

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 10:54:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081940.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_SRR3081940 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081940.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 10:54:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081940.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,645,729
Mapped reads	2,406,297 / 90.95%
Unmapped reads	239,432 / 9.05%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,889 / 0.52%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	126,836 / 4.79%
Duplication rate	3.98%
Clipped reads	992,727 / 37.52%

2.2. ACGT Content

Number/percentage of A's	44,891,910 / 27.73%
Number/percentage of C's	29,842,477 / 18.43%
Number/percentage of T's	51,113,496 / 31.57%
Number/percentage of G's	36,020,501 / 22.25%
Number/percentage of N's	20,357 / 0.01%
GC Percentage	40.68%

2.3. Coverage

Mean	0.0523

Standard Deviation	0.5074
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2.4. Mapping Quality

Mean Mapping Quality	45.47
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2.5. Mismatches and indels

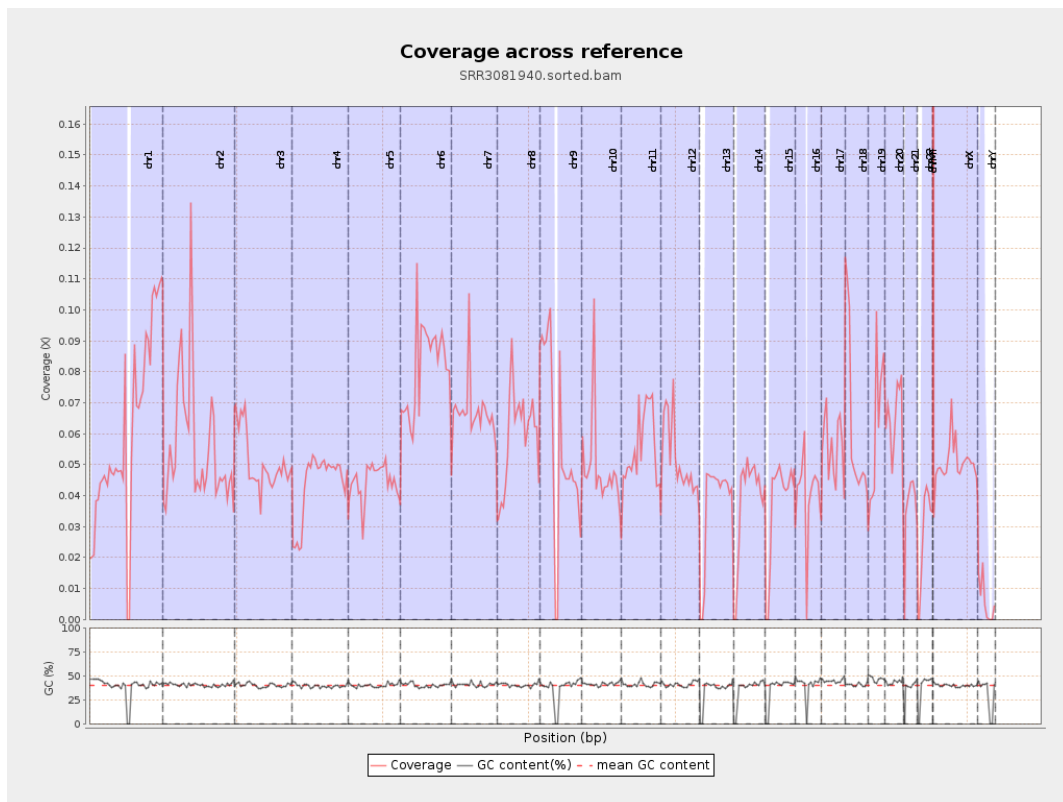
General error rate	0.81%
Mismatches	1,283,116
Insertions	11,614
Mapped reads with at least one insertion	0.48%
Deletions	36,855
Mapped reads with at least one deletion	1.52%
Homopolymer indels	47.04%

