

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 01:06:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081182.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_SRR3081182 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081182.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 01:06:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081182.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,273,539
Mapped reads	1,136,542 / 89.24%
Unmapped reads	136,997 / 10.76%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,878 / 1.33%
Read min/max/mean length	30 / 76 / 76.46
Duplicated reads (estimated)	38,356 / 3.01%
Duplication rate	2.13%
Clipped reads	538,481 / 42.28%

2.2. ACGT Content

Number/percentage of A's	21,567,064 / 28.49%
Number/percentage of C's	14,538,450 / 19.2%
Number/percentage of T's	22,405,514 / 29.6%
Number/percentage of G's	17,173,296 / 22.68%
Number/percentage of N's	22,158 / 0.03%
GC Percentage	41.89%

2.3. Coverage

Mean	0.0245

Standard Deviation	0.3292
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2.4. Mapping Quality

Mean Mapping Quality	43.3
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2.5. Mismatches and indels

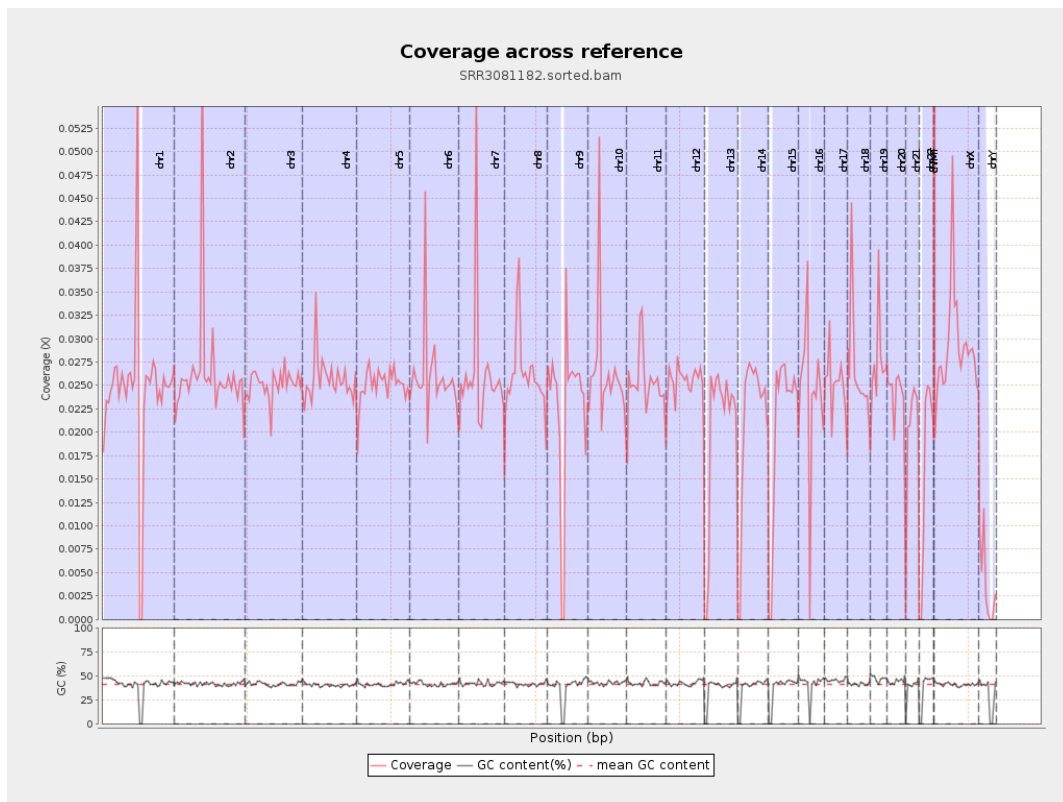
General error rate	0.88%
Mismatches	652,074
Insertions	6,854
Mapped reads with at least one insertion	0.6%
Deletions	15,391
Mapped reads with at least one deletion	1.34%
Homopolymer indels	43.04%

