

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/13 21:47:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004033.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_SRR6004033 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004033.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 13 21:47:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004033.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,153,861
Mapped reads	964,392 / 83.58%
Unmapped reads	189,469 / 16.42%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,969 / 0.69%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	27,622 / 2.39%
Duplication rate	1.97%
Clipped reads	471,043 / 40.82%

2.2. ACGT Content

Number/percentage of A's	18,063,286 / 28.26%
Number/percentage of C's	11,834,839 / 18.52%
Number/percentage of T's	19,773,927 / 30.94%
Number/percentage of G's	14,235,292 / 22.27%
Number/percentage of N's	11,210 / 0.02%
GC Percentage	40.79%

2.3. Coverage

Mean	0.0207

Standard Deviation	0.2486
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2.4. Mapping Quality

Mean Mapping Quality	42.91
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2.5. Mismatches and indels

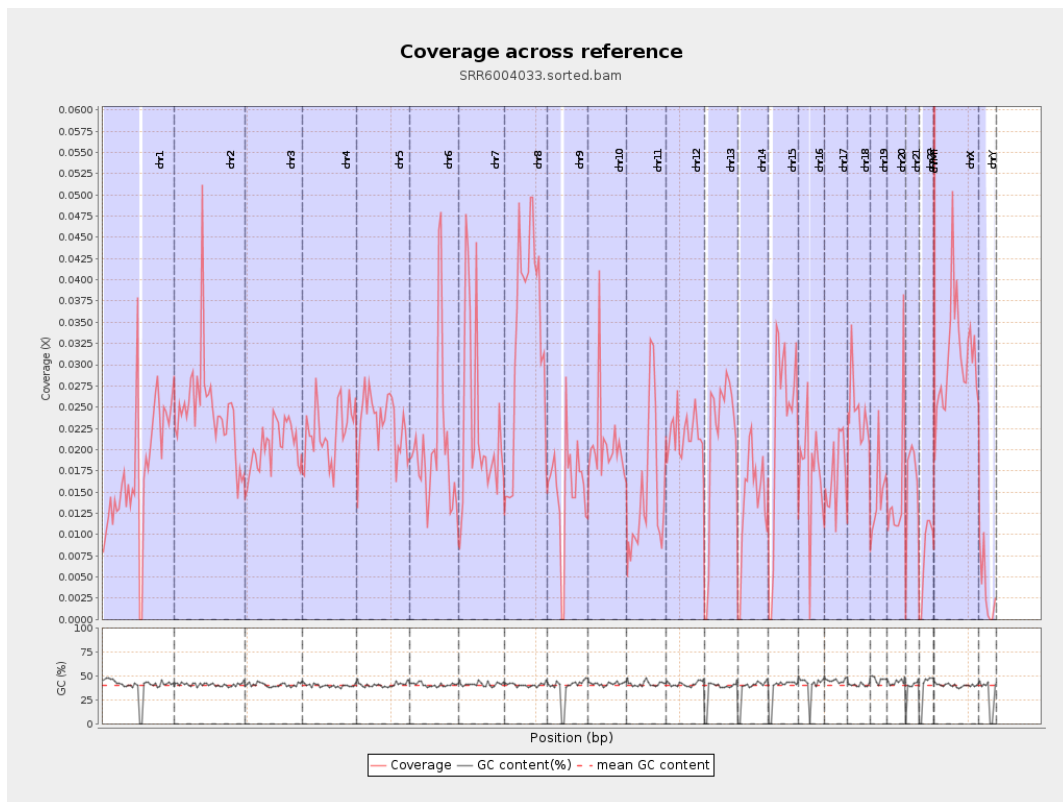
General error rate	1.03%
Mismatches	647,920
Insertions	5,795
Mapped reads with at least one insertion	0.6%
Deletions	18,525
Mapped reads with at least one deletion	1.9%
Homopolymer indels	44.61%