2.6. Chromosome stats

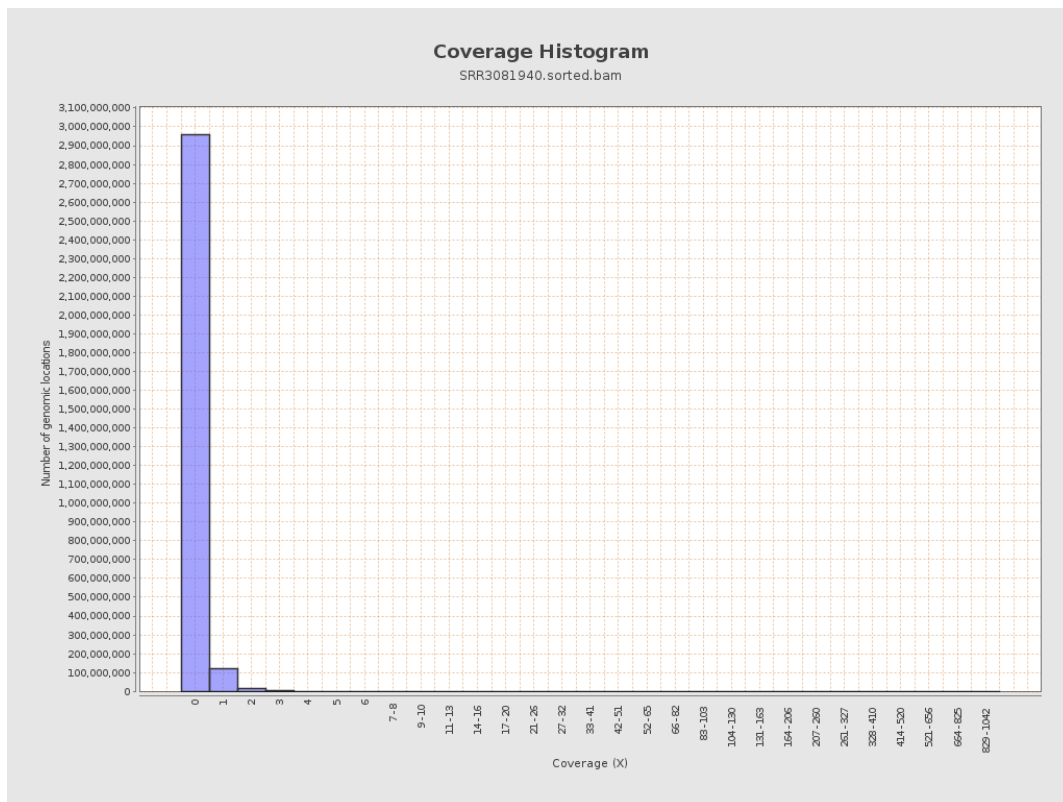
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	15165738	0.0608	0.923
chr2	243199373	13646729	0.0561	0.7122
chr3	198022430	10068023	0.0508	0.2547
chr4	191154276	8378325	0.0438	0.2571
chr5	180915260	8002081	0.0442	0.2391
chr6	171115067	13956024	0.0816	0.4465
chr7	159138663	10630738	0.0668	0.7213

chr8	146364022	8712916	0.0595	0.6117
chr9	141213431	7967573	0.0564	0.5528
chr10	135534747	6598406	0.0487	0.4868
chr11	135006516	7518175	0.0557	0.3741
chr12	133851895	6901987	0.0516	0.2727
chr13	115169878	4265320	0.037	0.2168
chr14	107349540	4135616	0.0385	0.2668
chr15	102531392	3783406	0.0369	0.2221
chr16	90354753	3591236	0.0397	0.2762
chr17	81195210	4567422	0.0563	0.3067
chr18	78077248	4813881	0.0617	0.8895
chr19	59128983	3672778	0.0621	0.6618
chr20	63025520	4122192	0.0654	0.297
chr21	48129895	1712438	0.0356	0.242
chr22	51304566	1409836	0.0275	0.1836
chrMT	16571	132033	7.9677	4.826
chrX	155270560	7843130	0.0505	0.3196
chrY	59373566	356986	0.006	0.1548