2.6. Chromosome stats

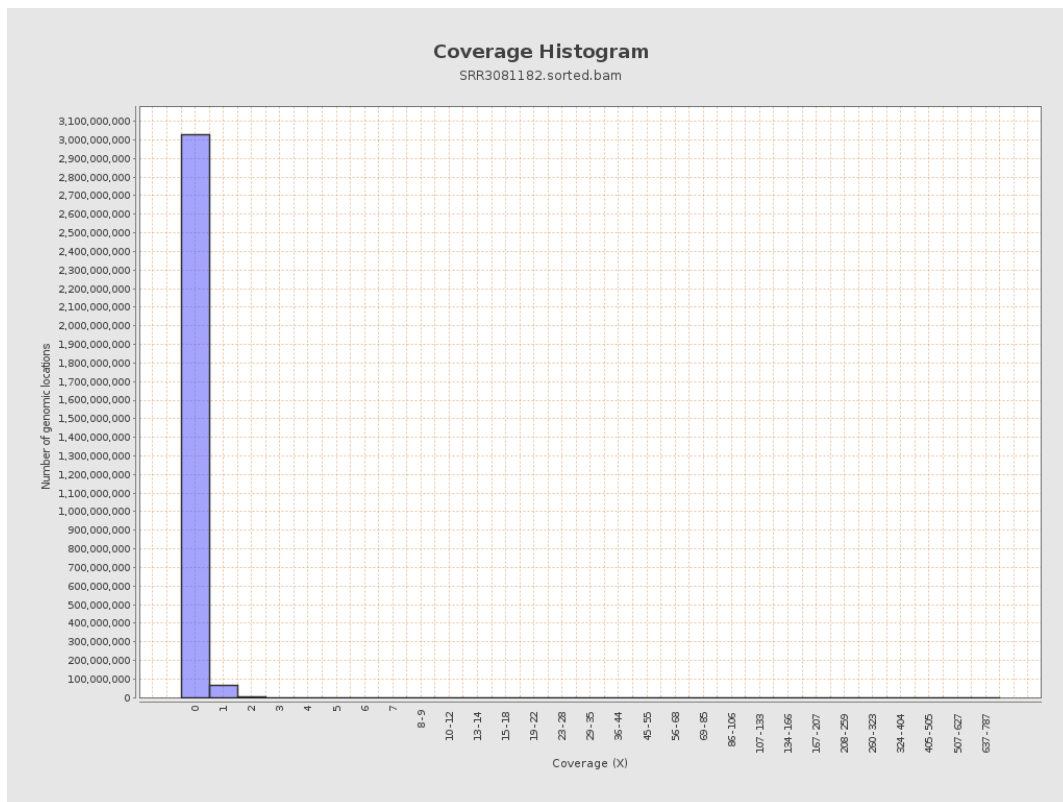
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	6085303	0.0244	0.6711
chr2	243199373	6406761	0.0263	0.3357
chr3	198022430	4982892	0.0252	0.1653
chr4	191154276	4895992	0.0256	0.1769
chr5	180915260	4560699	0.0252	0.1696
chr6	171115067	4427074	0.0259	0.2609
chr7	159138663	4169431	0.0262	0.4706

chr8	146364022	3840370	0.0262	0.3494
chr9	141213431	3217078	0.0228	0.2925
chr10	135534747	3558388	0.0263	0.2889
chr11	135006516	3450261	0.0256	0.2936
chr12	133851895	3412818	0.0255	0.1727
chr13	115169878	2315455	0.0201	0.1466
chr14	107349540	2283552	0.0213	0.1913
chr15	102531392	2130603	0.0208	0.1527
chr16	90354753	2155420	0.0239	0.208
chr17	81195210	2033654	0.025	0.2131
chr18	78077248	2073342	0.0266	0.6521
chr19	59128983	1637597	0.0277	0.4812
chr20	63025520	1502442	0.0238	0.1691
chr21	48129895	973339	0.0202	0.1679
chr22	51304566	834049	0.0163	0.1322
chrMT	16571	24677	1.4892	1.4465
chrX	155270560	4536368	0.0292	0.2171
chrY	59373566	224774	0.0038	0.1003

