

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 07:36:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081745.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_SRR3081745 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081745.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 07:36:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081745.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,408,084
Mapped reads	2,203,819 / 91.52%
Unmapped reads	204,265 / 8.48%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,241 / 0.67%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	86,769 / 3.6%
Duplication rate	2.76%
Clipped reads	917,859 / 38.12%

2.2. ACGT Content

Number/percentage of A's	40,704,271 / 27.44%
Number/percentage of C's	28,606,772 / 19.28%
Number/percentage of T's	45,250,510 / 30.5%
Number/percentage of G's	33,791,761 / 22.78%
Number/percentage of N's	1,697 / 0%
GC Percentage	42.06%

2.3. Coverage

Mean	0.0479

Standard Deviation	0.4594
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2.4. Mapping Quality

Mean Mapping Quality	44.25
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2.5. Mismatches and indels

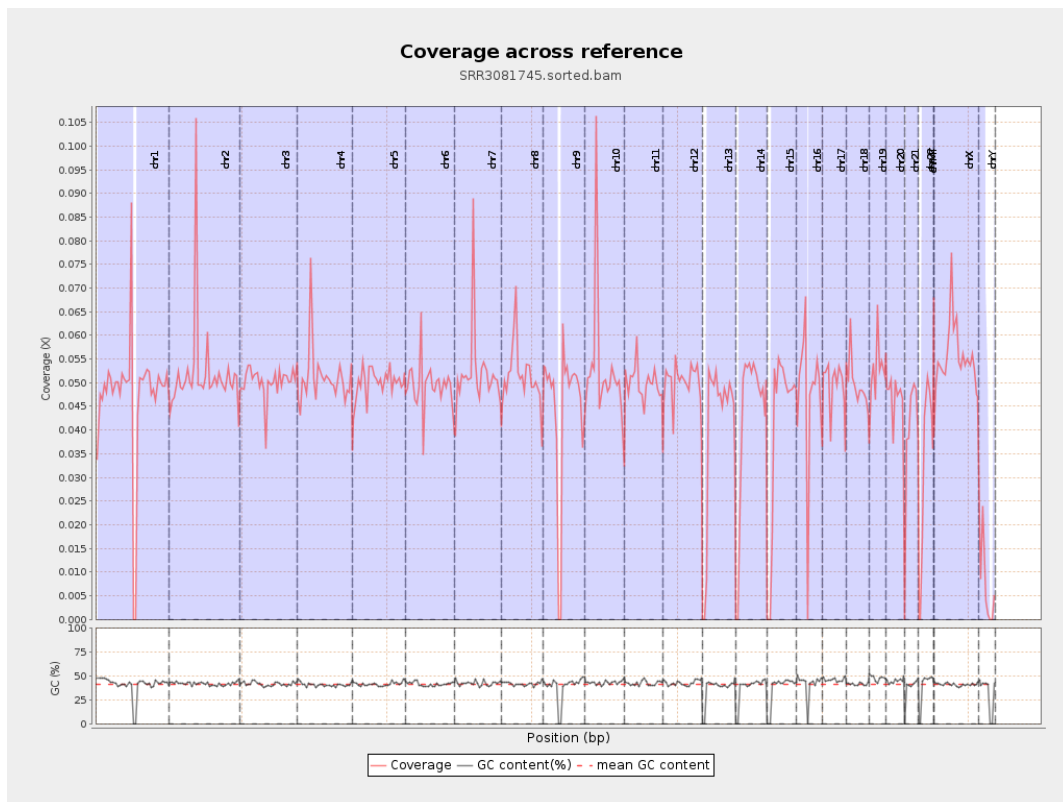
General error rate	0.83%
Mismatches	1,215,381
Insertions	11,165
Mapped reads with at least one insertion	0.5%
Deletions	33,556
Mapped reads with at least one deletion	1.51%
Homopolymer indels	46.09%