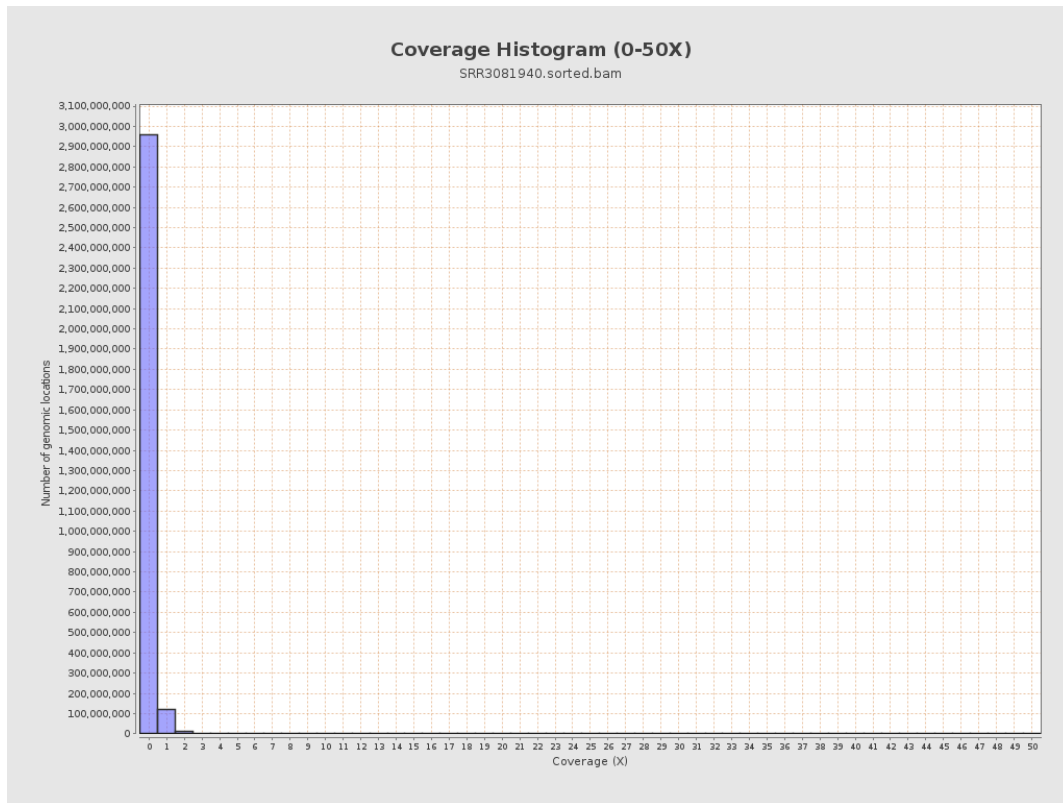
3. Results : Coverage across reference



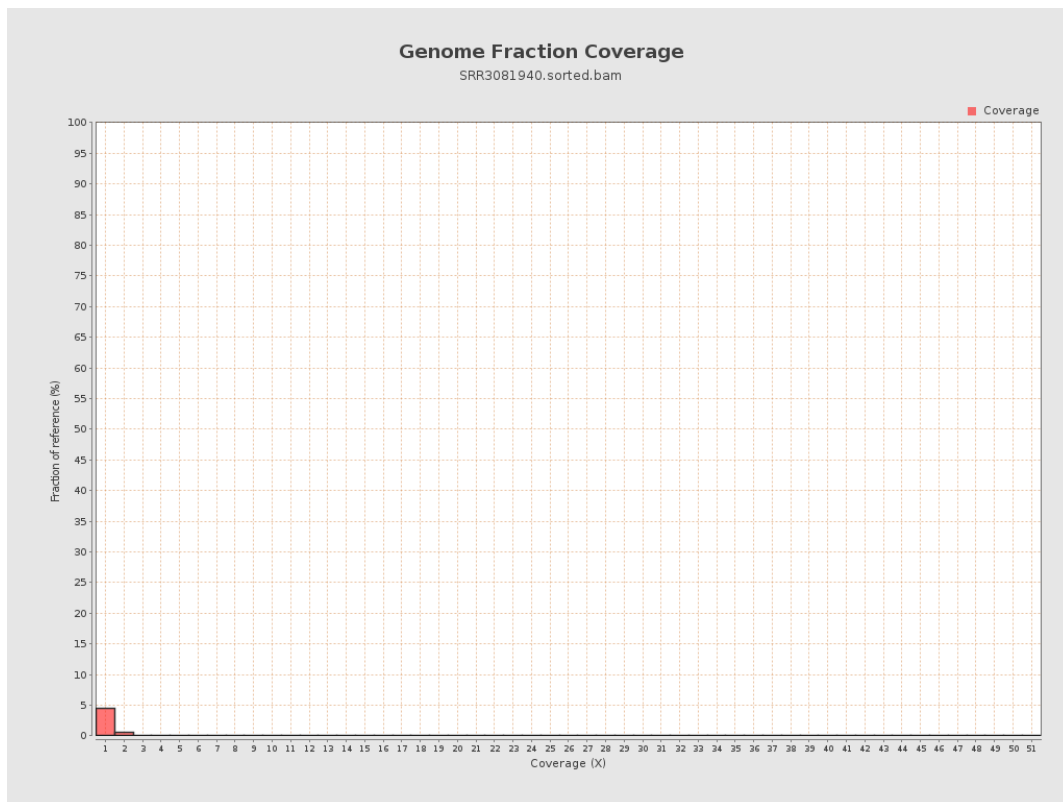
