

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 19:24:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6236077.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_SRR6236077 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6236077.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 19:24:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6236077.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,238,989
Mapped reads	1,060,584 / 85.6%
Unmapped reads	178,405 / 14.4%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,019 / 0.73%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	58,668 / 4.74%
Duplication rate	4.63%
Clipped reads	531,043 / 42.86%

2.2. ACGT Content

Number/percentage of A's	18,834,981 / 27.22%
Number/percentage of C's	12,465,355 / 18.02%
Number/percentage of T's	22,212,406 / 32.1%
Number/percentage of G's	15,639,431 / 22.6%
Number/percentage of N's	35,073 / 0.05%
GC Percentage	40.62%

2.3. Coverage

Mean	0.0224

Standard Deviation	0.2405
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2.4. Mapping Quality

Mean Mapping Quality	44.35
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2.5. Mismatches and indels

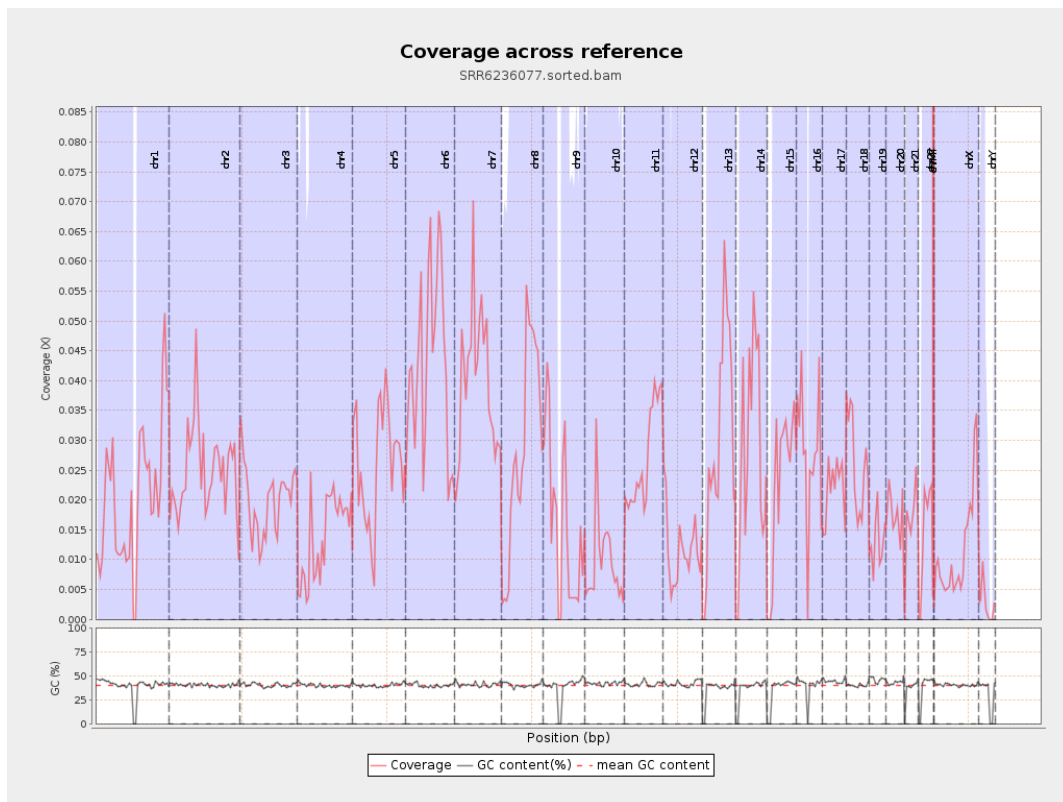
General error rate	0.87%
Mismatches	594,143
Insertions	5,089
Mapped reads with at least one insertion	0.48%
Deletions	24,524
Mapped reads with at least one deletion	2.28%
Homopolymer indels	45.45%