2.6. Chromosome stats

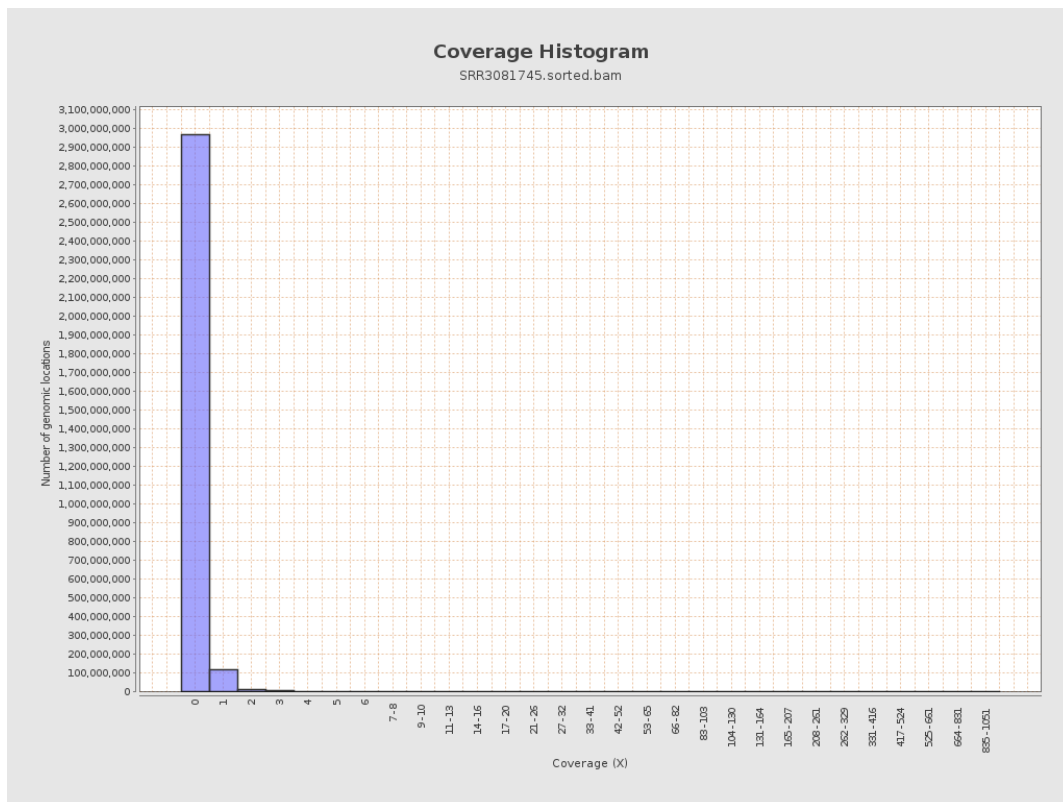
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	11780433	0.0473	0.9146
chr2	243199373	12614454	0.0519	0.5621
chr3	198022430	9942592	0.0502	0.2566
chr4	191154276	9735430	0.0509	0.2919
chr5	180915260	9060547	0.0501	0.2508
chr6	171115067	8438115	0.0493	0.2975
chr7	159138663	8302387	0.0522	0.6256

chr8	146364022	7506209	0.0513	0.5049
chr9	141213431	6271254	0.0444	0.4125
chr10	135534747	7106439	0.0524	0.5258
chr11	135006516	6703592	0.0497	0.3473
chr12	133851895	6726990	0.0503	0.2553
chr13	115169878	4653898	0.0404	0.223
chr14	107349540	4554126	0.0424	0.2594
chr15	102531392	4209339	0.0411	0.231
chr16	90354753	4295847	0.0475	0.3018
chr17	81195210	3999868	0.0493	0.274
chr18	78077248	3900892	0.05	0.7264
chr19	59128983	3131882	0.053	0.6582
chr20	63025520	2919129	0.0463	0.2534
chr21	48129895	1903420	0.0395	0.2537
chr22	51304566	1647380	0.0321	0.199
chrMT	16571	1126	0.068	0.2871
chrX	155270560	8578770	0.0553	0.3077
chrY	59373566	430724	0.0073	0.2028