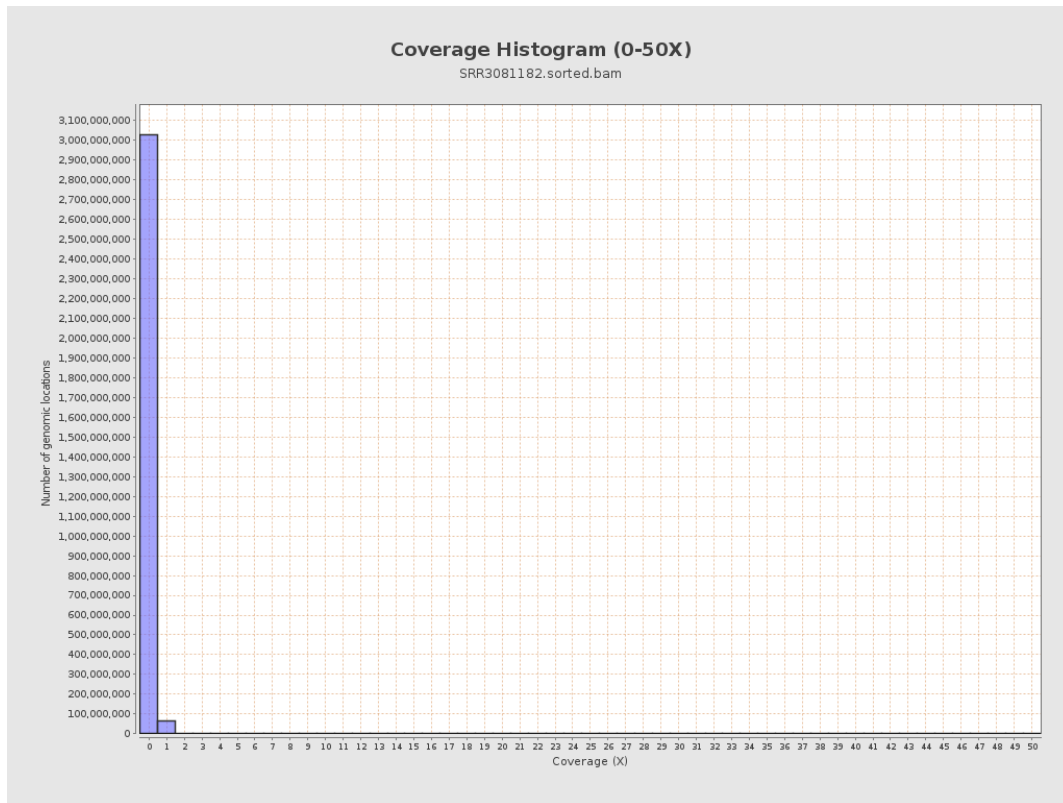
3. Results : Coverage across reference



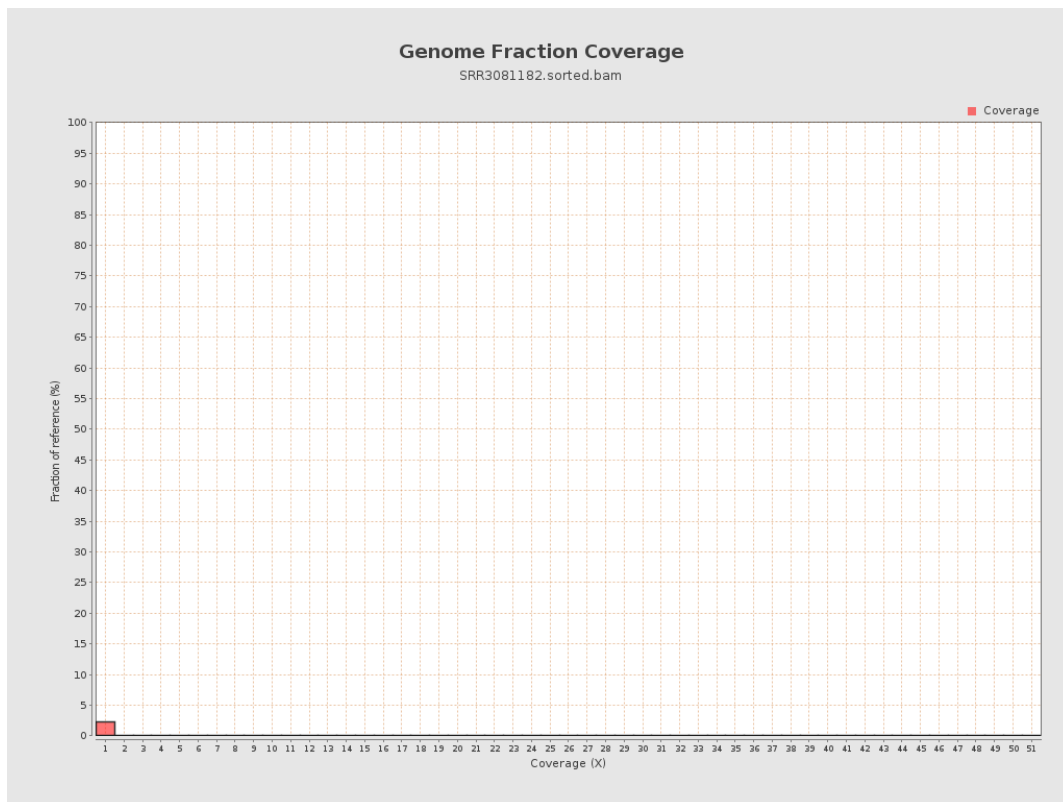