2.6. Chromosome stats

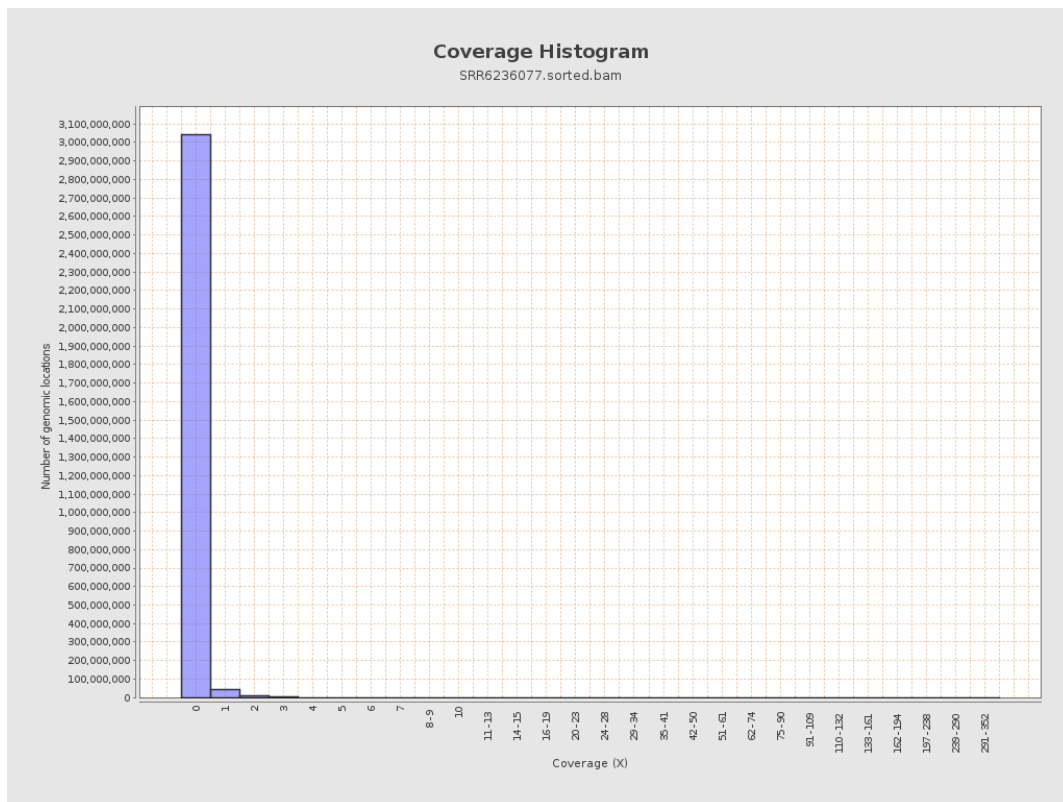
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	5092447	0.0204	0.3097
chr2	243199373	6085231	0.025	0.2763
chr3	198022430	3934613	0.0199	0.1667
chr4	191154276	2624942	0.0137	0.1572
chr5	180915260	4681468	0.0259	0.1926
chr6	171115067	7224185	0.0422	0.2934
chr7	159138663	6353534	0.0399	0.4456

chr8	146364022	4147803	0.0283	0.318
chr9	141213431	2244715	0.0159	0.1965
chr10	135534747	1292945	0.0095	0.1822
chr11	135006516	3633471	0.0269	0.2198
chr12	133851895	1578503	0.0118	0.1311
chr13	115169878	3382669	0.0294	0.2052
chr14	107349540	2929425	0.0273	0.2032
chr15	102531392	2343325	0.0229	0.1826
chr16	90354753	2493979	0.0276	0.2062
chr17	81195210	1755523	0.0216	0.1851
chr18	78077248	2040379	0.0261	0.3542
chr19	59128983	772300	0.0131	0.2203
chr20	63025520	1113133	0.0177	0.1613
chr21	48129895	803627	0.0167	0.1657
chr22	51304566	732014	0.0143	0.1396
chrMT	16571	35924	2.1679	2.0935
chrX	155270560	1780200	0.0115	0.1352
chrY	59373566	153626	0.0026	0.089

