

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 00:18:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004079.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_SRR6004079 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004079.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 00:18:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004079.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,026,184
Mapped reads	2,712,215 / 89.62%
Unmapped reads	313,969 / 10.38%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	22,824 / 0.75%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	91,667 / 3.03%
Duplication rate	2.25%
Clipped reads	1,422,985 / 47.02%

2.2. ACGT Content

Number/percentage of A's	48,479,237 / 27.48%
Number/percentage of C's	34,309,163 / 19.45%
Number/percentage of T's	52,694,567 / 29.87%
Number/percentage of G's	40,884,515 / 23.18%
Number/percentage of N's	36,343 / 0.02%
GC Percentage	42.63%

2.3. Coverage

Mean	0.057

Standard Deviation	0.4837
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2.4. Mapping Quality

Mean Mapping Quality	42.07
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2.5. Mismatches and indels

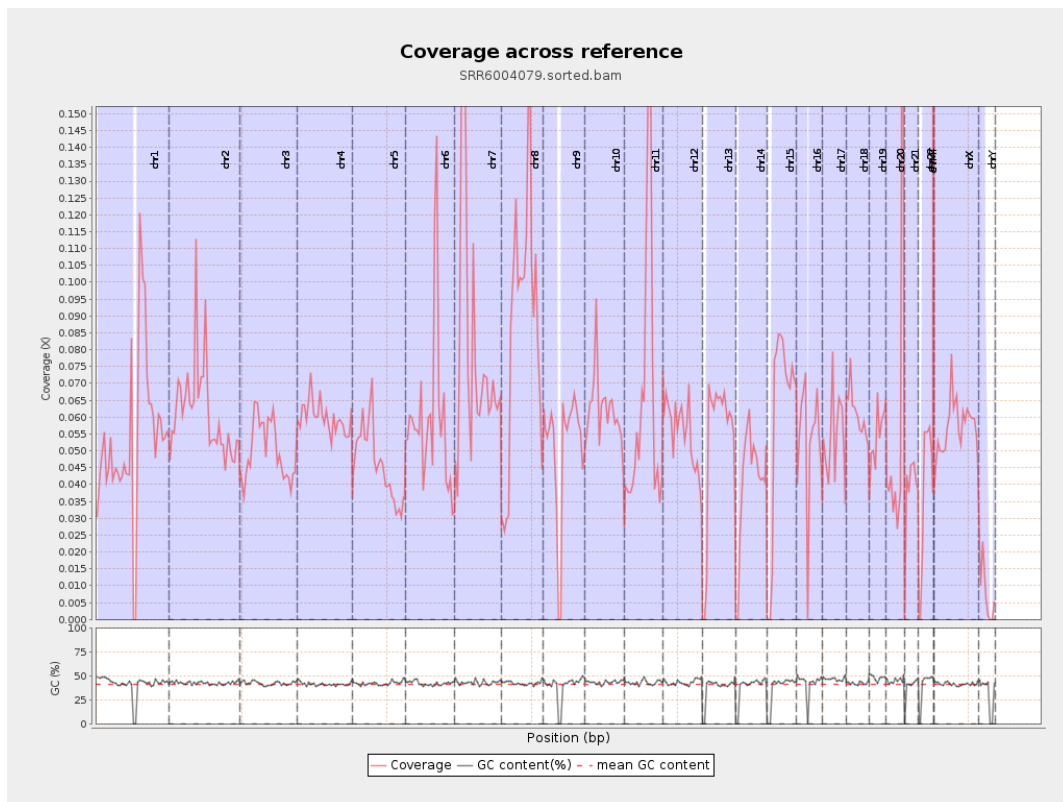
General error rate	0.88%
Mismatches	1,530,222
Insertions	14,454
Mapped reads with at least one insertion	0.53%
Deletions	53,708
Mapped reads with at least one deletion	1.95%
Homopolymer indels	43.32%