4. Results : Coverage Histogram



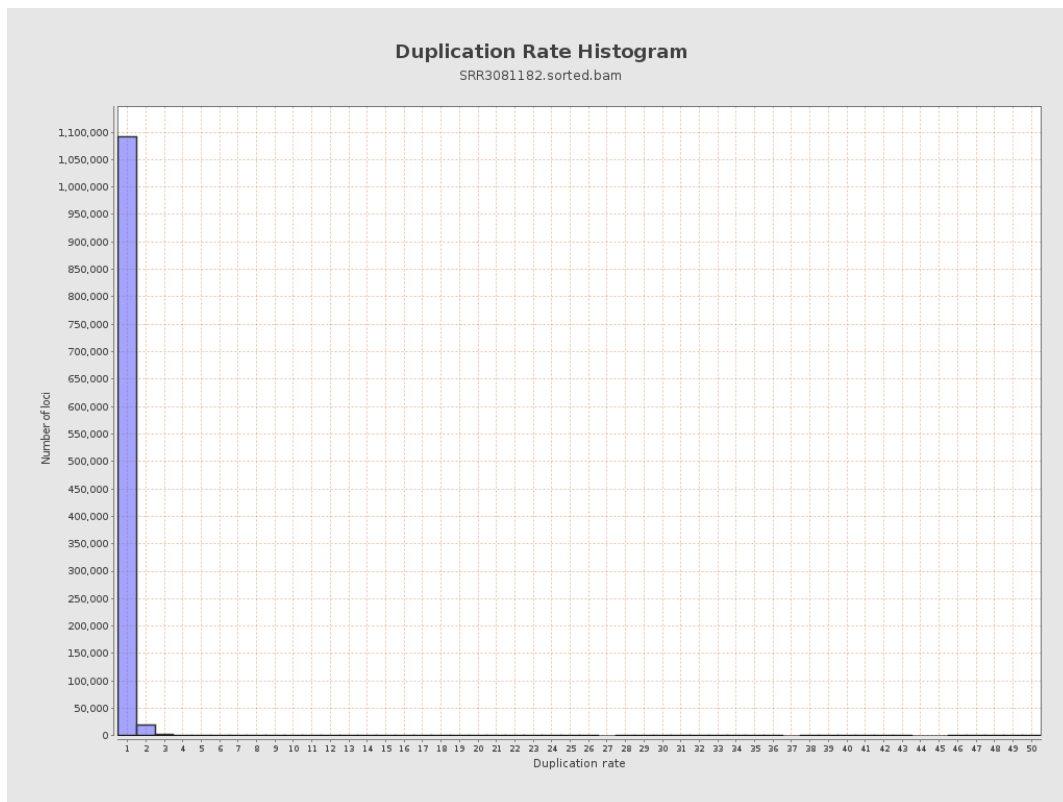
5. Results : Coverage Histogram (0-50X)