2.6. Chromosome stats

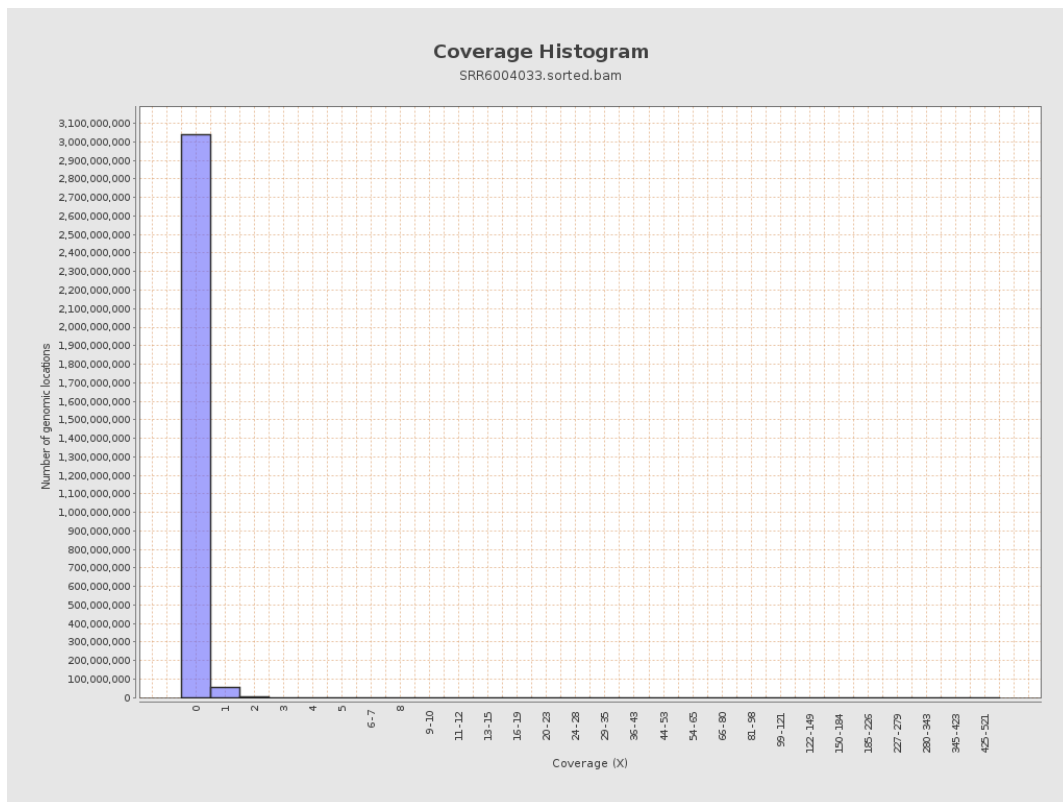
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	4389689	0.0176	0.4574
chr2	243199373	5974158	0.0246	0.2756
chr3	198022430	4036384	0.0204	0.1504
chr4	191154276	4221041	0.0221	0.1627
chr5	180915260	4219624	0.0233	0.1631
chr6	171115067	3473380	0.0203	0.1588
chr7	159138663	3584527	0.0225	0.3454

chr8	146364022	4931449	0.0337	0.3399
chr9	141213431	2173656	0.0154	0.2348
chr10	135534747	2782751	0.0205	0.2251
chr11	135006516	1993777	0.0148	0.1807
chr12	133851895	2915051	0.0218	0.1606
chr13	115169878	2434837	0.0211	0.1533
chr14	107349540	1504583	0.014	0.1447
chr15	102531392	2383537	0.0232	0.1618
chr16	90354753	1549090	0.0171	0.1694
chr17	81195210	1393163	0.0172	0.1482
chr18	78077248	1907198	0.0244	0.4368
chr19	59128983	867407	0.0147	0.3317
chr20	63025520	975356	0.0155	0.1376
chr21	48129895	793299	0.0165	0.1496
chr22	51304566	399056	0.0078	0.0915
chrMT	16571	32457	1.9587	2.0108
chrX	155270560	4812245	0.031	0.2089
chrY	59373566	201533	0.0034	0.0873