2.6. Chromosome stats

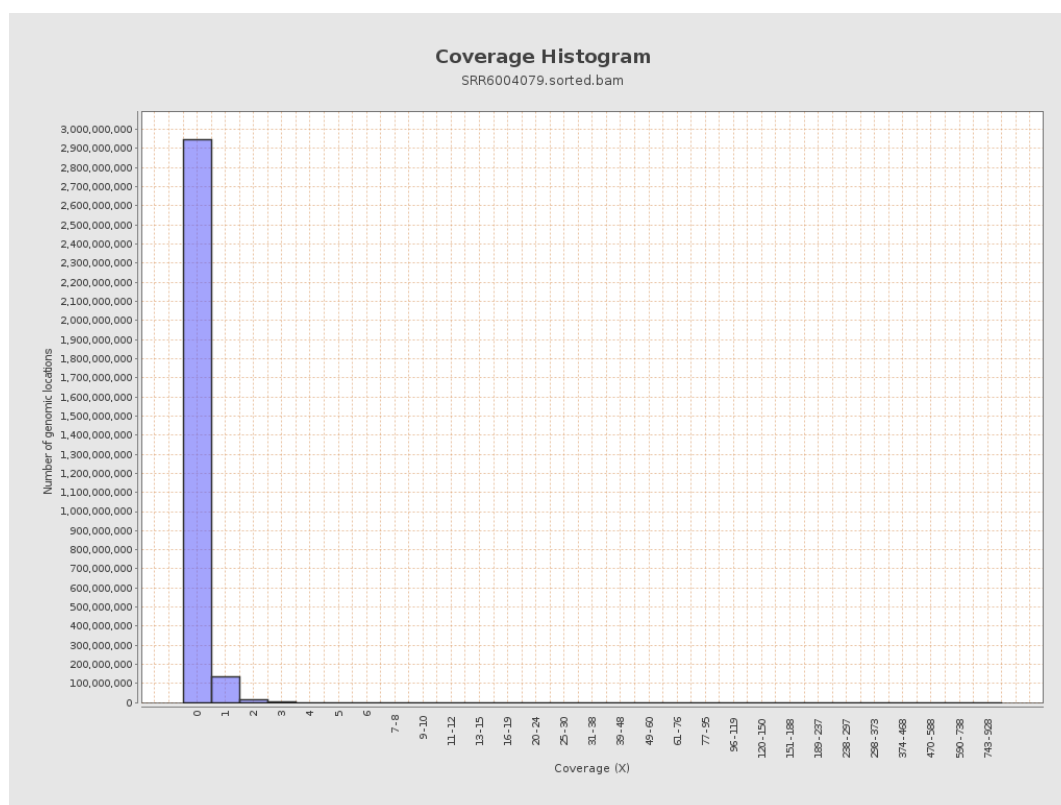
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	13397715	0.0538	0.83
chr2	243199373	14951175	0.0615	0.61
chr3	198022430	9873956	0.0499	0.2511
chr4	191154276	11439517	0.0598	0.2911
chr5	180915260	8299631	0.0459	0.2471
chr6	171115067	10163490	0.0594	0.3422
chr7	159138663	12972651	0.0815	0.7723

chr8	146364022	12554495	0.0858	0.6018
chr9	141213431	7137511	0.0505	0.4806
chr10	135534747	8450509	0.0623	0.4539
chr11	135006516	8795365	0.0651	0.4473
chr12	133851895	7391273	0.0552	0.2751
chr13	115169878	6057370	0.0526	0.2545
chr14	107349540	4356555	0.0406	0.3027
chr15	102531392	6240301	0.0609	0.2952
chr16	90354753	4811817	0.0533	0.3247
chr17	81195210	4370195	0.0538	0.2906
chr18	78077248	4778734	0.0612	0.8717
chr19	59128983	3226242	0.0546	0.6305
chr20	63025520	4167719	0.0661	0.3356
chr21	48129895	1842165	0.0383	0.2582
chr22	51304566	1906562	0.0372	0.2132
chrMT	16571	9668	0.5834	0.9161
chrX	155270560	8835671	0.0569	0.3278
chrY	59373566	463705	0.0078	0.1556