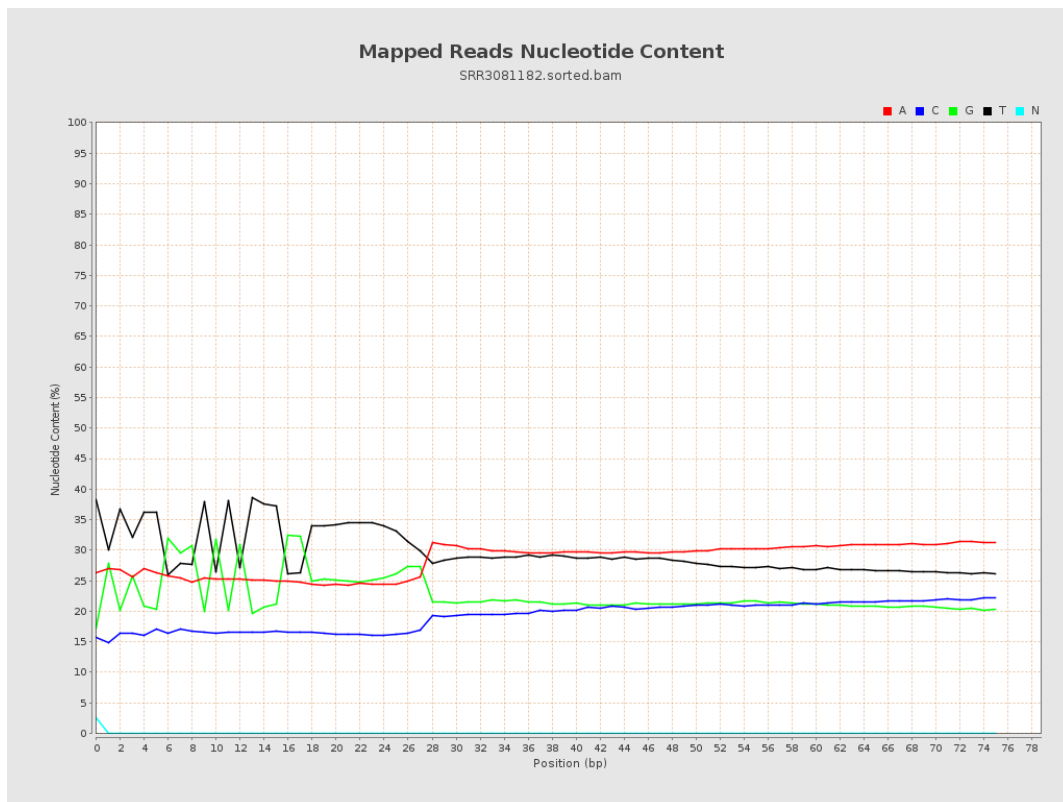
6. Results : Genome Fraction Coverage



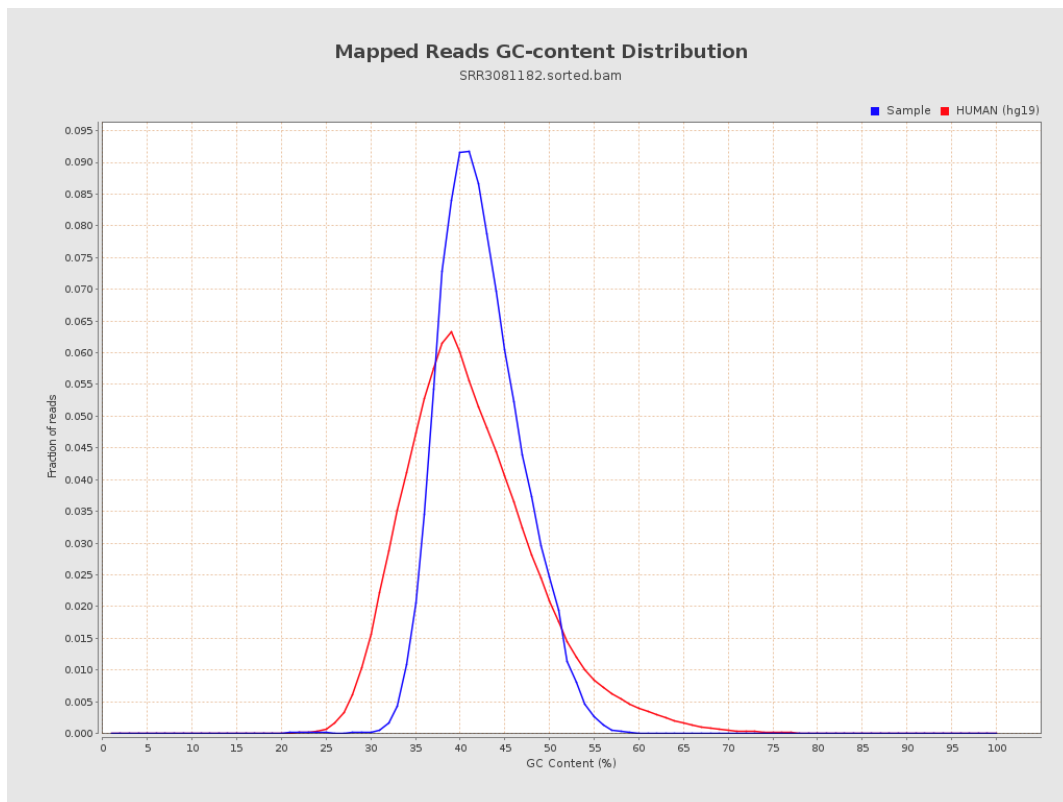