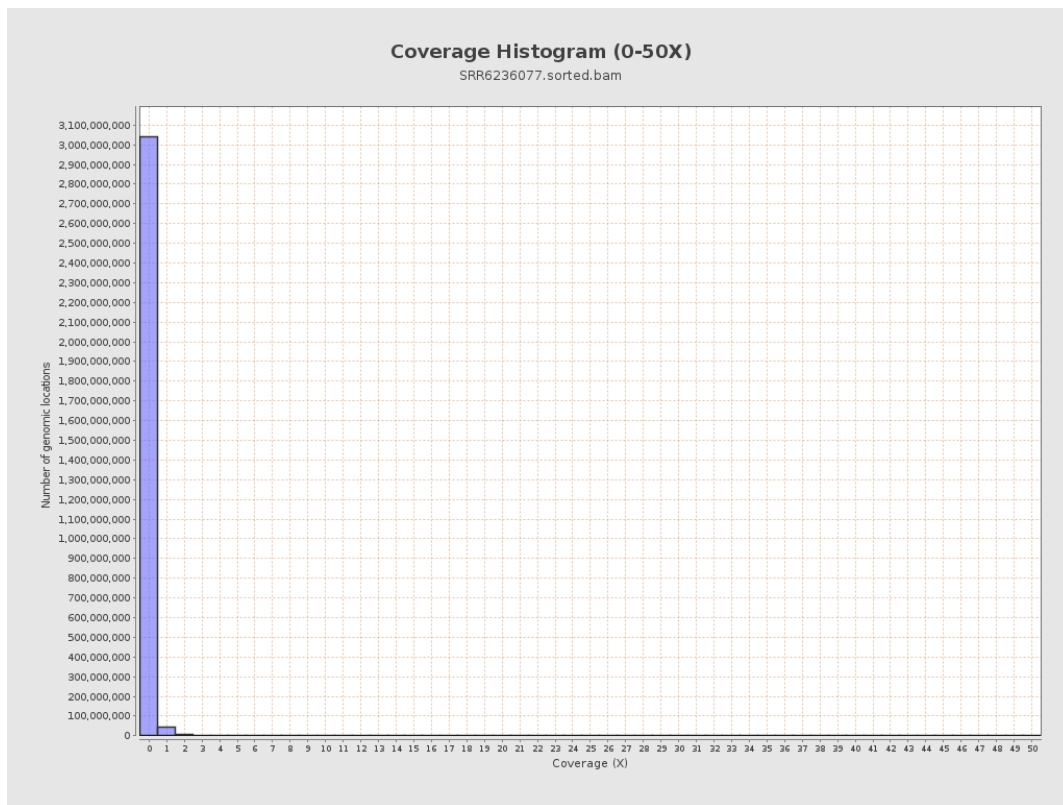
3. Results : Coverage across reference



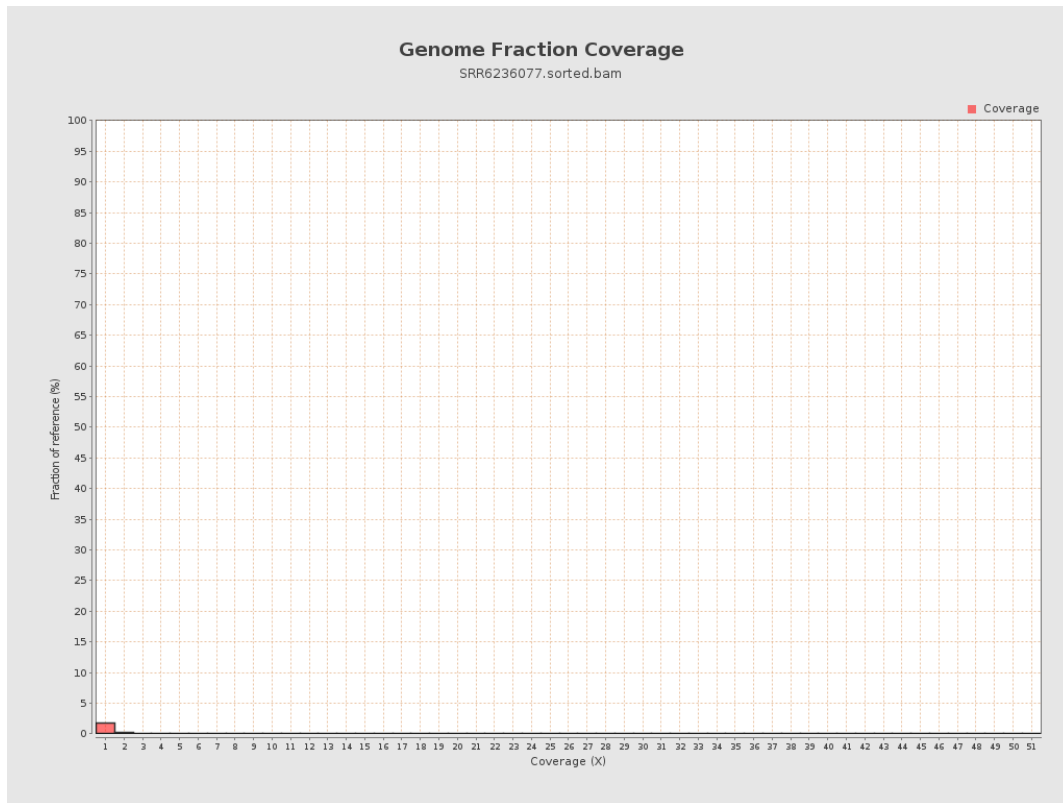