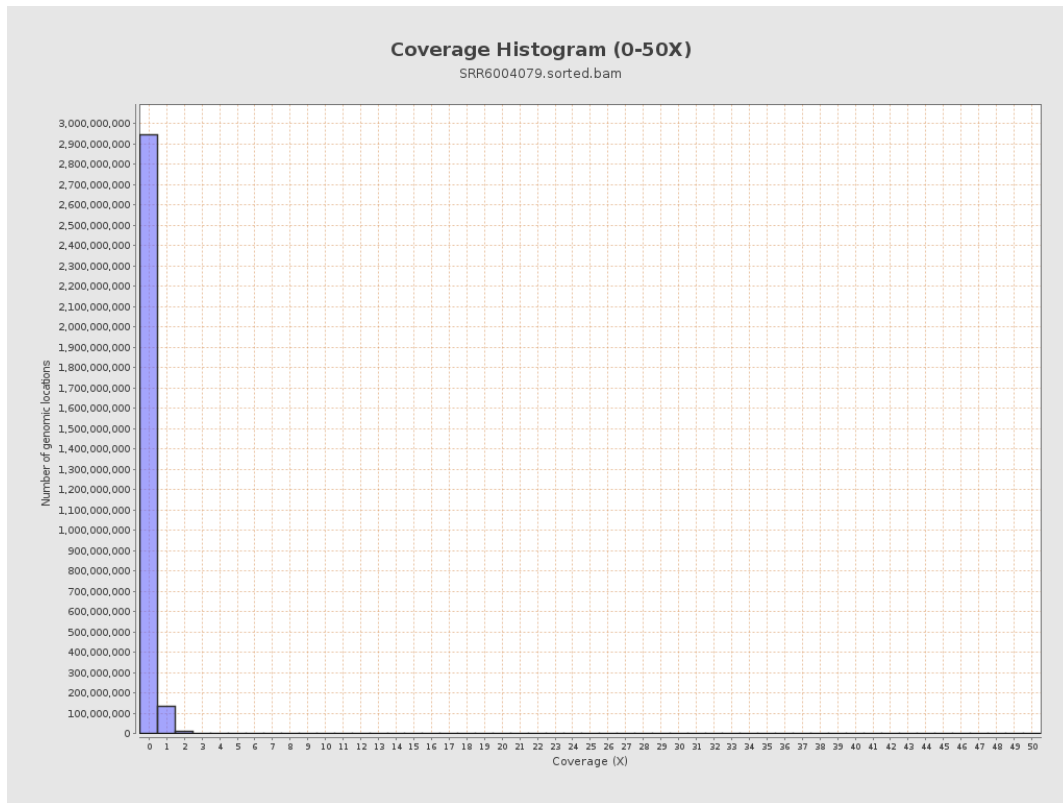
3. Results : Coverage across reference



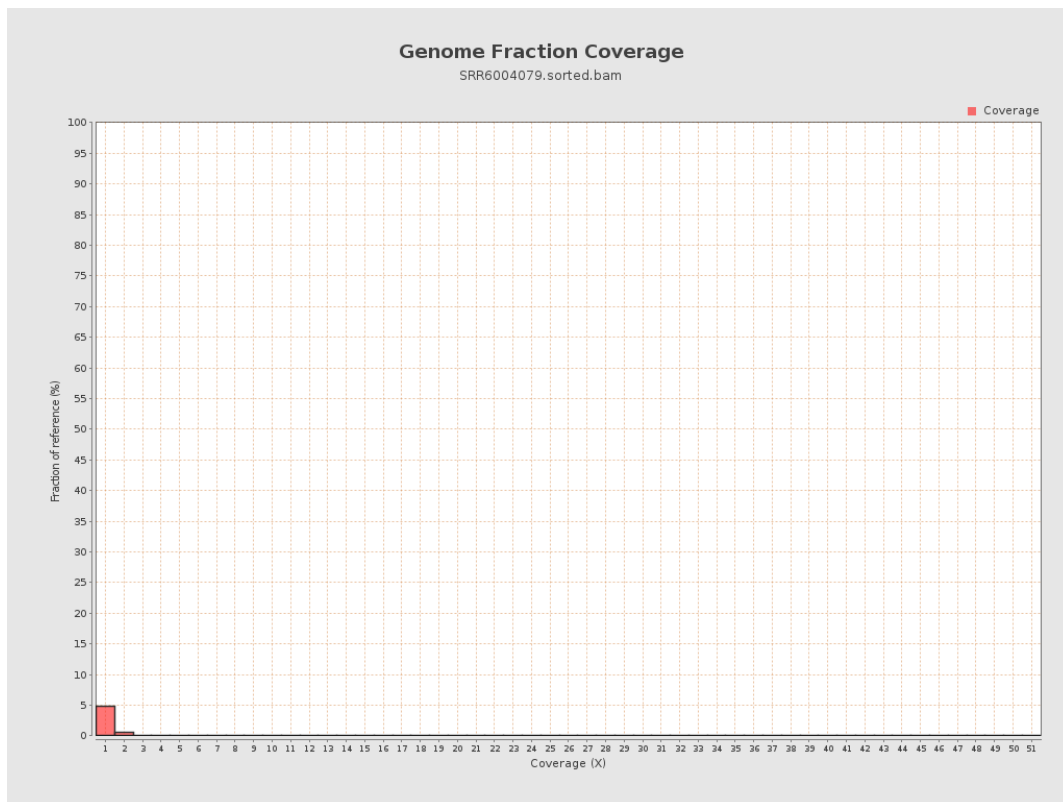