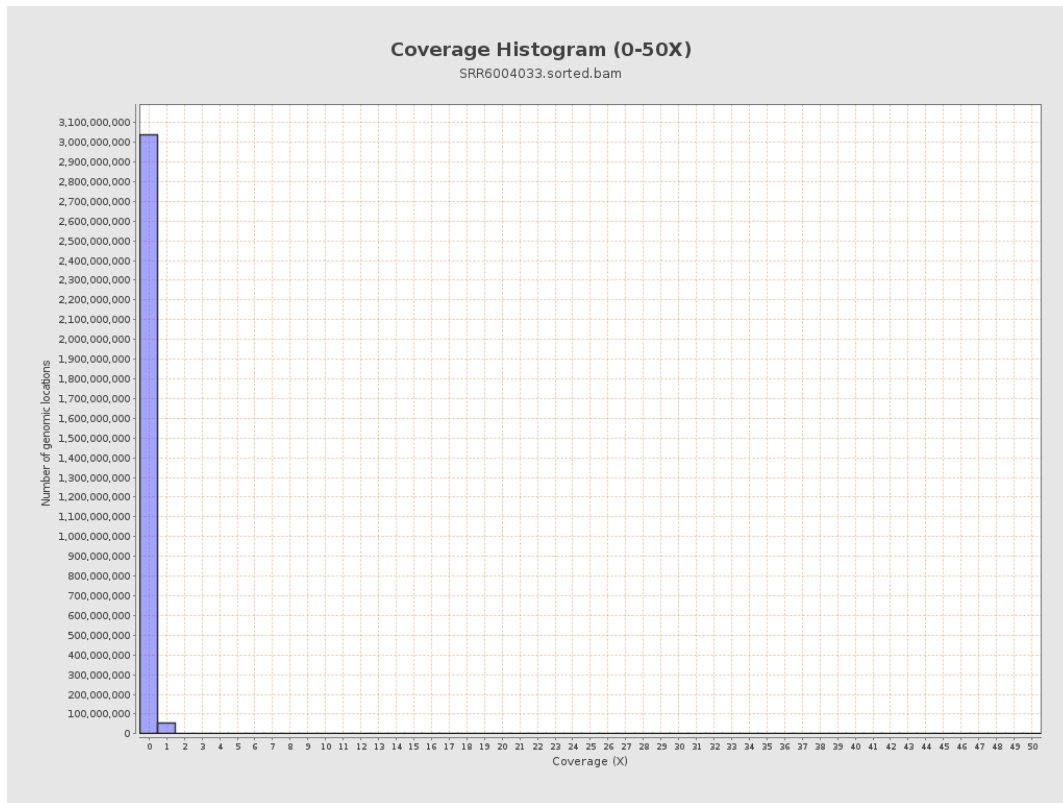
3. Results : Coverage across reference



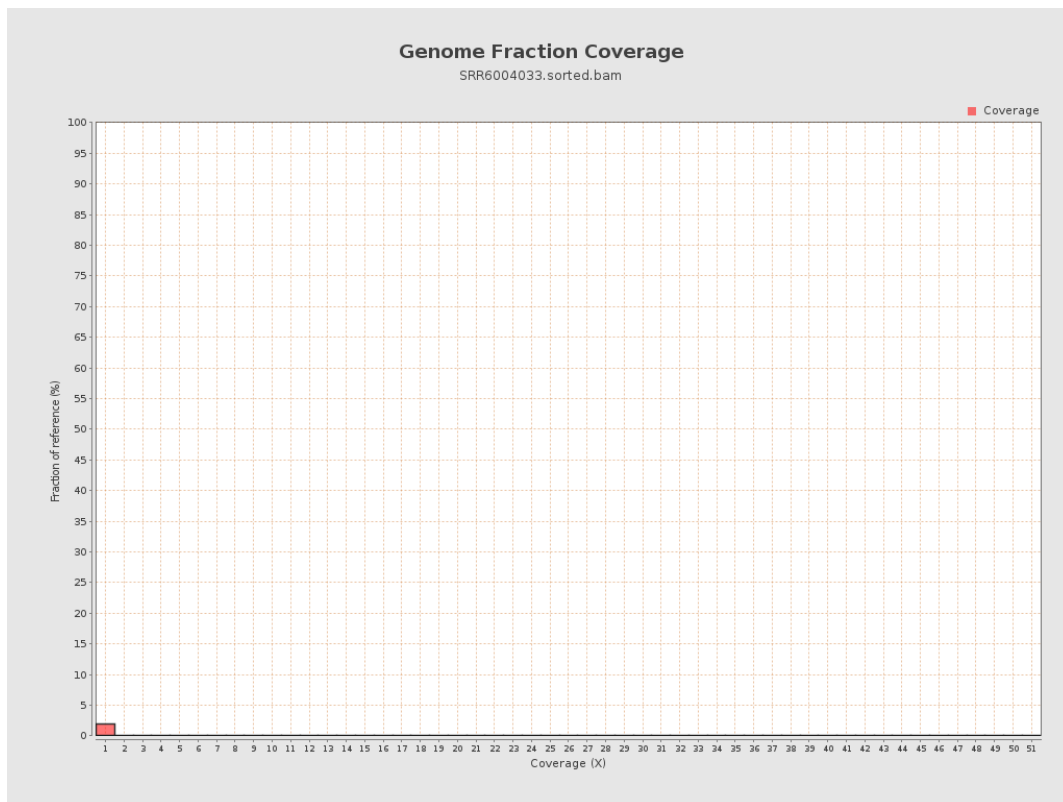