4. Results : Coverage Histogram



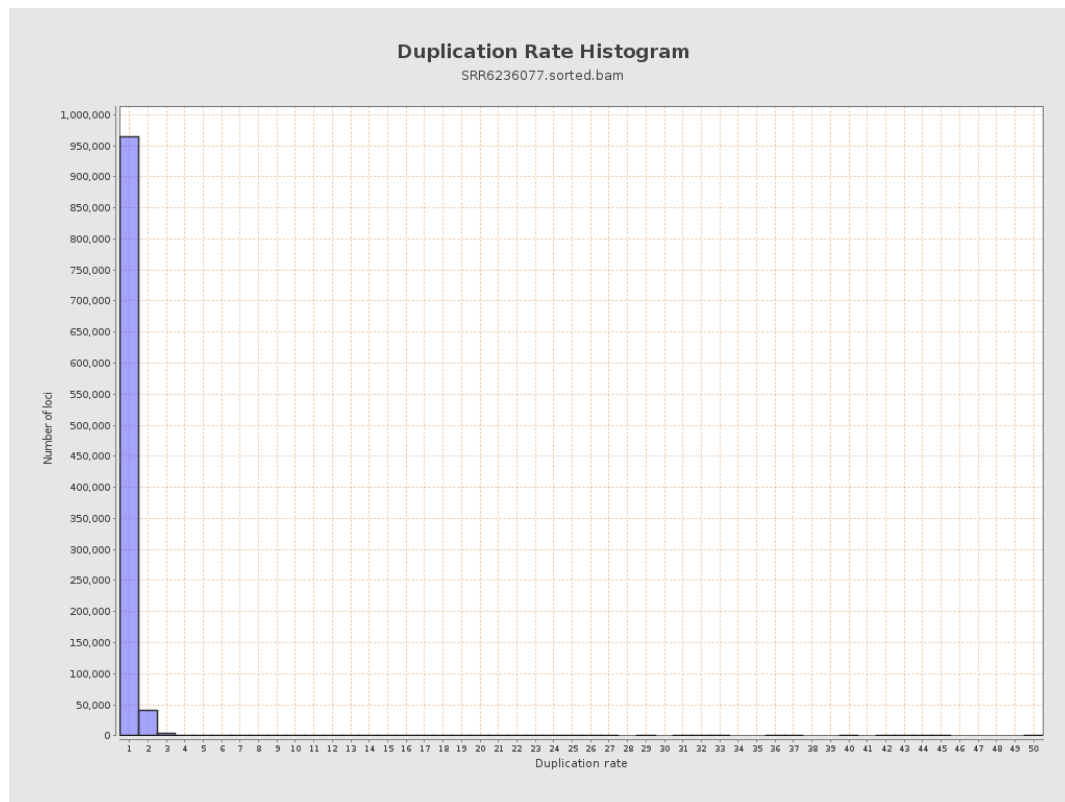
5. Results : Coverage Histogram (0-50X)