4. Results : Coverage Histogram



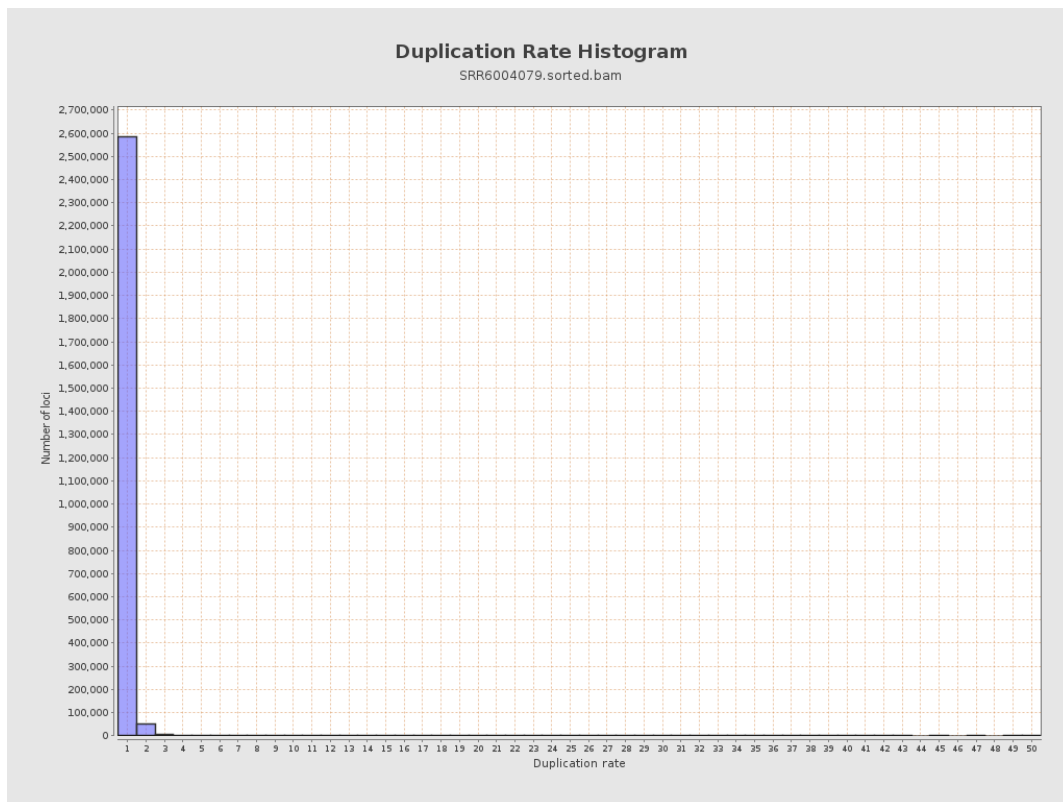
5. Results : Coverage Histogram (0-50X)



