

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 11:57:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008797.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_SRR6008797 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008797.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 11:57:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008797.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,270,993
Mapped reads	1,141,487 / 89.81%
Unmapped reads	129,506 / 10.19%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,418 / 0.58%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	40,624 / 3.2%
Duplication rate	2.02%
Clipped reads	501,214 / 39.43%

2.2. ACGT Content

Number/percentage of A's	21,356,787 / 28.04%
Number/percentage of C's	14,130,294 / 18.55%
Number/percentage of T's	23,480,511 / 30.83%
Number/percentage of G's	17,171,117 / 22.54%
Number/percentage of N's	26,269 / 0.03%
GC Percentage	41.1%

2.3. Coverage

Mean	0.0246

Standard Deviation	0.3765
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2.4. Mapping Quality

Mean Mapping Quality	43.83
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2.5. Mismatches and indels

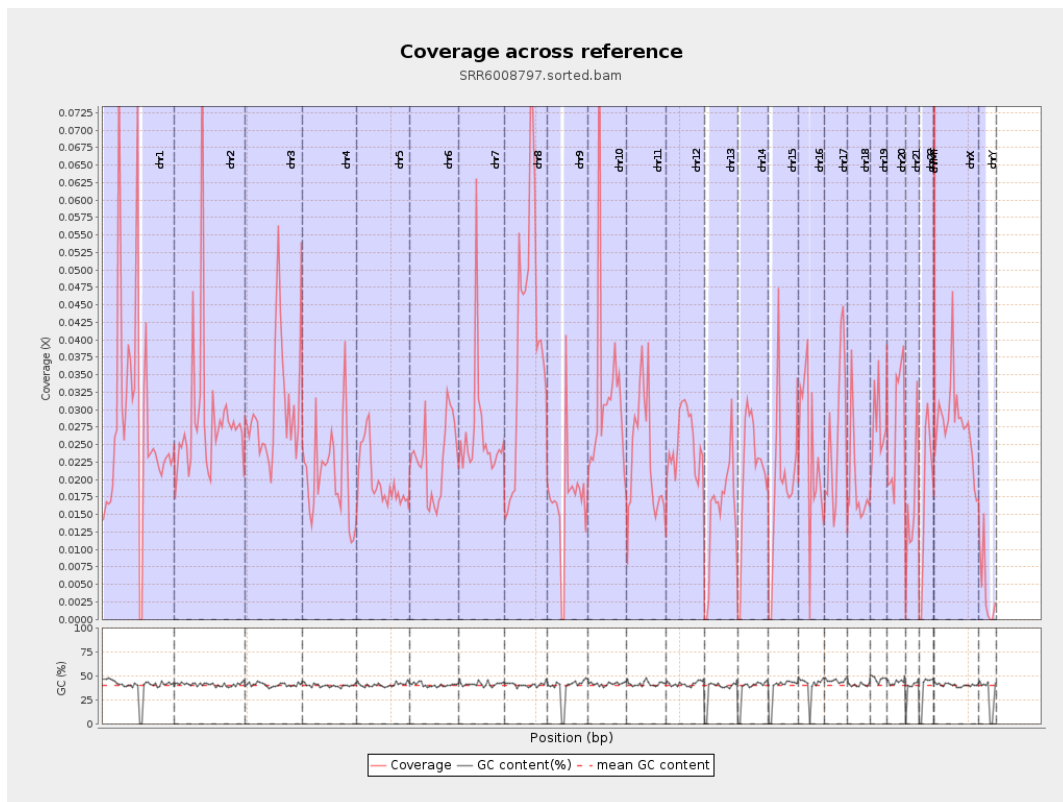
General error rate	0.89%
Mismatches	665,325
Insertions	6,107
Mapped reads with at least one insertion	0.53%
Deletions	23,200
Mapped reads with at least one deletion	2.01%
Homopolymer indels	44.74%