4. Results : Coverage Histogram



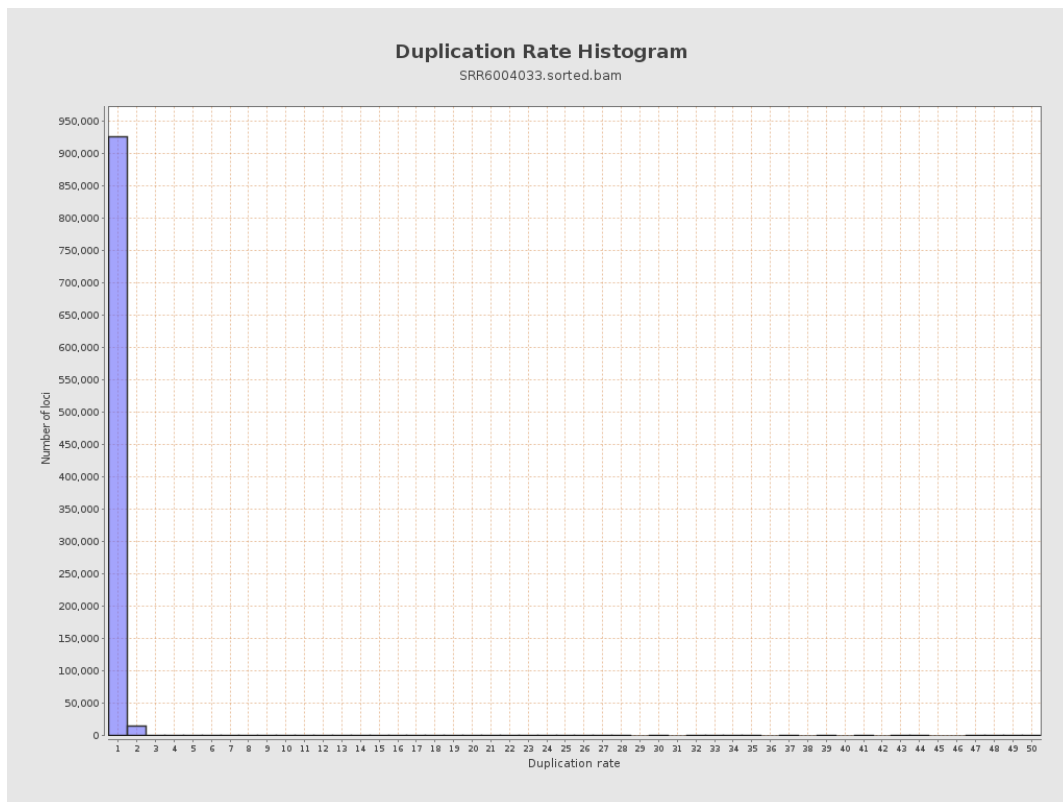
5. Results : Coverage Histogram (0-50X)