4. Results : Coverage Histogram



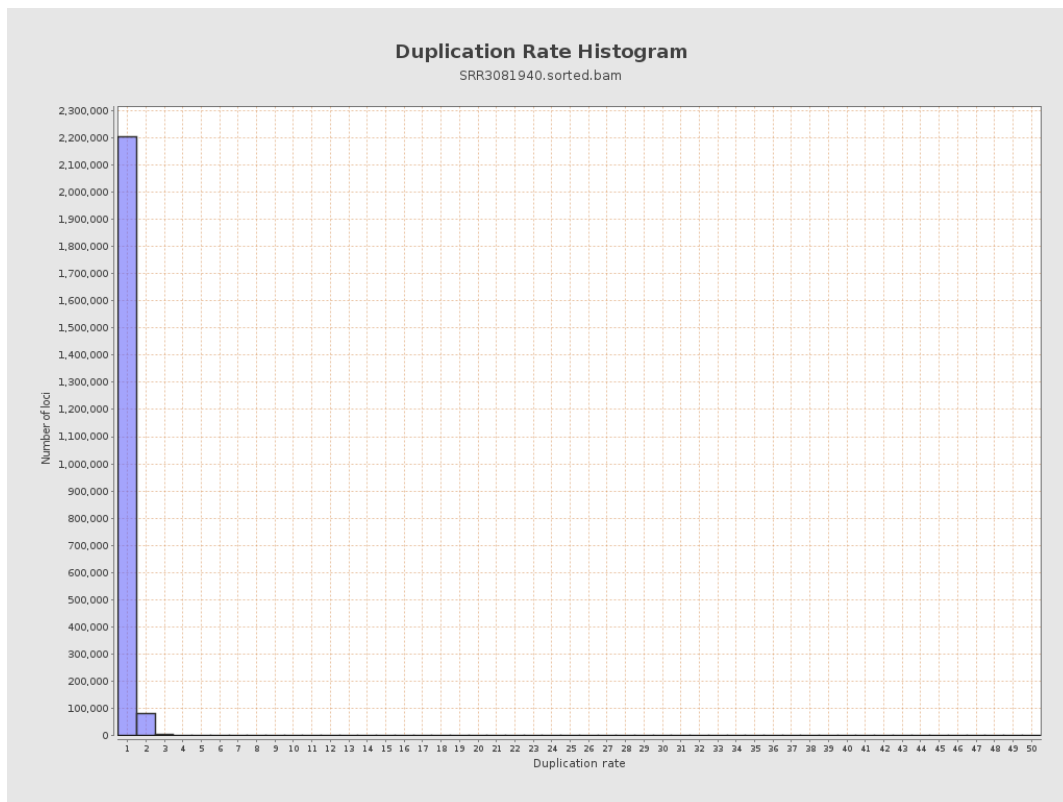
5. Results : Coverage Histogram (0-50X)