2.6. Chromosome stats

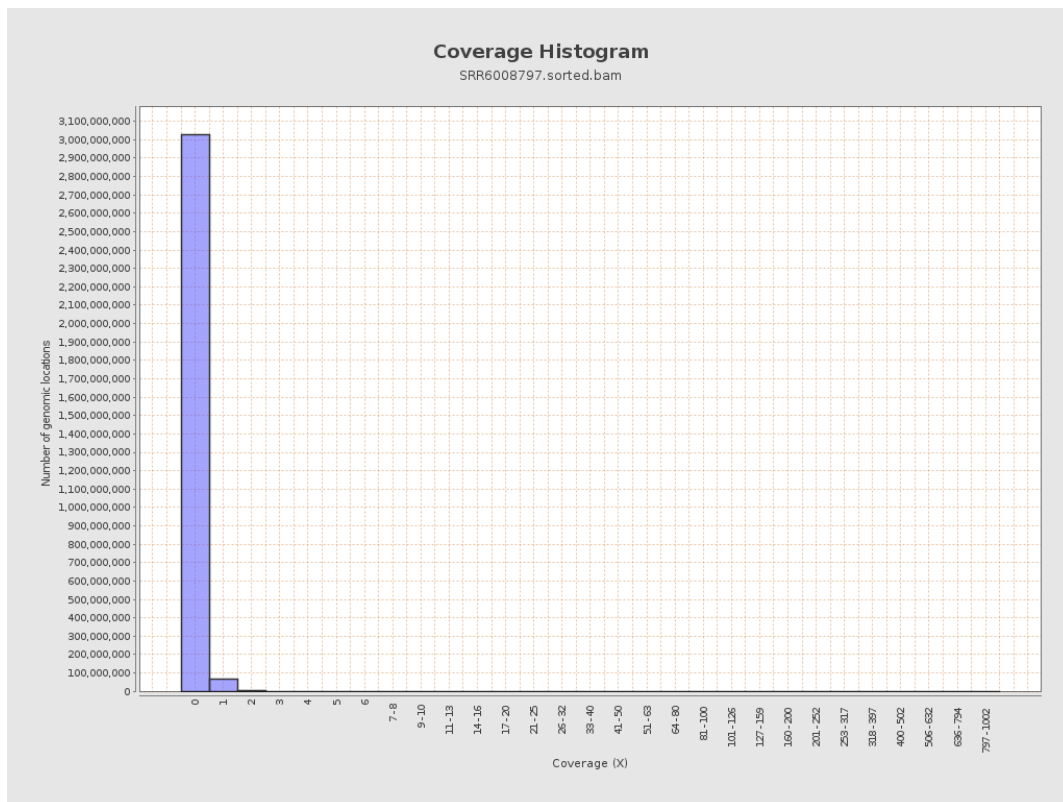
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	6789090	0.0272	0.8382
chr2	243199373	6987773	0.0287	0.4196
chr3	198022430	5962229	0.0301	0.2075
chr4	191154276	3989247	0.0209	0.1679
chr5	180915260	3621822	0.02	0.1528
chr6	171115067	3913977	0.0229	0.1891
chr7	159138663	4221025	0.0265	0.4355

chr8	146364022	5854149	0.04	0.3896
chr9	141213431	2380837	0.0169	0.3191
chr10	135534747	4352118	0.0321	0.5376
chr11	135006516	3197531	0.0237	0.3024
chr12	133851895	3370385	0.0252	0.1725
chr13	115169878	1776293	0.0154	0.129
chr14	107349540	2277410	0.0212	0.1677
chr15	102531392	1997831	0.0195	0.1497
chr16	90354753	2146892	0.0238	0.234
chr17	81195210	2150999	0.0265	0.2259
chr18	78077248	1483259	0.019	0.6128
chr19	59128983	1665406	0.0282	0.5141
chr20	63025520	1739860	0.0276	0.1852
chr21	48129895	796413	0.0165	0.1551
chr22	51304566	935629	0.0182	0.1429
chrMT	16571	7381	0.4454	0.7077
chrX	155270560	4338753	0.0279	0.2163
chrY	59373566	249329	0.0042	0.1427