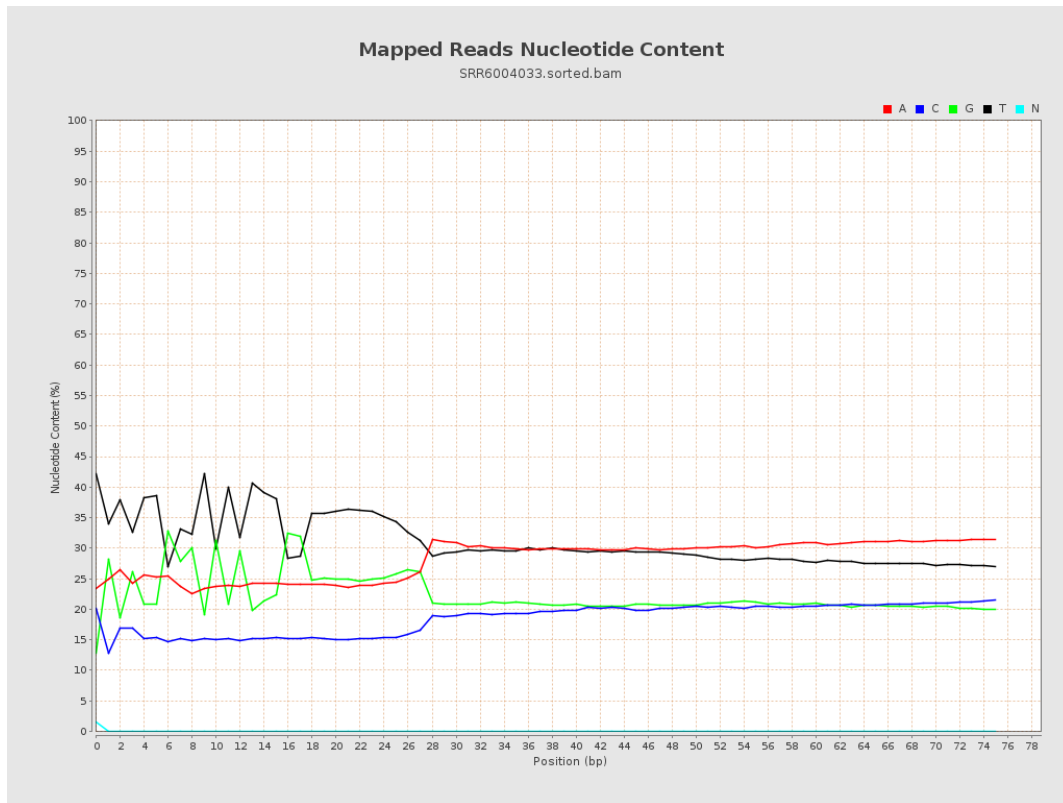
6. Results : Genome Fraction Coverage



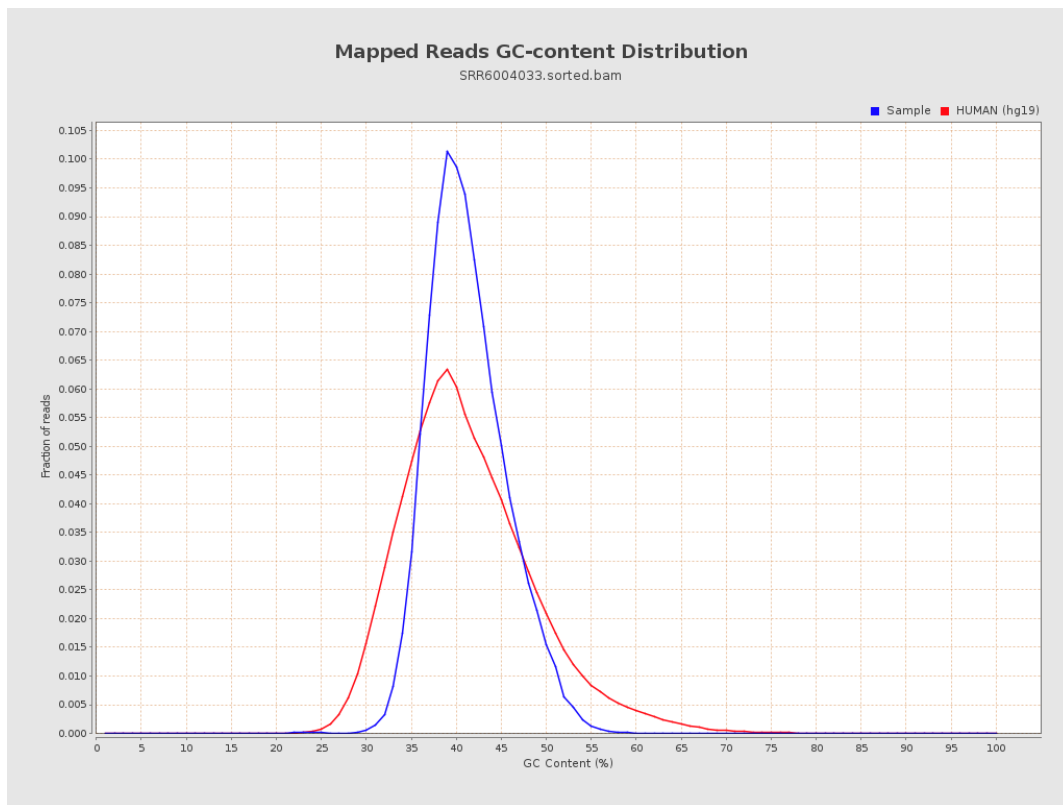