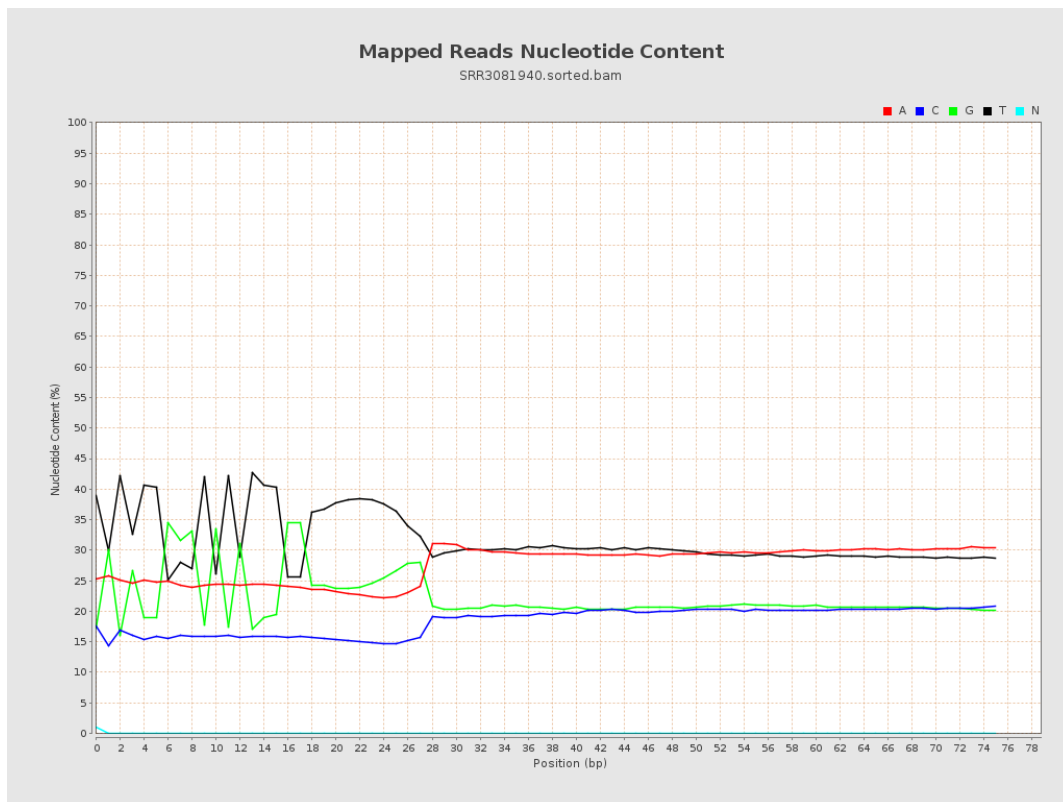
6. Results : Genome Fraction Coverage



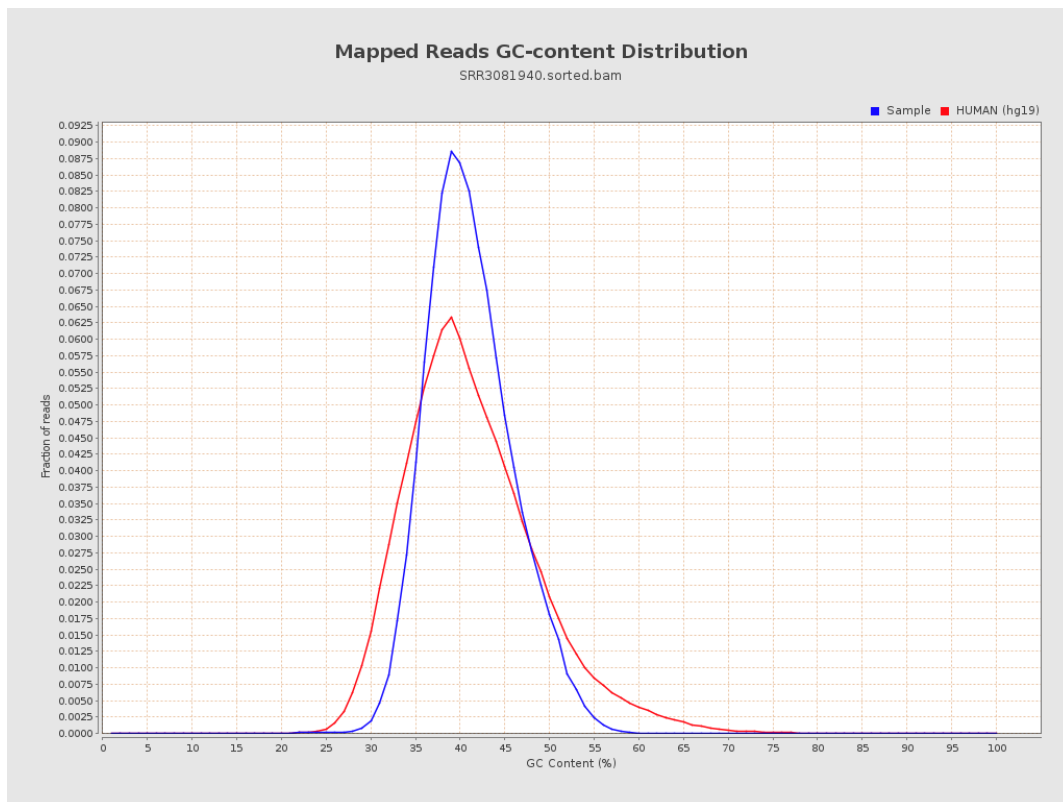