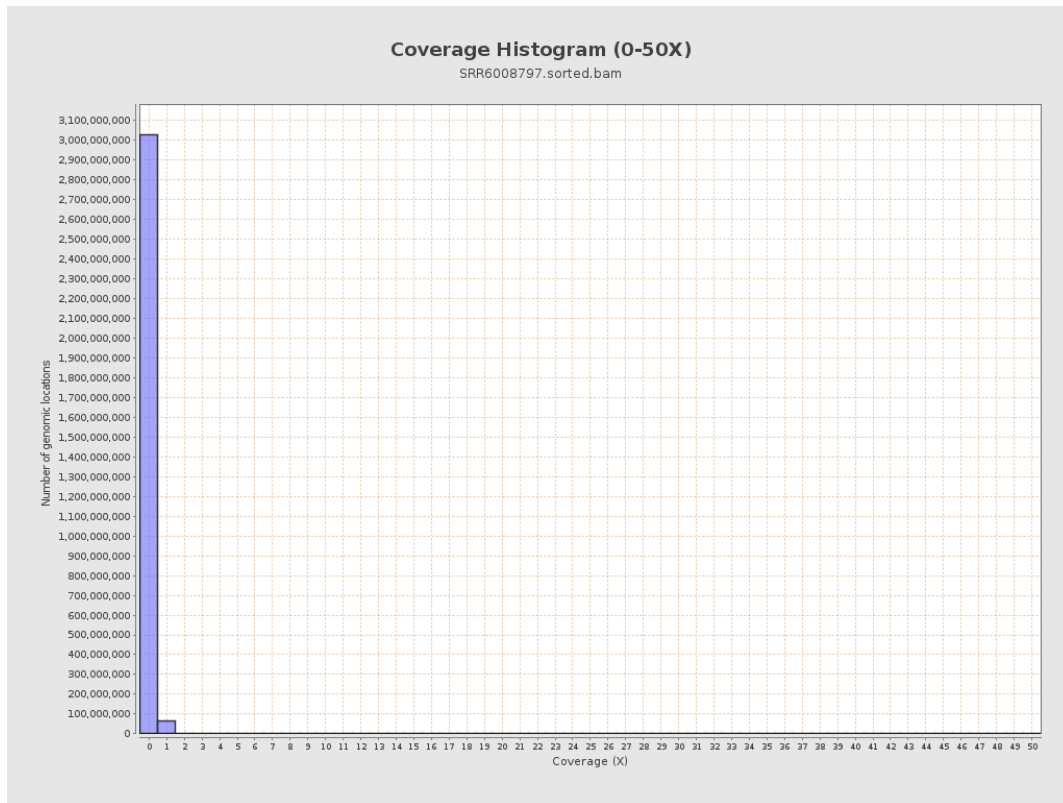
3. Results : Coverage across reference



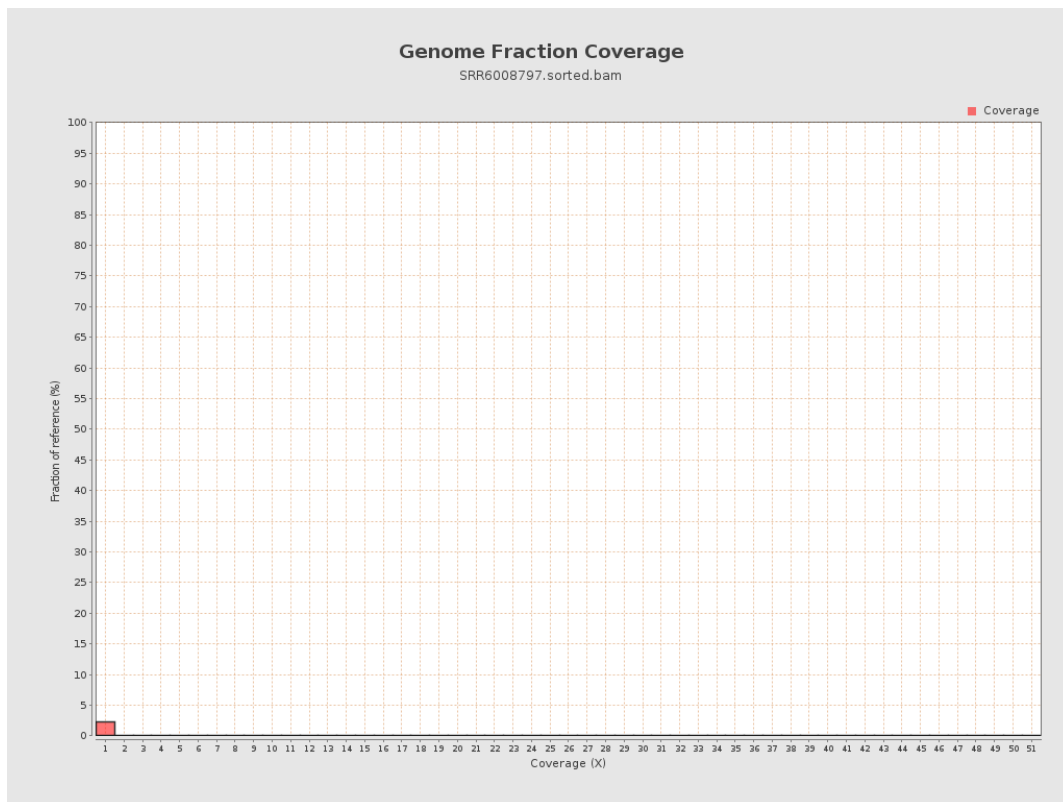