7. Results : Duplication Rate Histogram



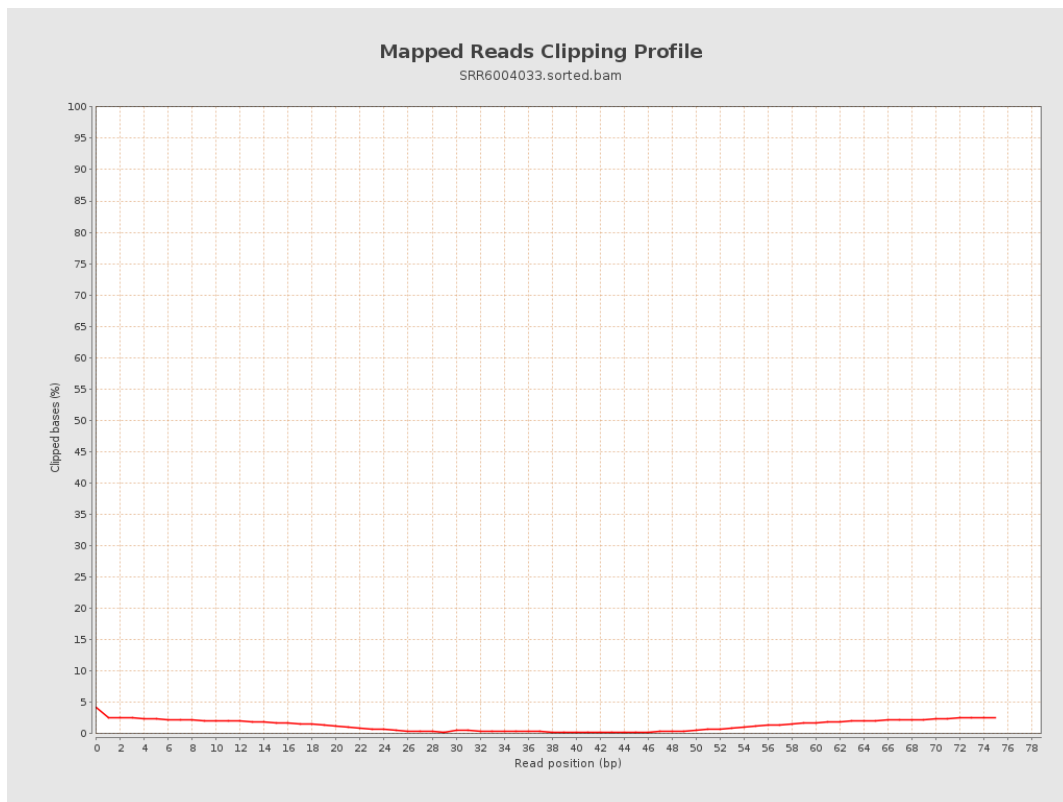
8. Results : Mapped Reads Nucleotide Content