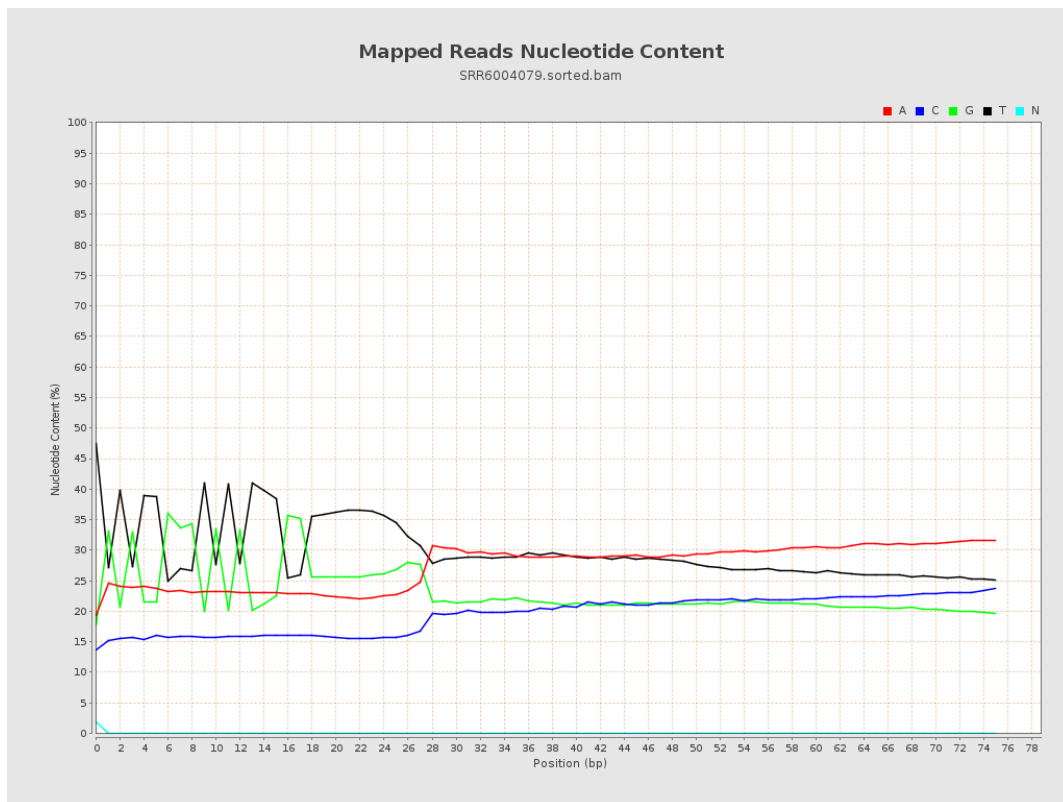
6. Results : Genome Fraction Coverage



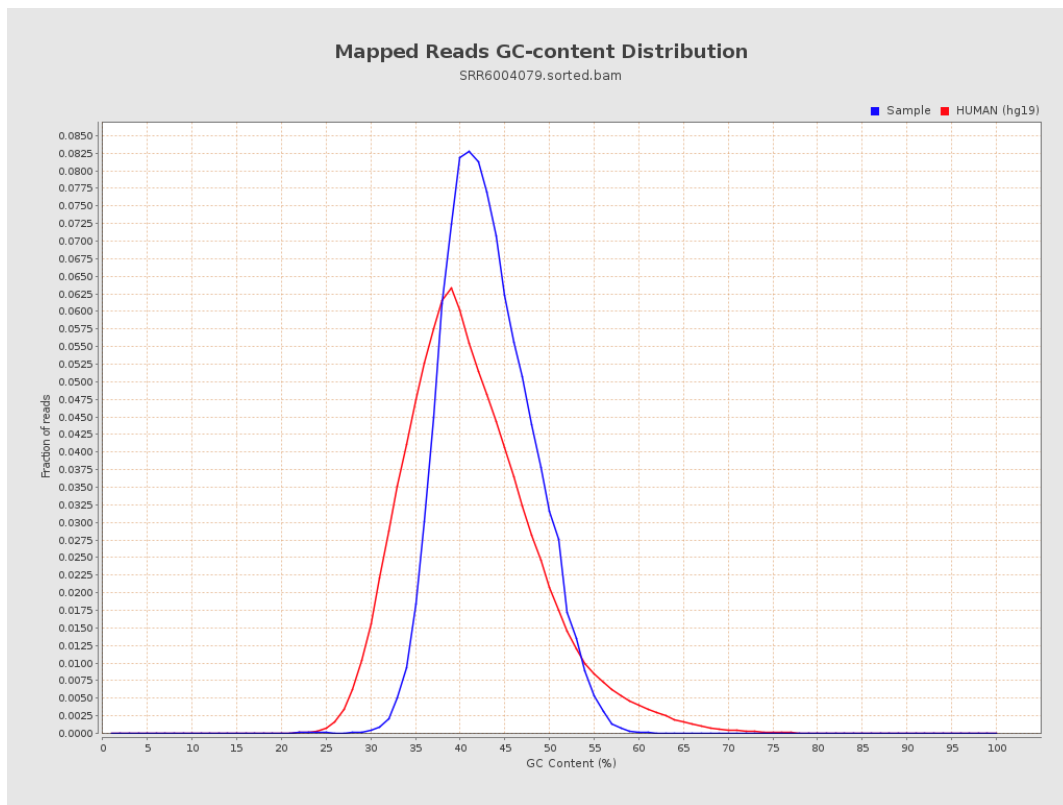