4. Results : Coverage Histogram



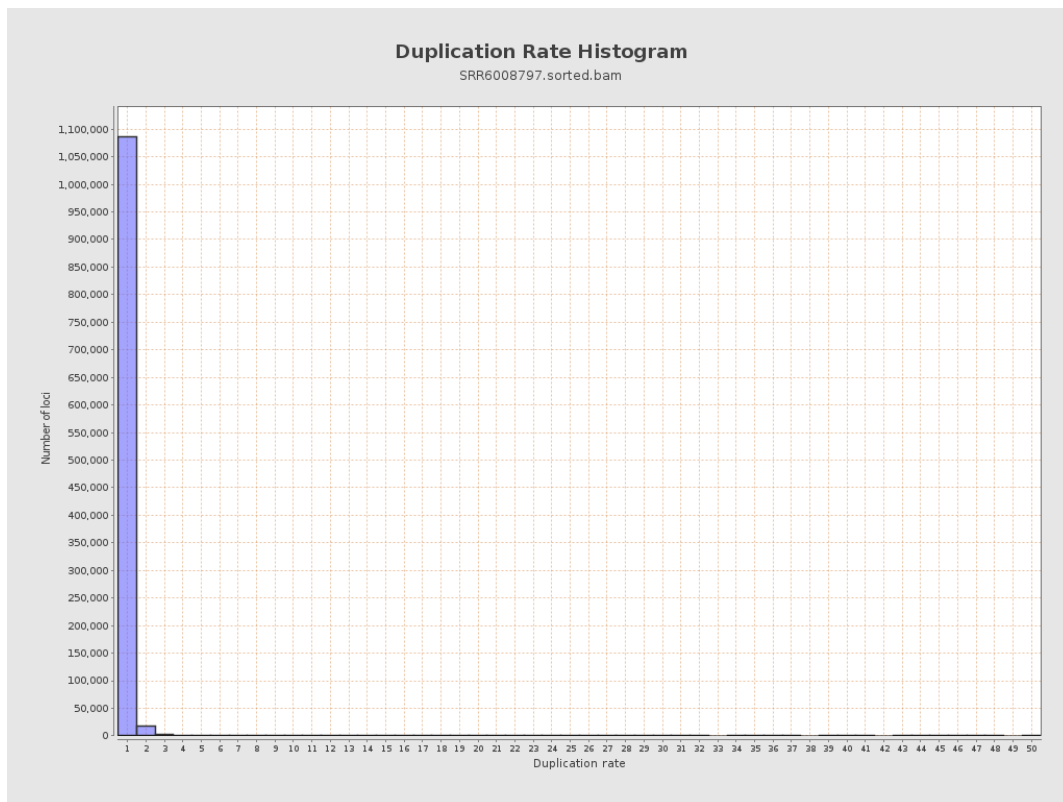
5. Results : Coverage Histogram (0-50X)