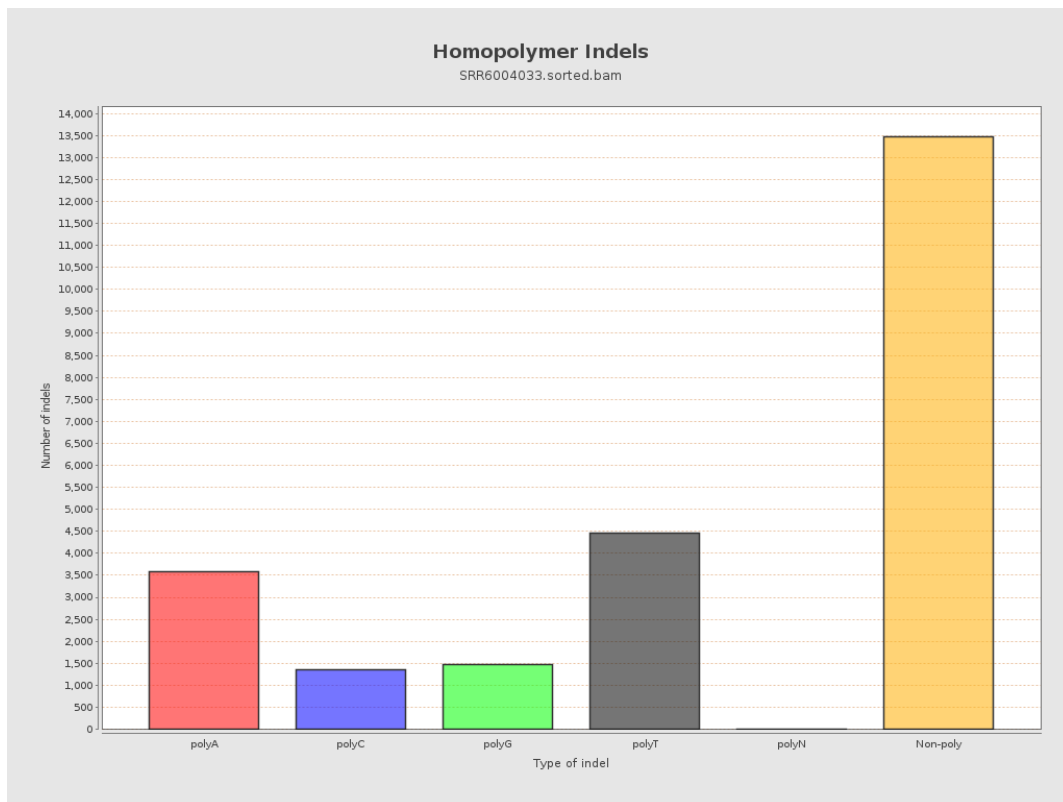
9. Results : Mapped Reads GC-content Distribution



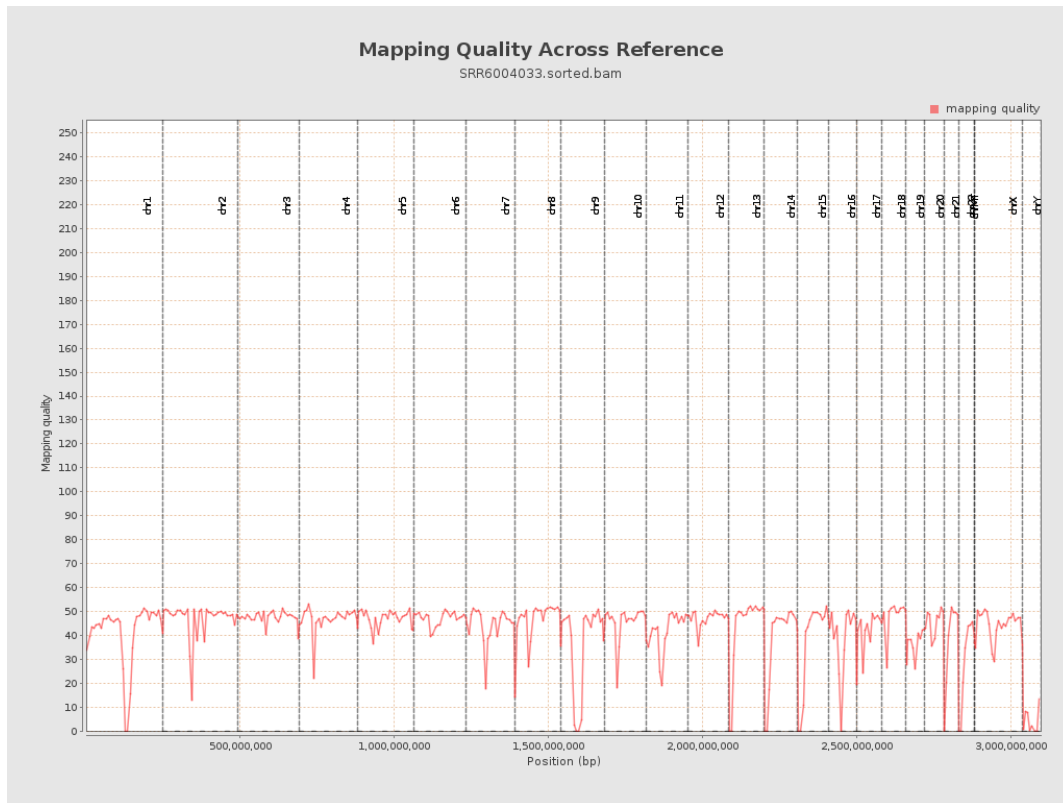
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