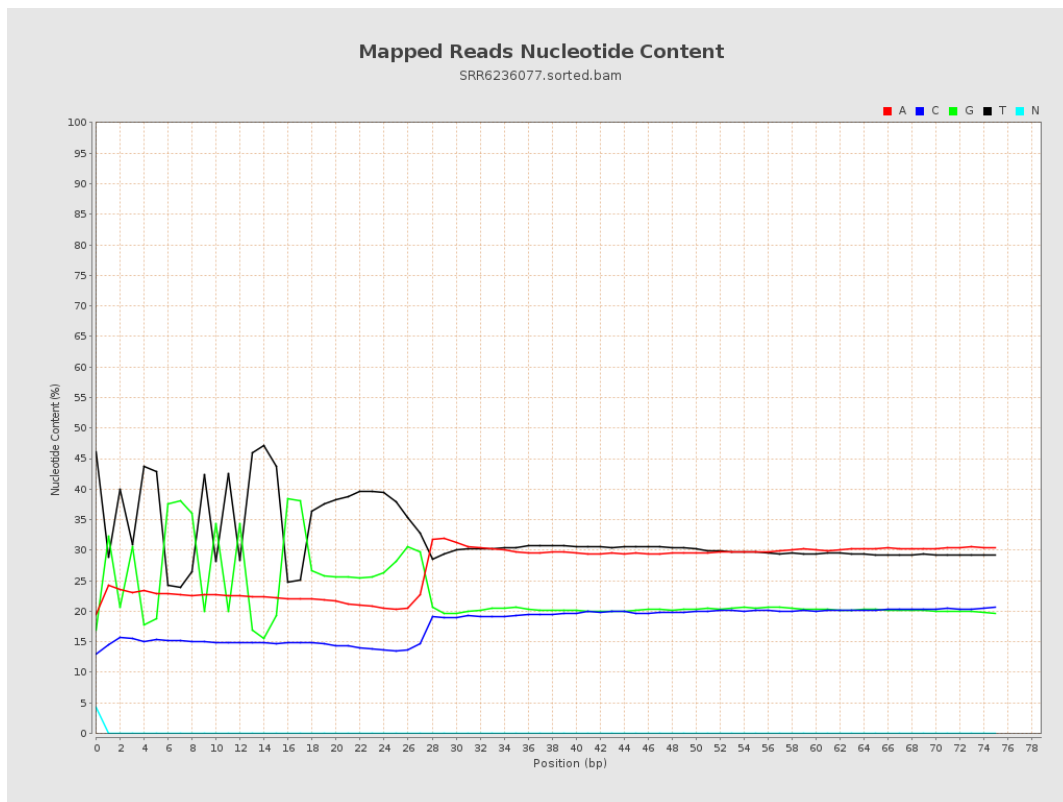
6. Results : Genome Fraction Coverage



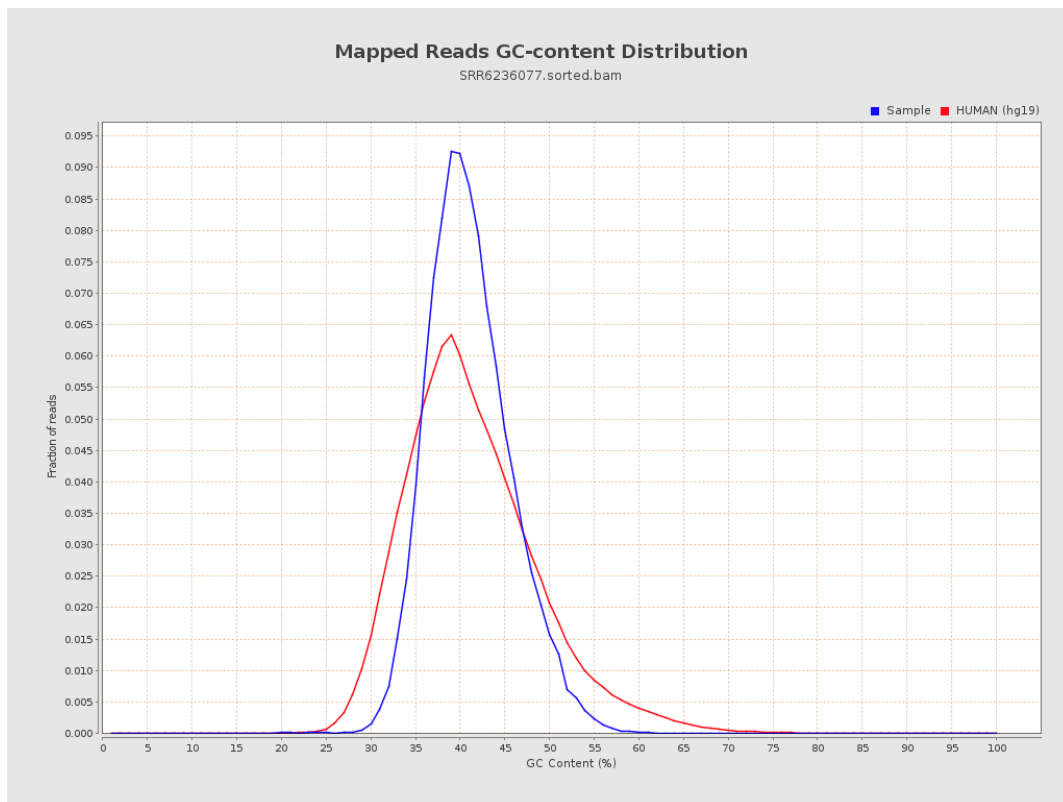