7. Results : Duplication Rate Histogram



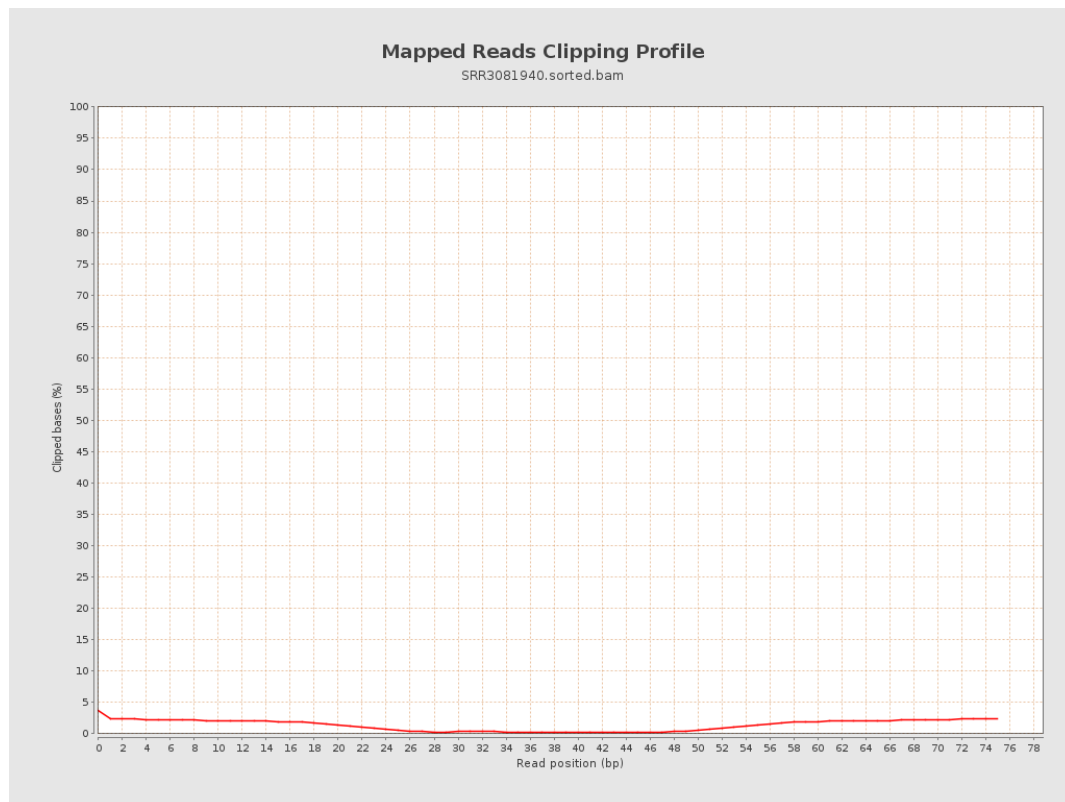
8. Results : Mapped Reads Nucleotide Content



