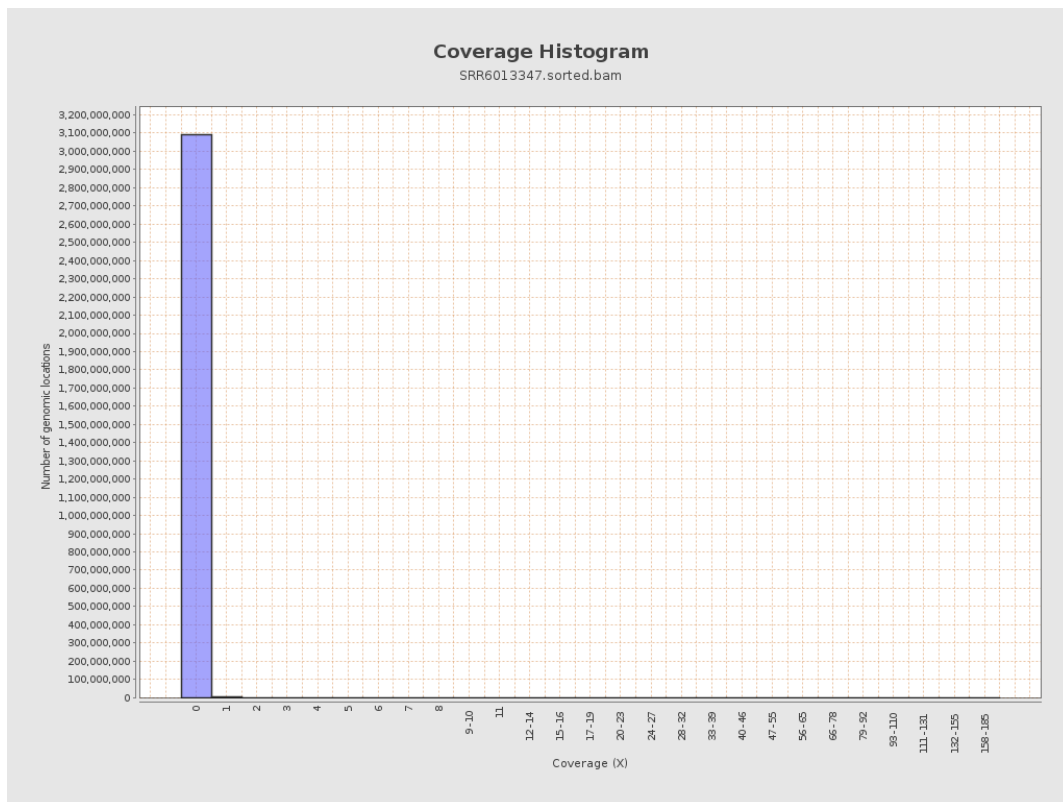
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	1221091	0.0049	0.1669
chr2	243199373	2266139	0.0093	0.2506
chr3	198022430	808624	0.0041	0.1543
chr4	191154276	885108	0.0046	0.1548
chr5	180915260	942545	0.0052	0.168