7. Results : Duplication Rate Histogram



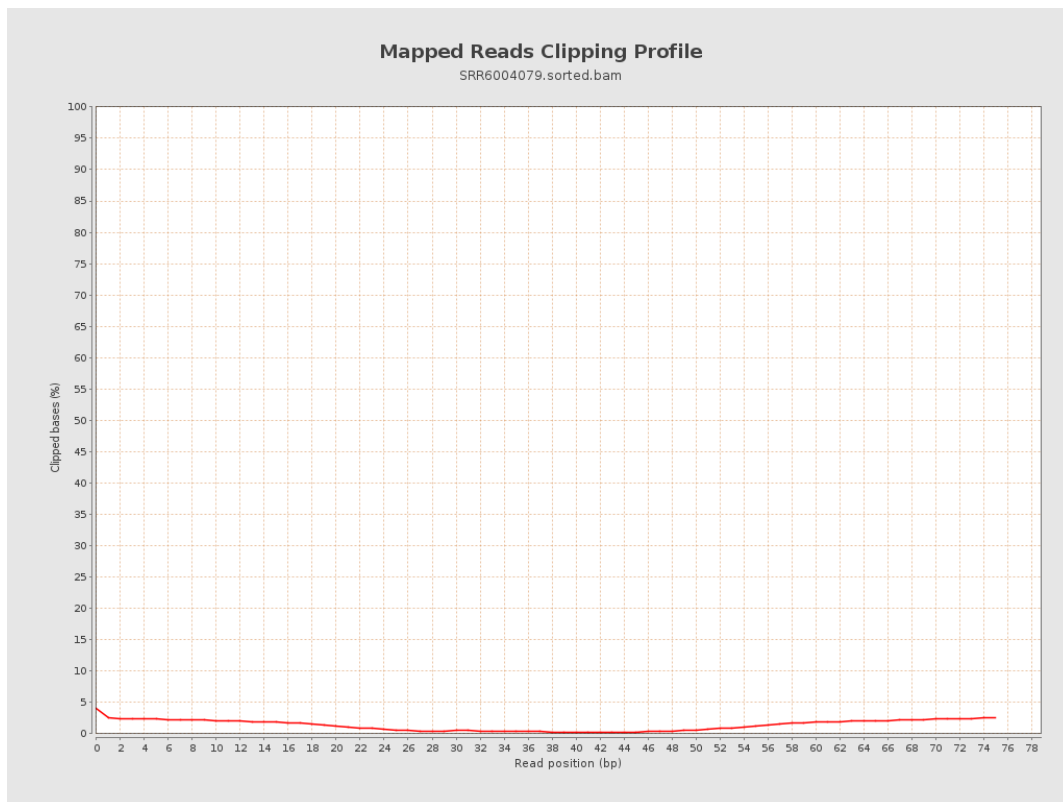
8. Results : Mapped Reads Nucleotide Content