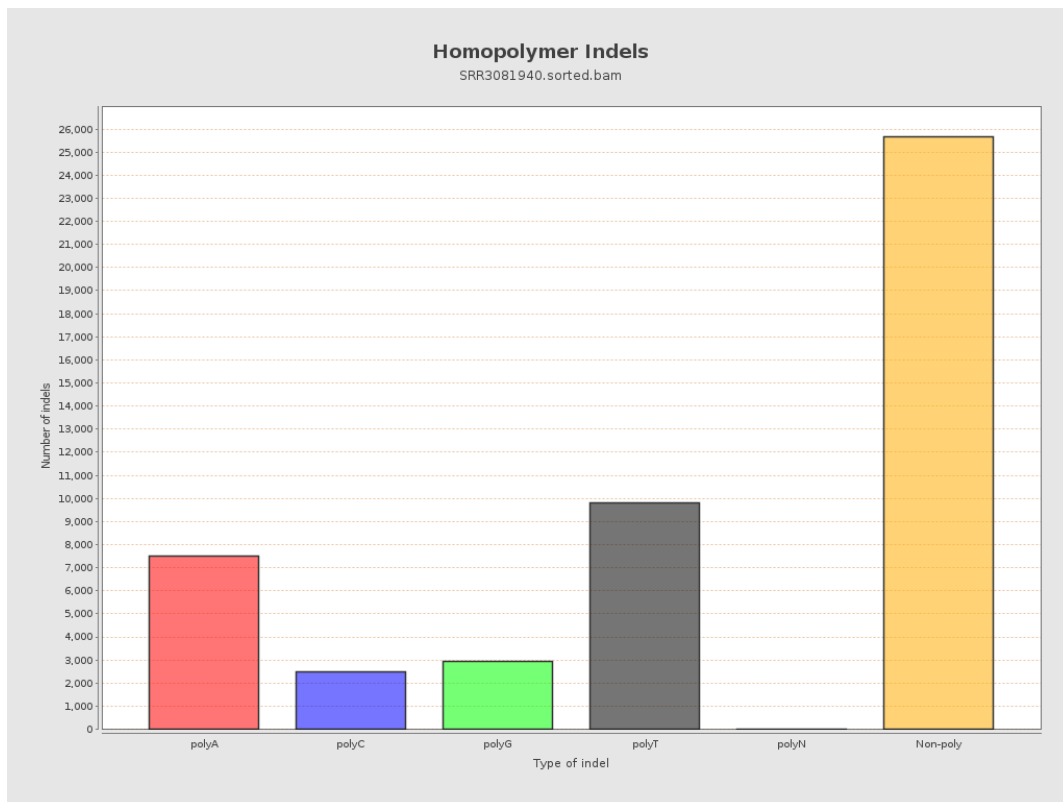
9. Results : Mapped Reads GC-content Distribution



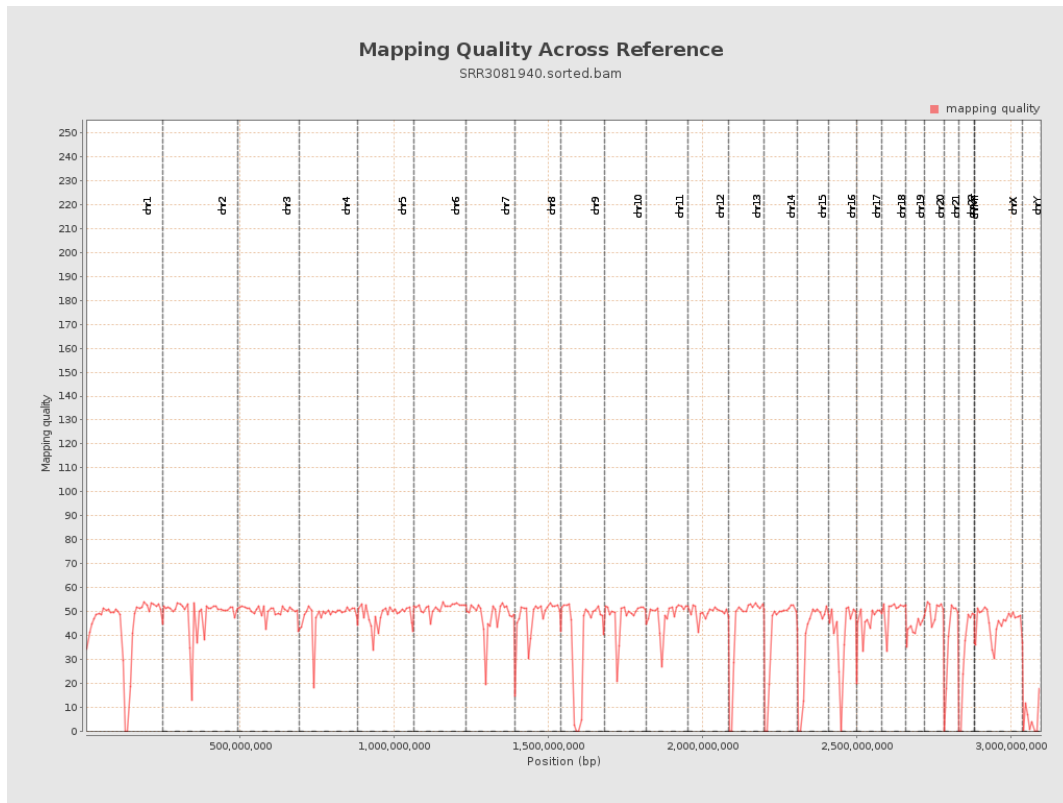
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