chr6	171115067	2447103	0.0143	0.3093
chr7	159138663	1227268	0.0077	0.2587

chr8	146364022	625595	0.0043	0.1547
chr9	141213431	579040	0.0041	0.1496
chr10	135534747	842093	0.0062	0.1824
chr11	135006516	523149	0.0039	0.1349
chr12	133851895	626497	0.0047	0.1572
chr13	115169878	595369	0.0052	0.1693
chr14	107349540	669241	0.0062	0.1909
chr15	102531392	416716	0.0041	0.1532
chr16	90354753	371668	0.0041	0.1466
chr17	81195210	435217	0.0054	0.1668
chr18	78077248	480997	0.0062	0.2972
chr19	59128983	259754	0.0044	0.1469
chr20	63025520	277295	0.0044	0.1484
chr21	48129895	239599	0.005	0.159
chr22	51304566	147176	0.0029	0.1189
chrMT	16571	15233	0.9193	2.1739
chrX	155270560	1325383	0.0085	0.223
chrY	59373566	54974	0.0009	0.0481

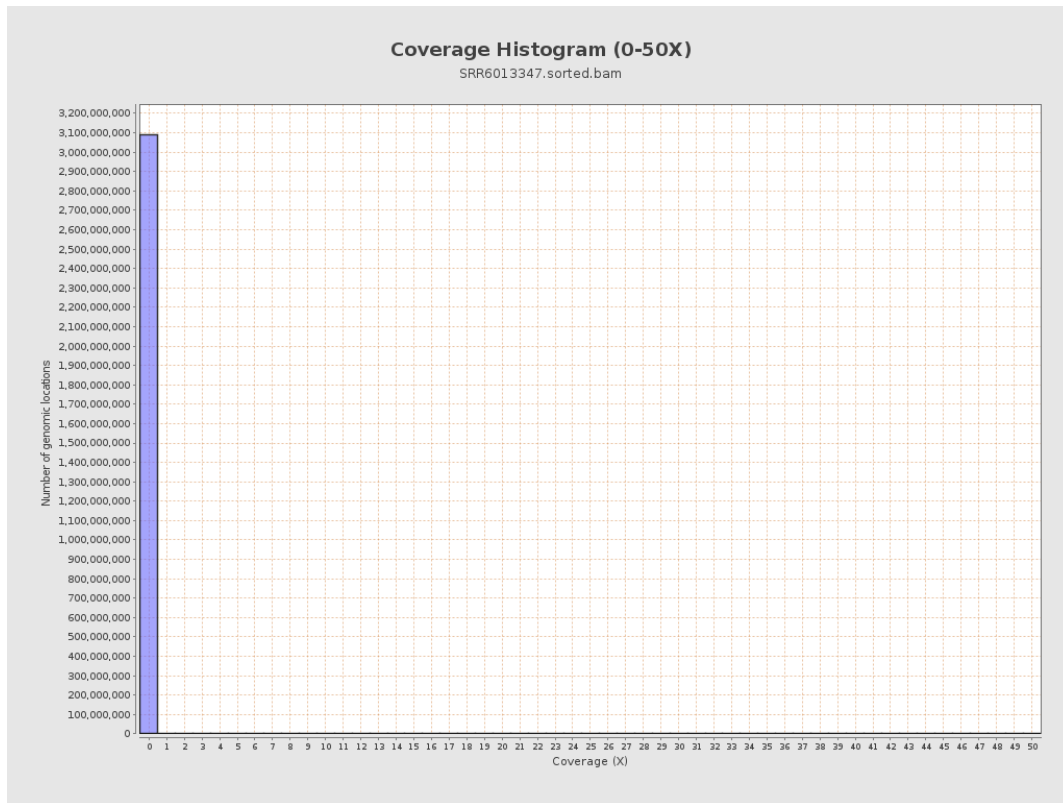
3. Results : Coverage across reference



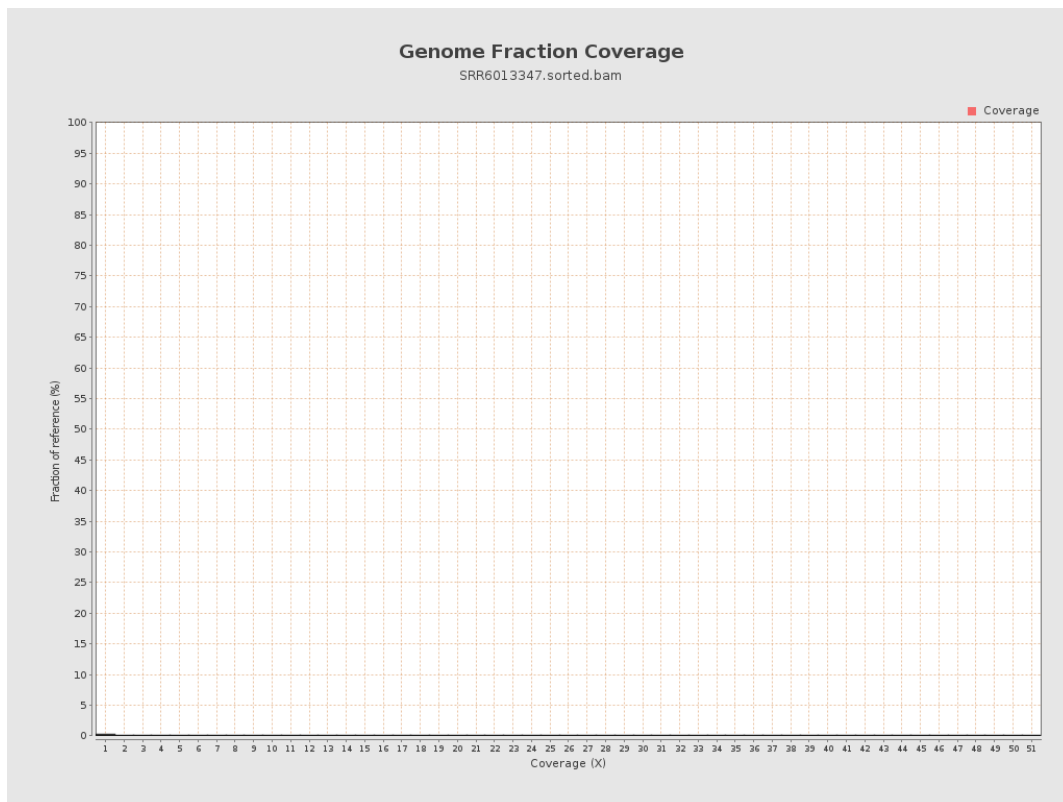