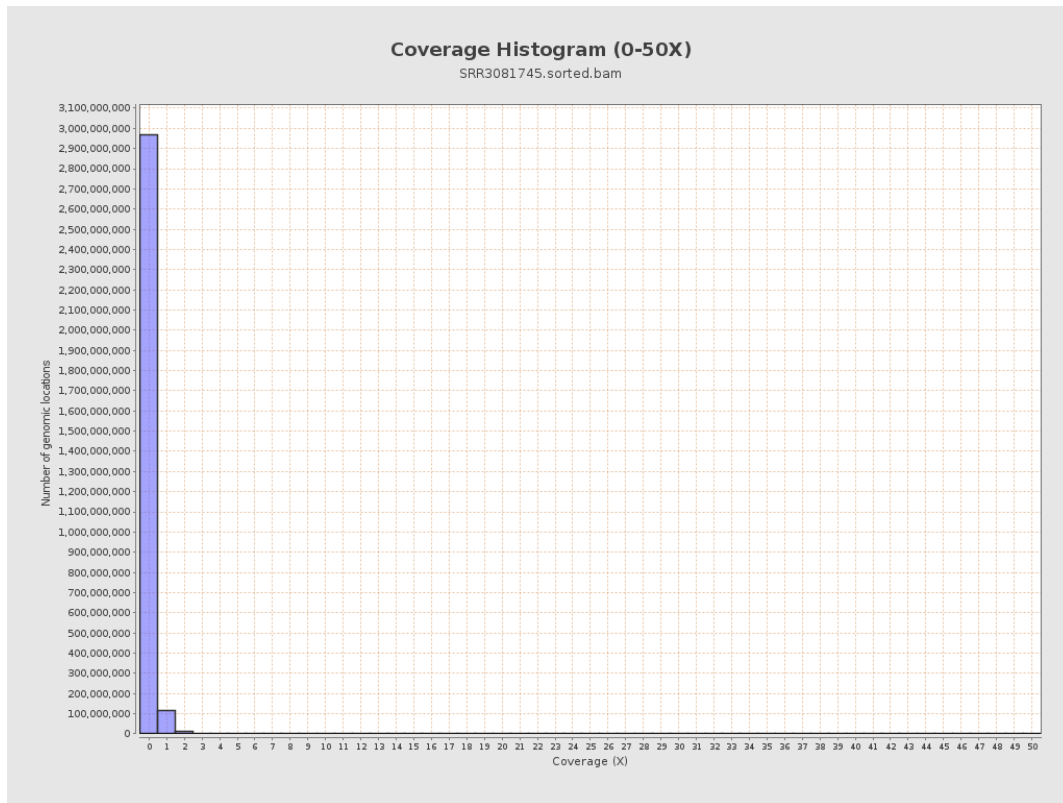
3. Results : Coverage across reference



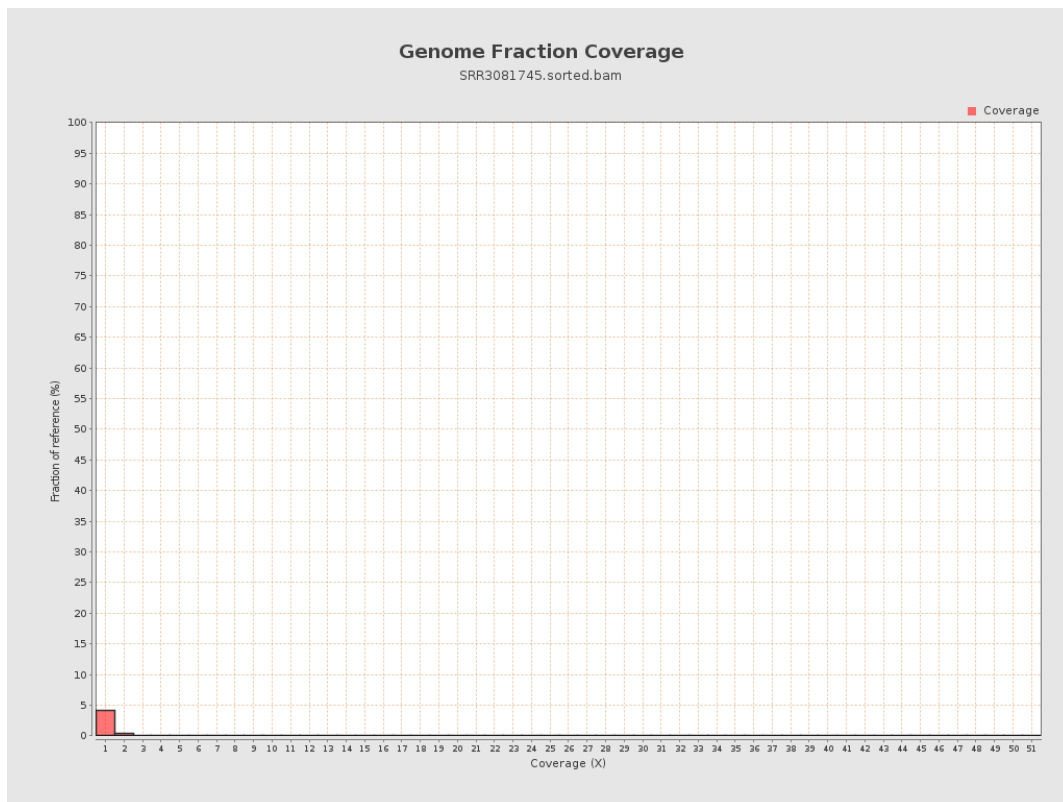