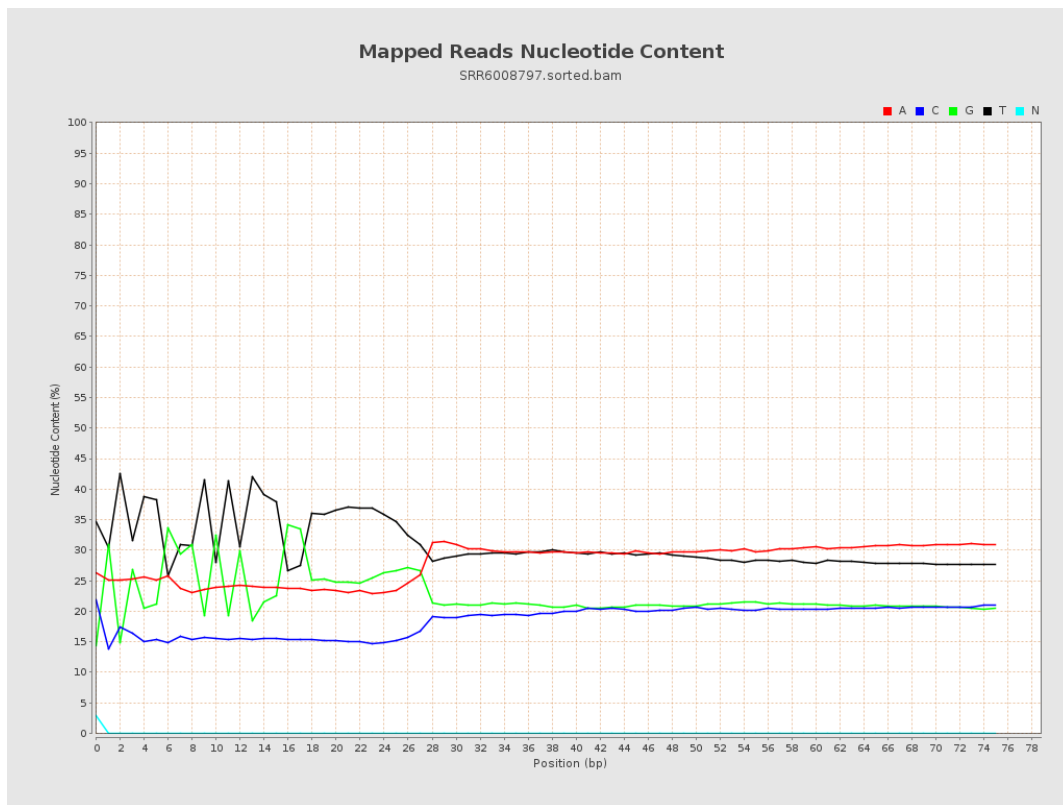
6. Results : Genome Fraction Coverage



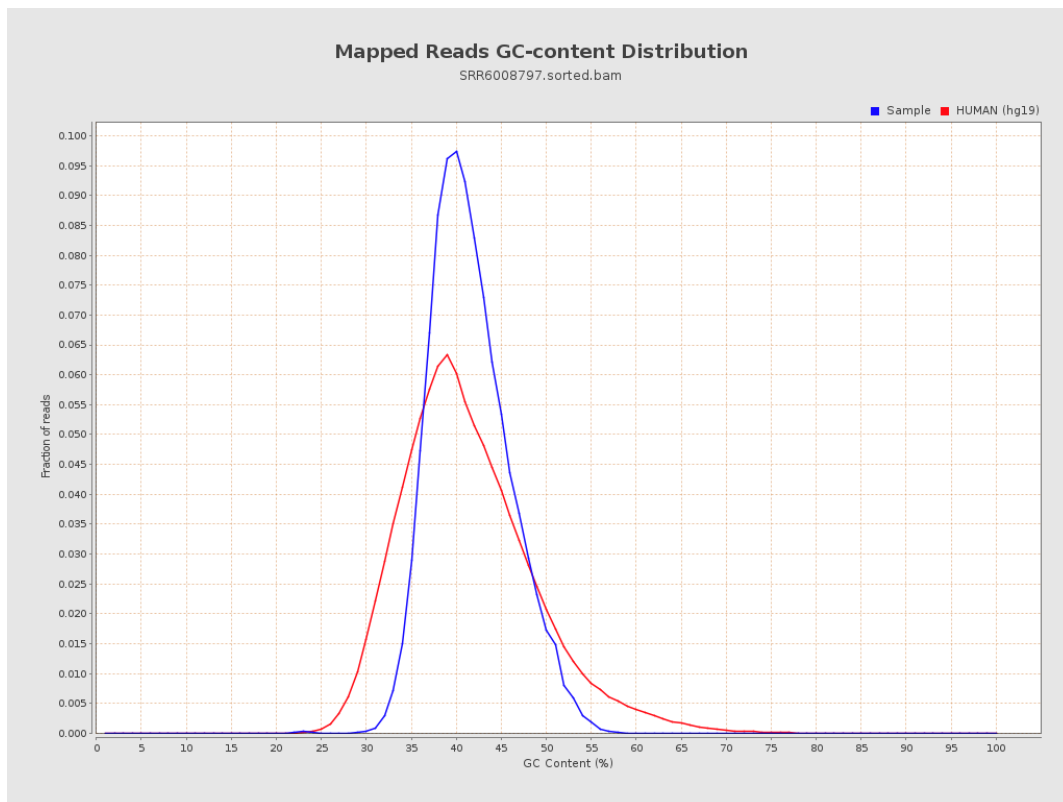