4. Results : Coverage Histogram



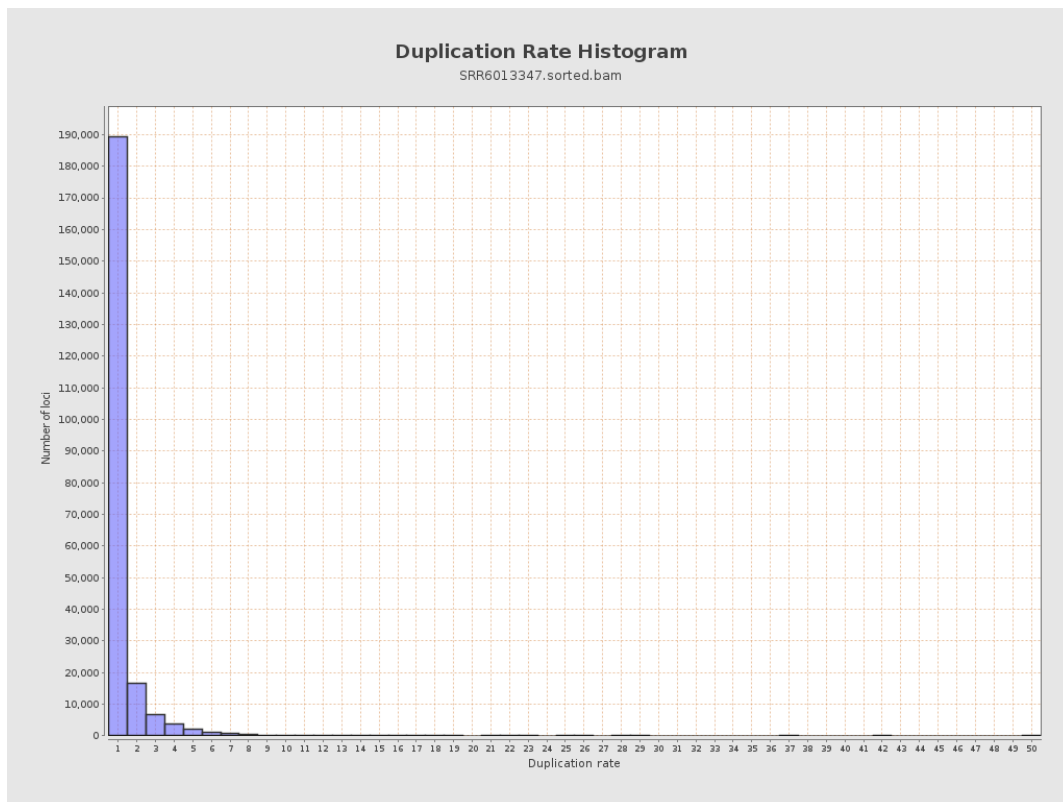
5. Results : Coverage Histogram (0-50X)



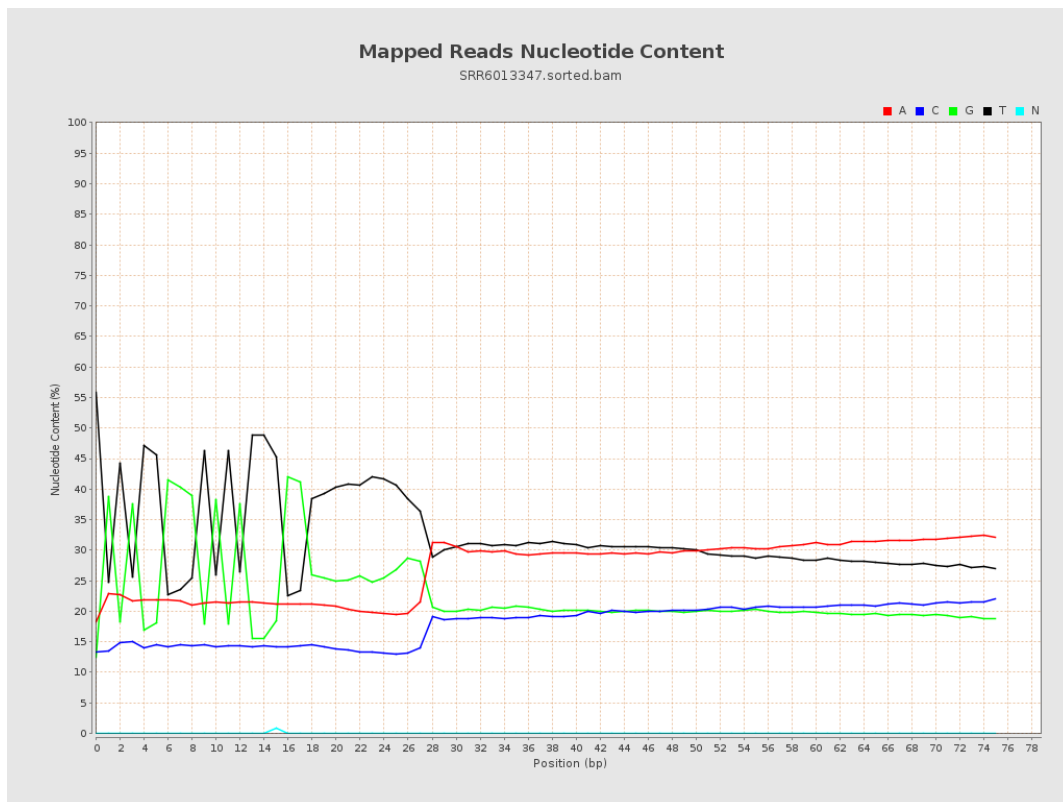
6. Results : Genome Fraction Coverage



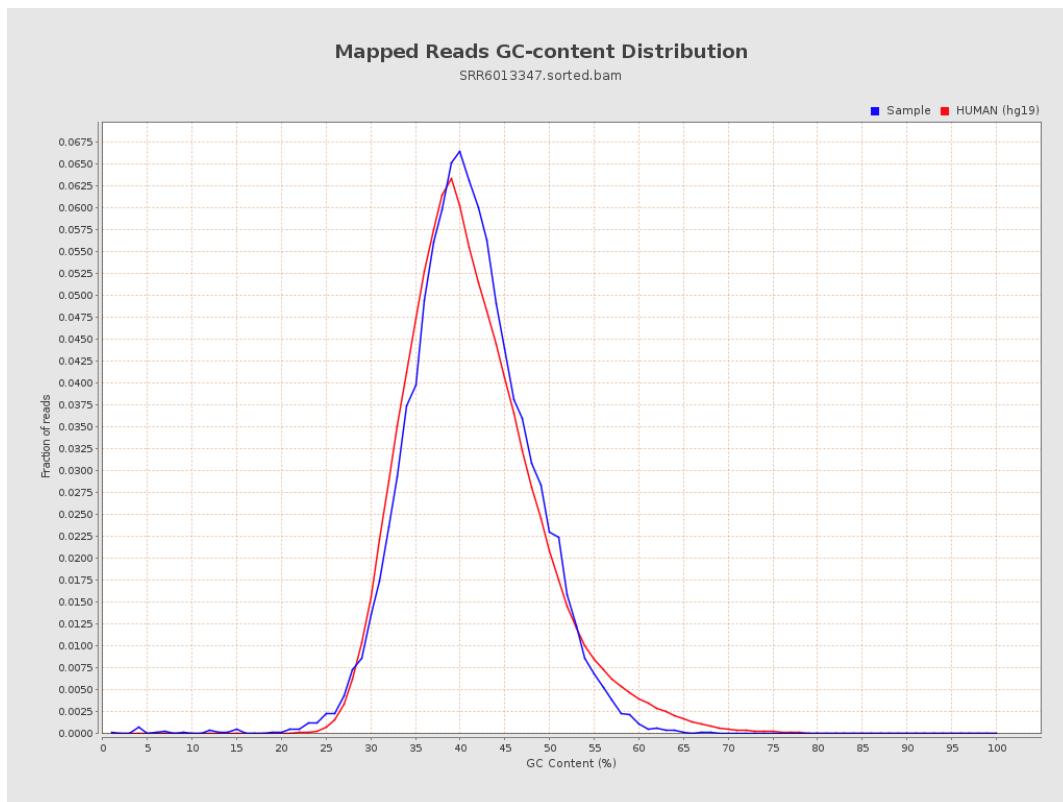
7. Results : Duplication Rate Histogram