4. Results : Coverage Histogram



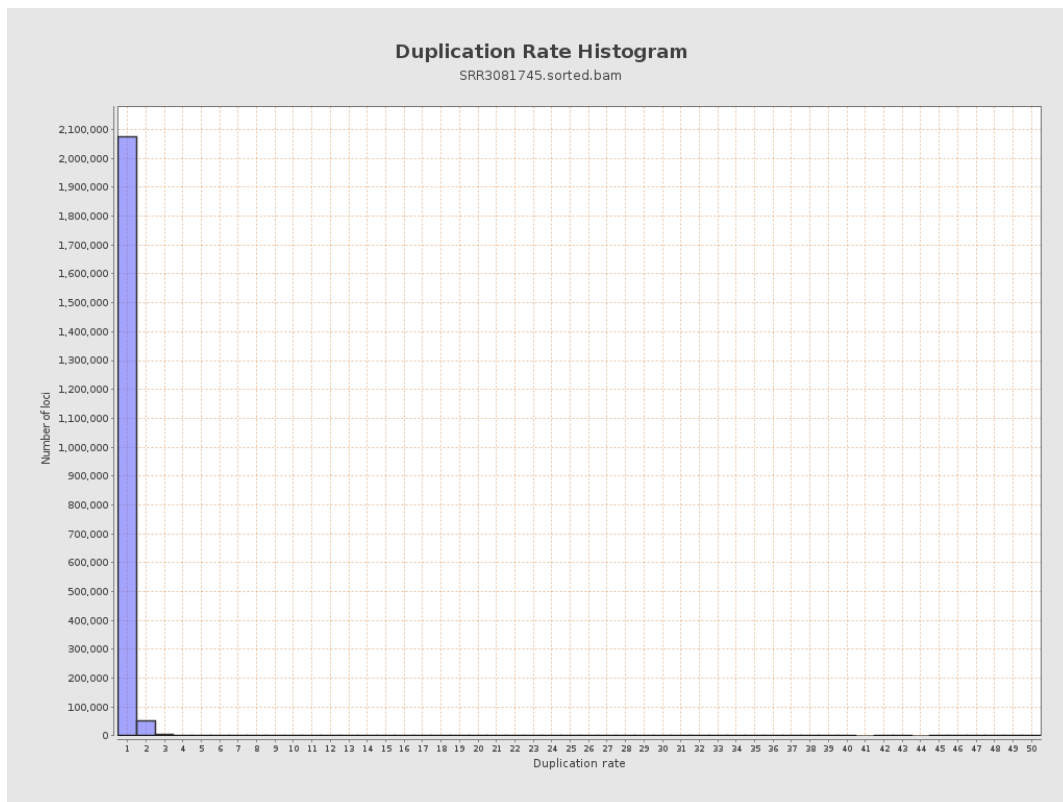
5. Results : Coverage Histogram (0-50X)