7. Results : Duplication Rate Histogram



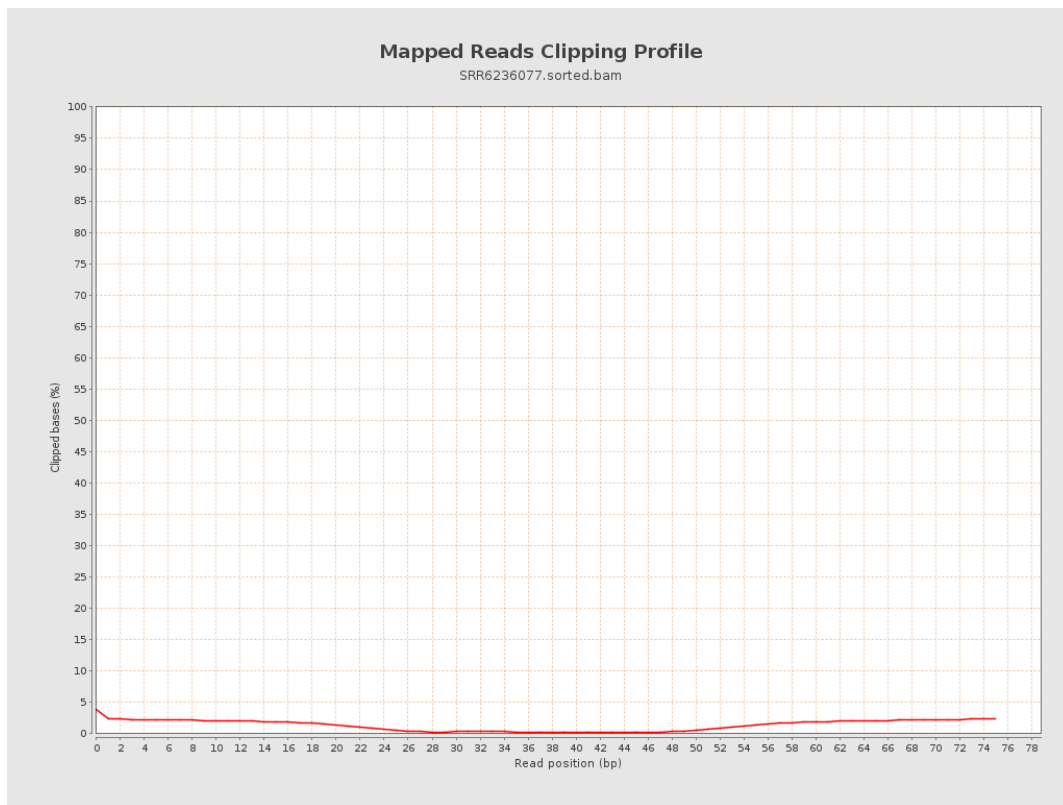
8. Results : Mapped Reads Nucleotide Content