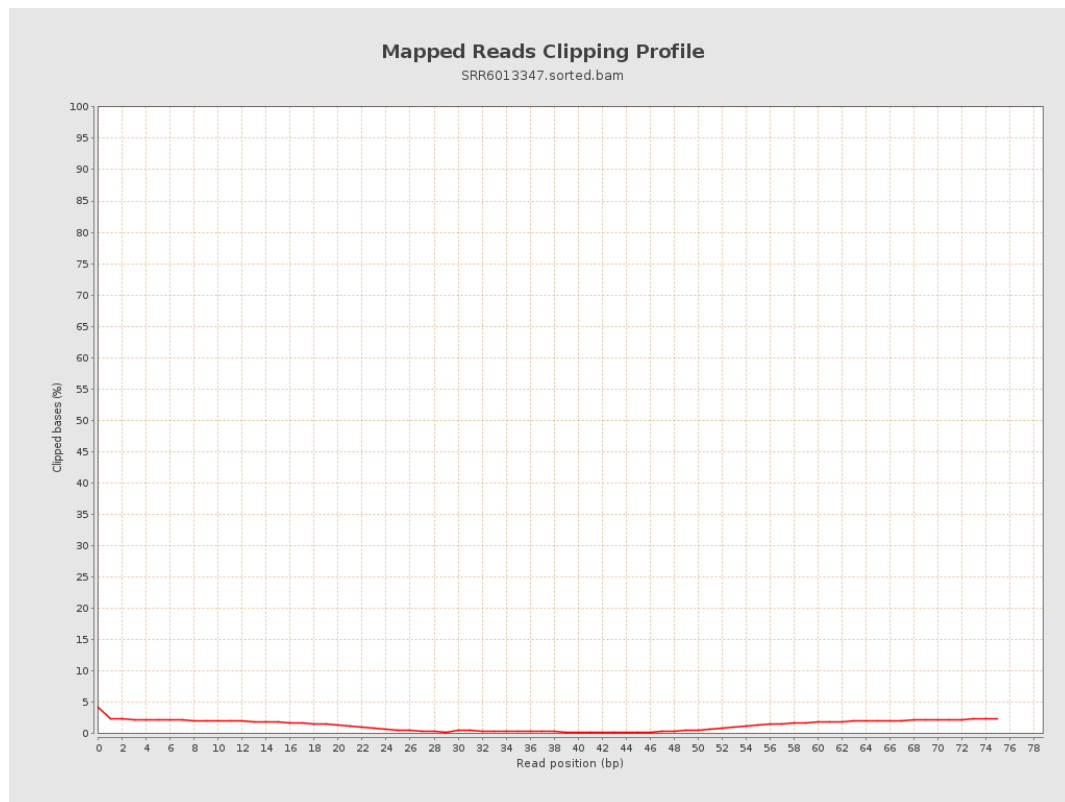
8. Results : Mapped Reads Nucleotide Content



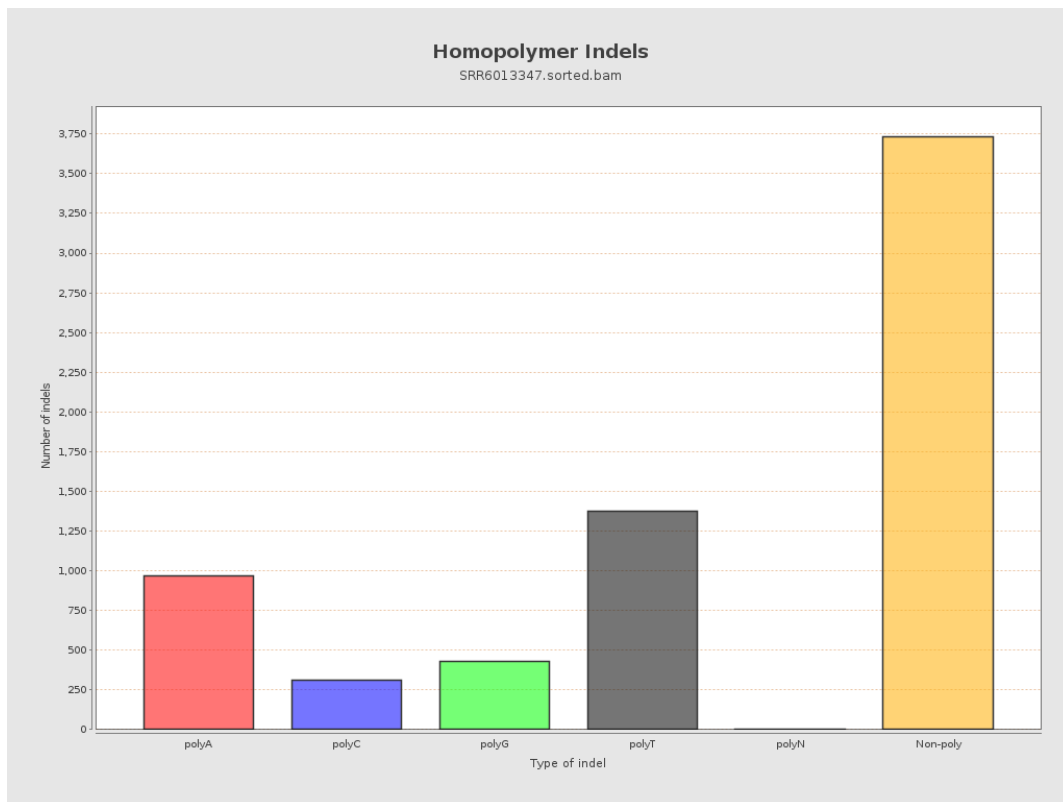
9. Results : Mapped Reads GC-content Distribution



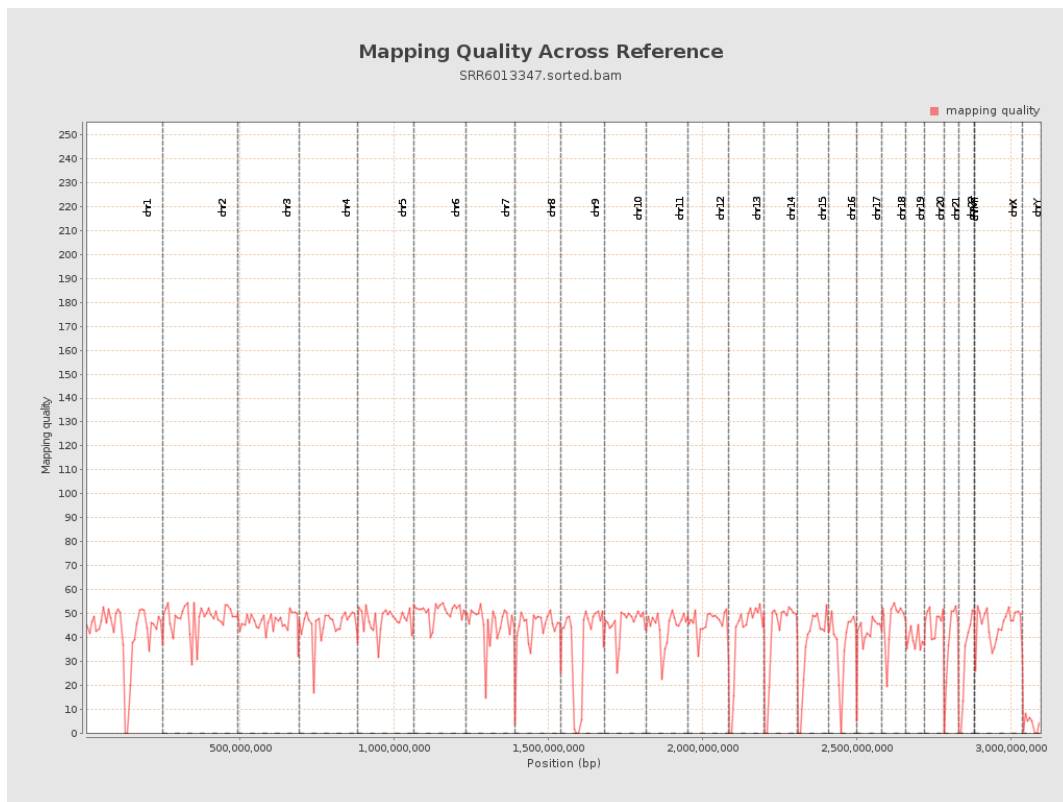
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