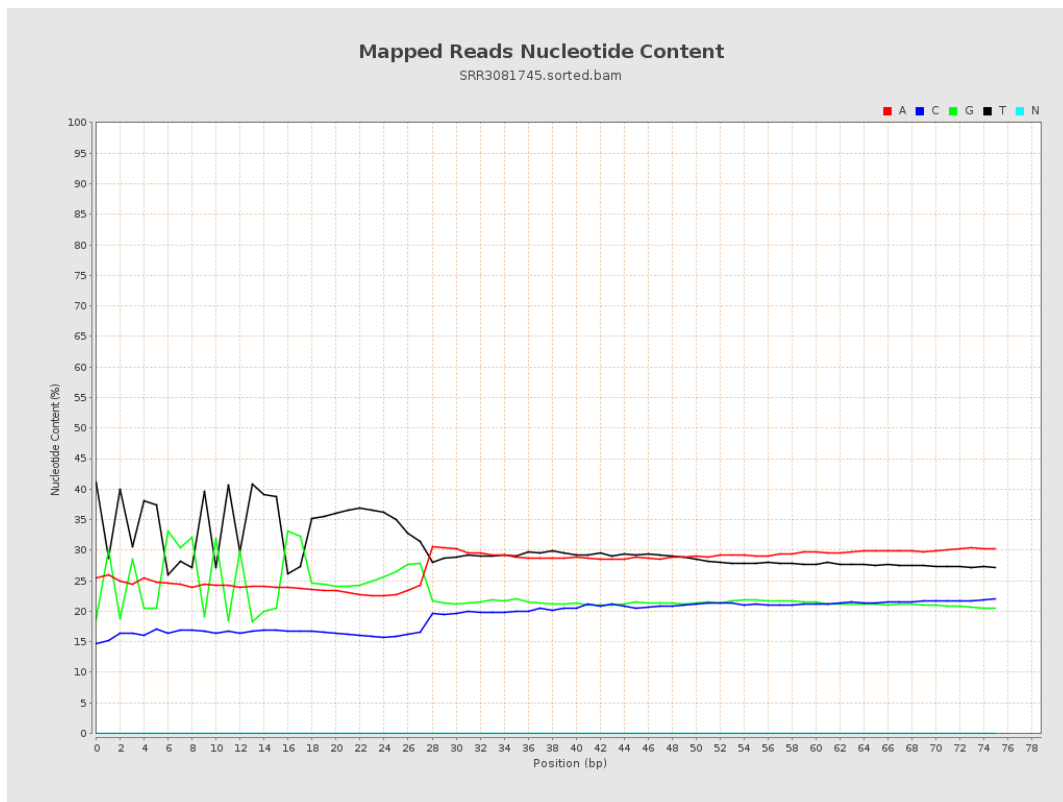
6. Results : Genome Fraction Coverage



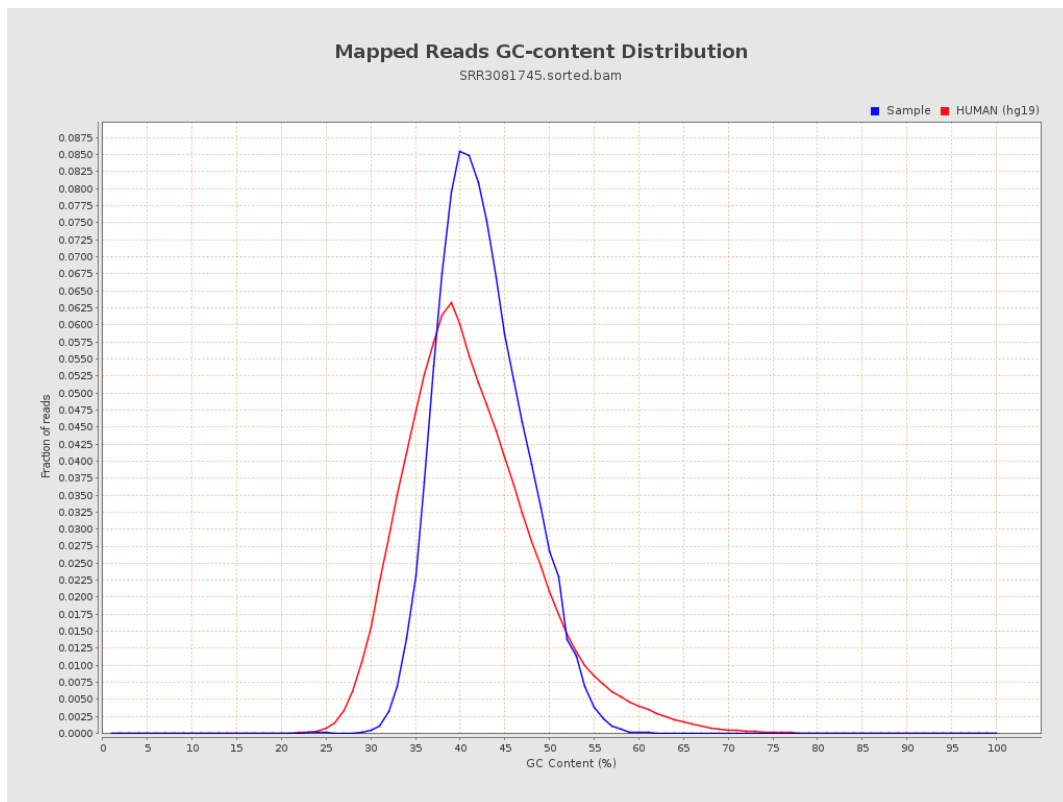