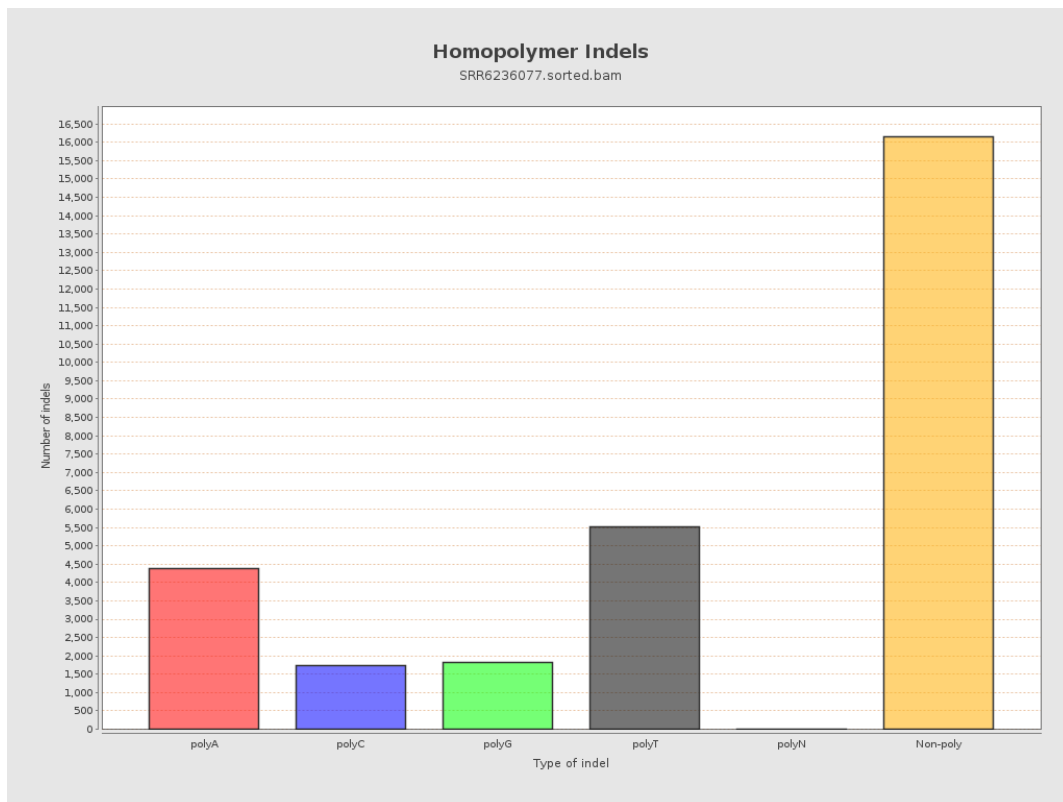
9. Results : Mapped Reads GC-content Distribution



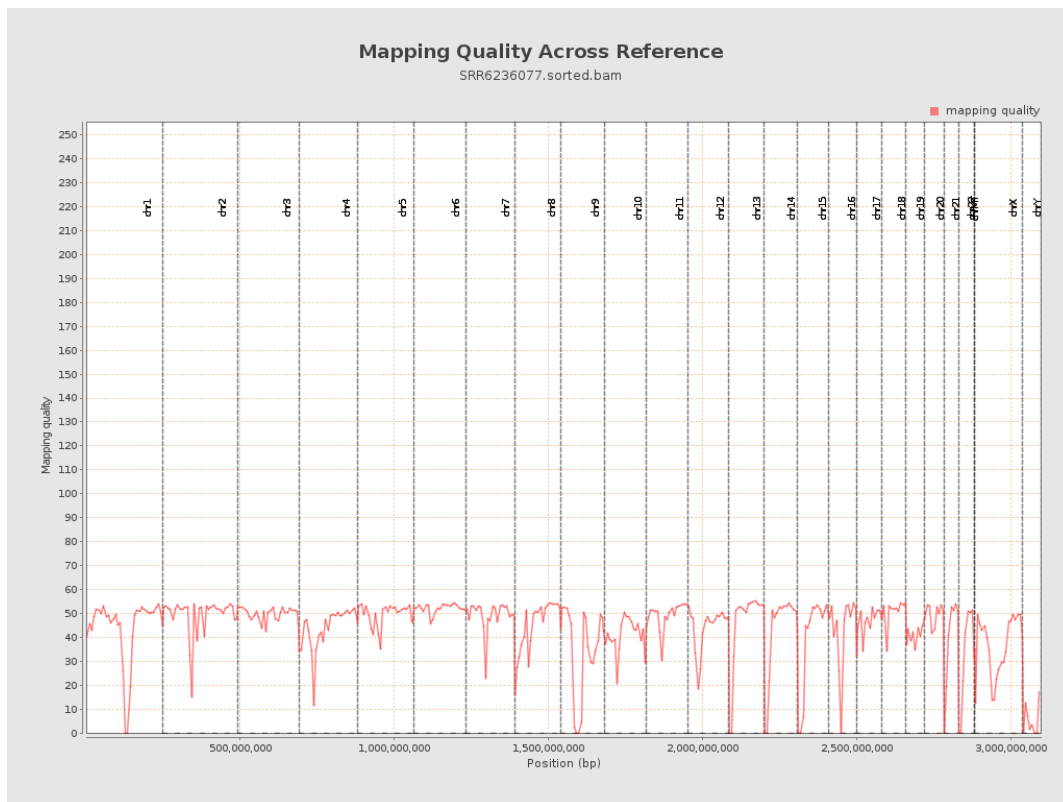
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