7. Results : Duplication Rate Histogram



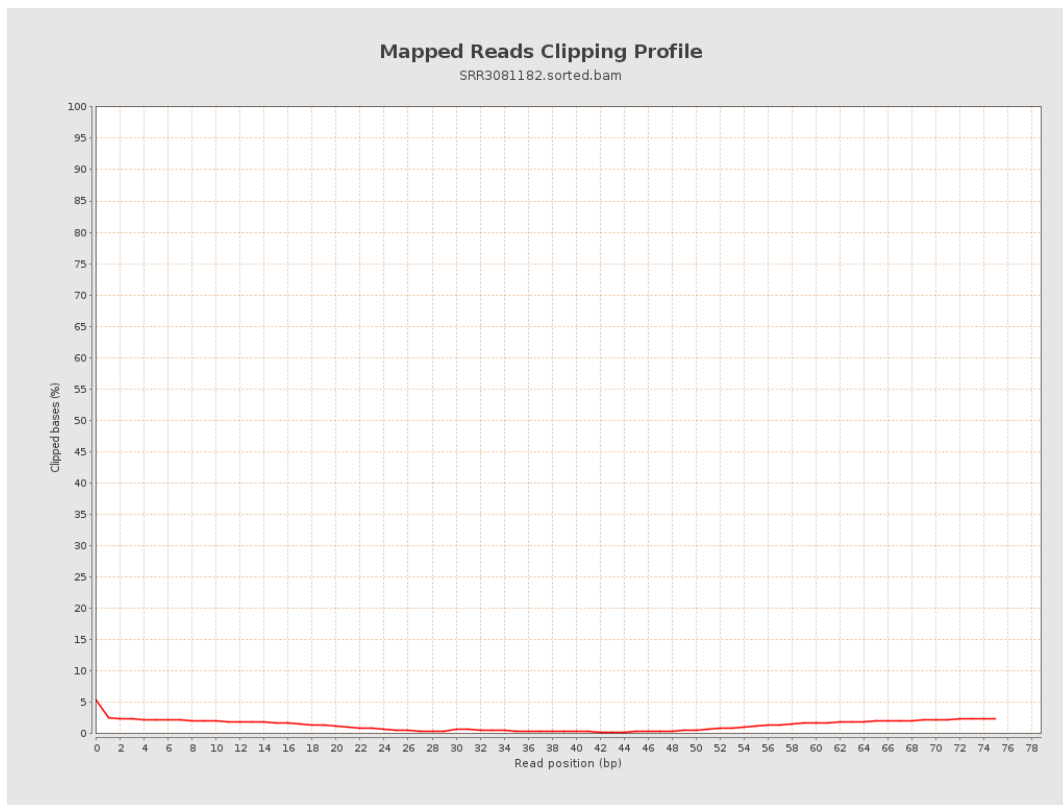
8. Results : Mapped Reads Nucleotide Content