7. Results : Duplication Rate Histogram



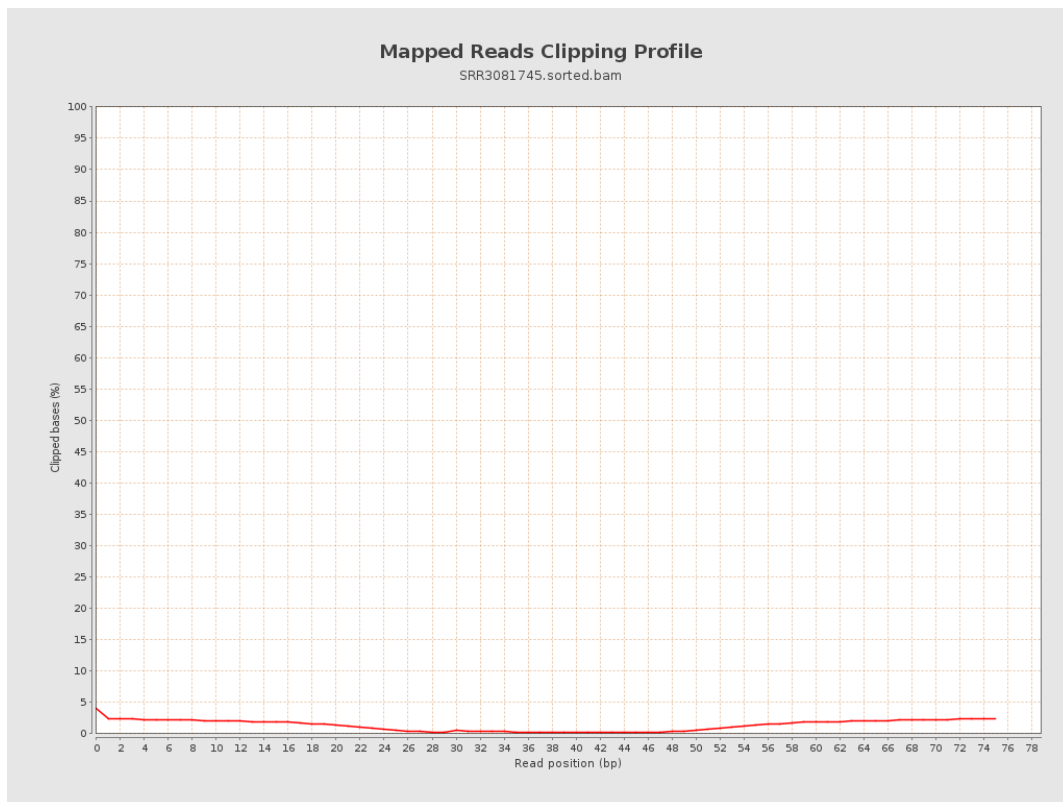
8. Results : Mapped Reads Nucleotide Content