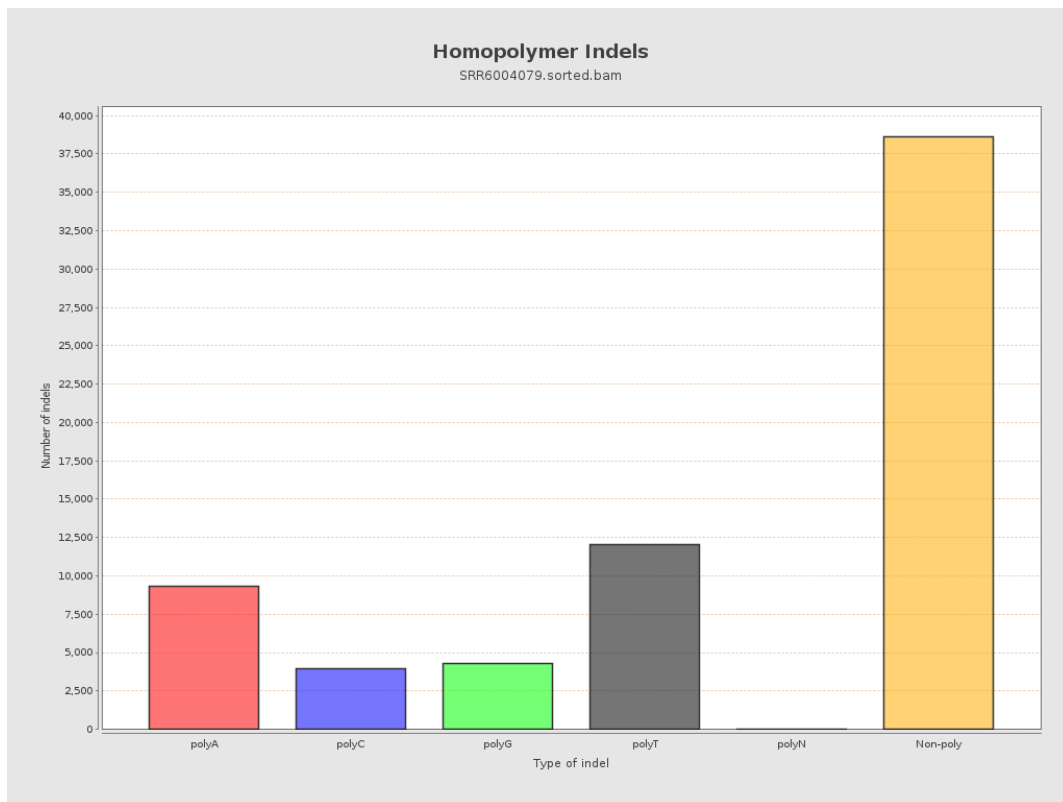
9. Results : Mapped Reads GC-content Distribution



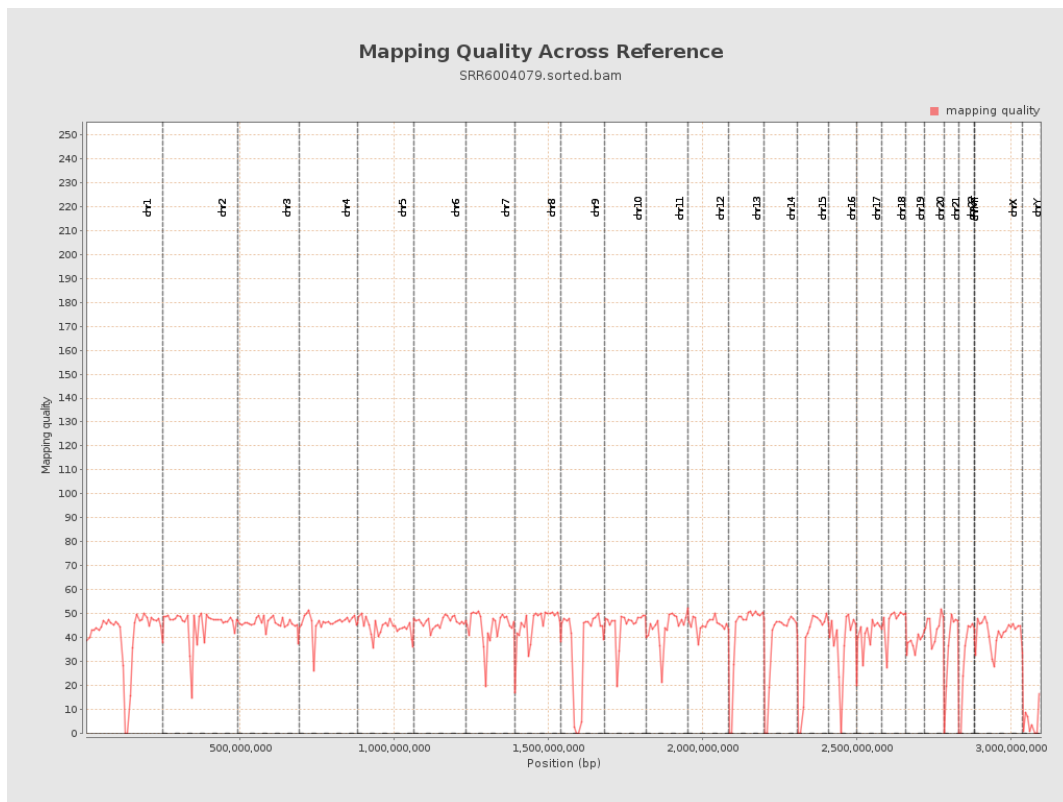
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