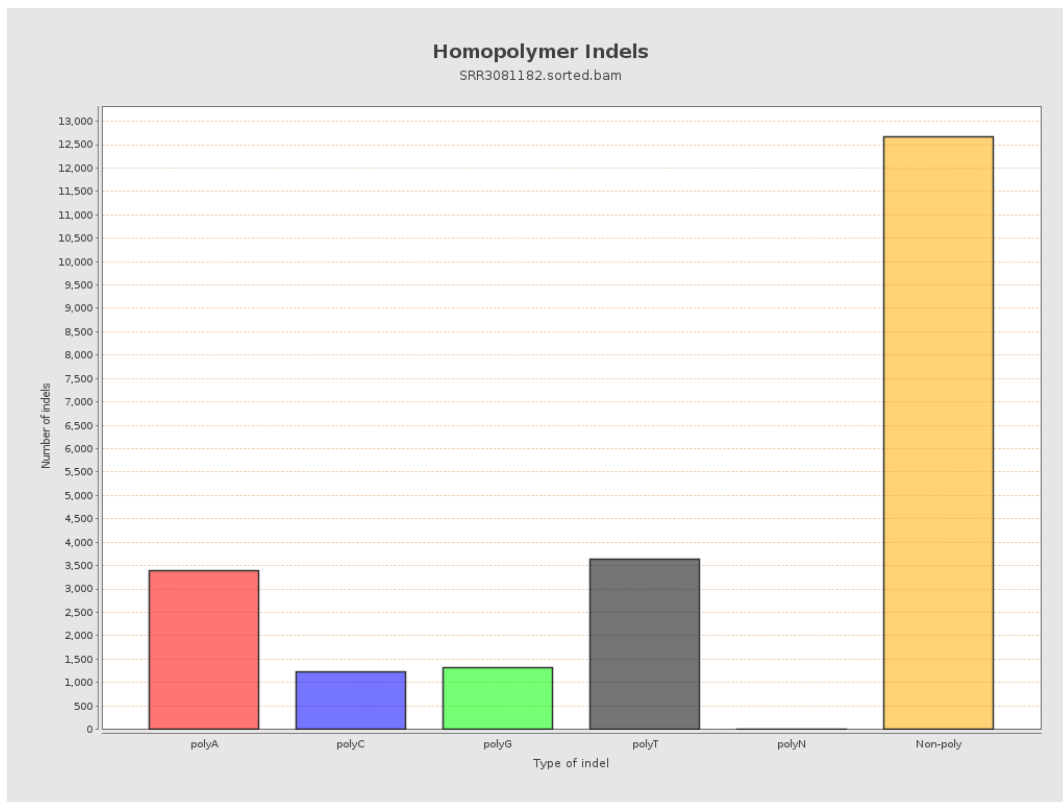
9. Results : Mapped Reads GC-content Distribution



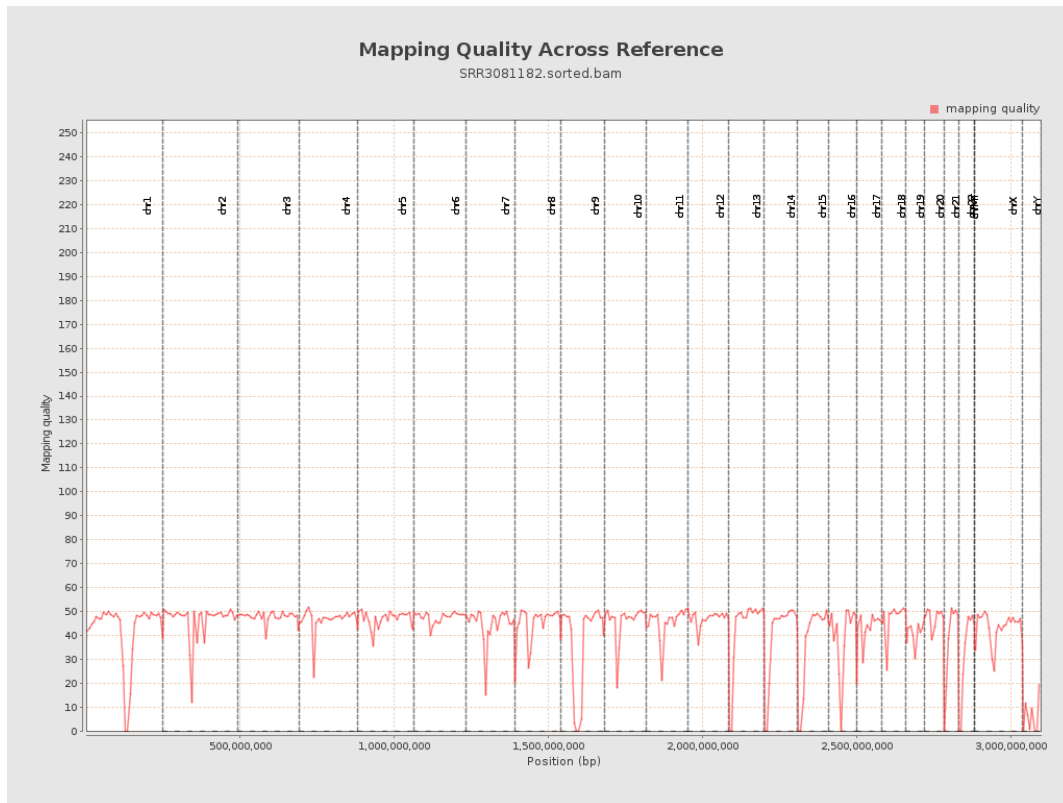
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