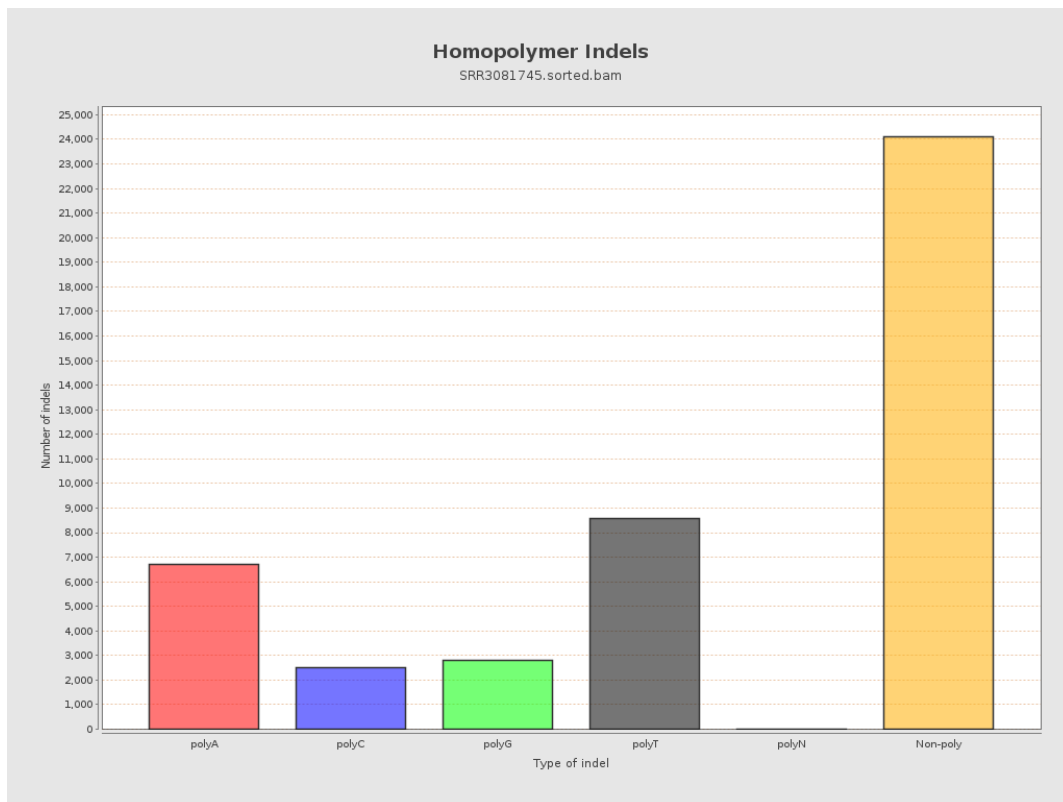
9. Results : Mapped Reads GC-content Distribution



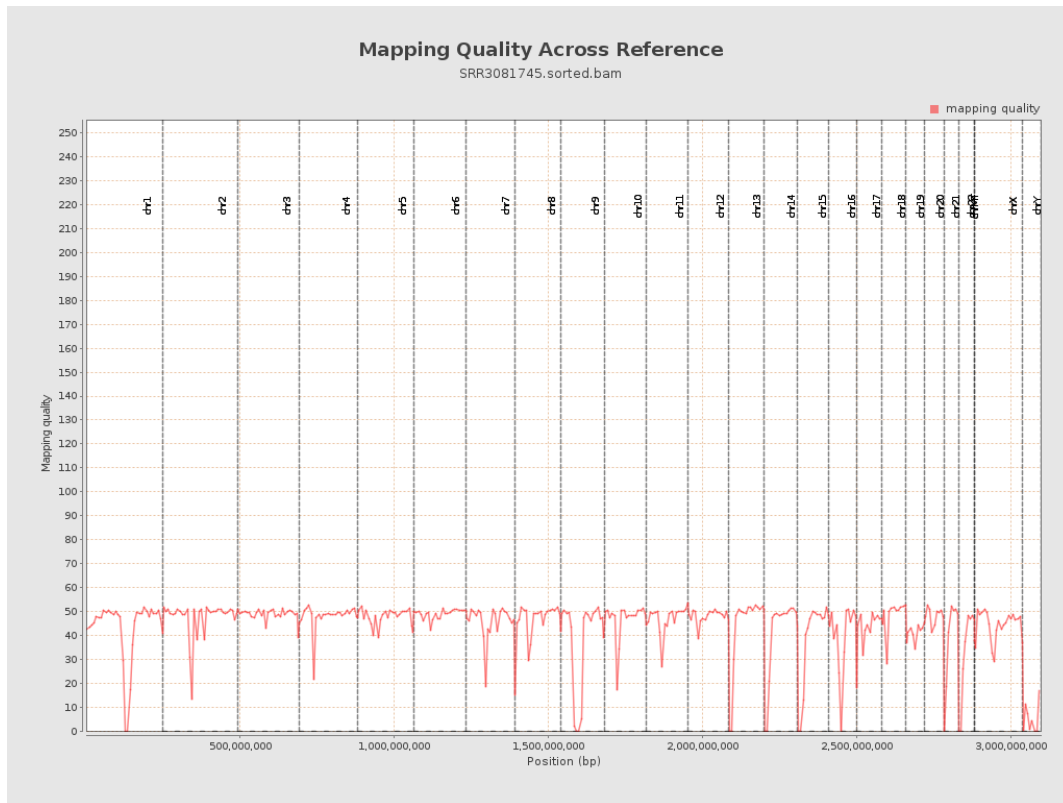
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