7. Results : Duplication Rate Histogram



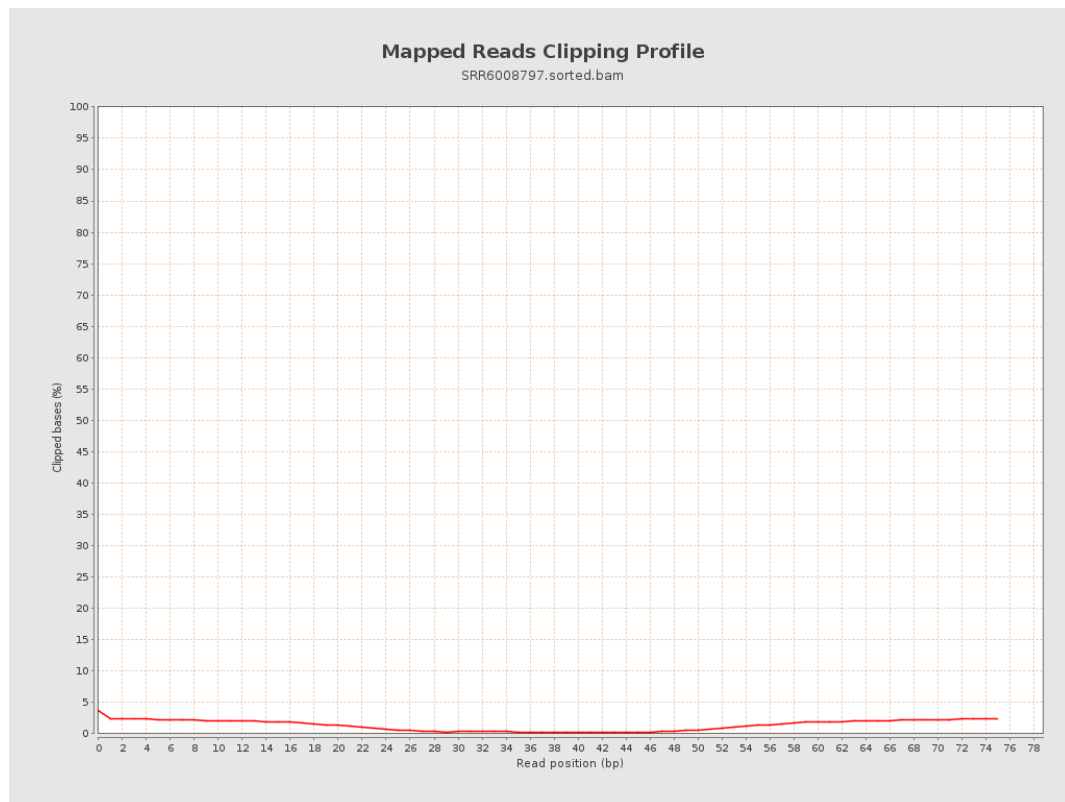
8. Results : Mapped Reads Nucleotide Content



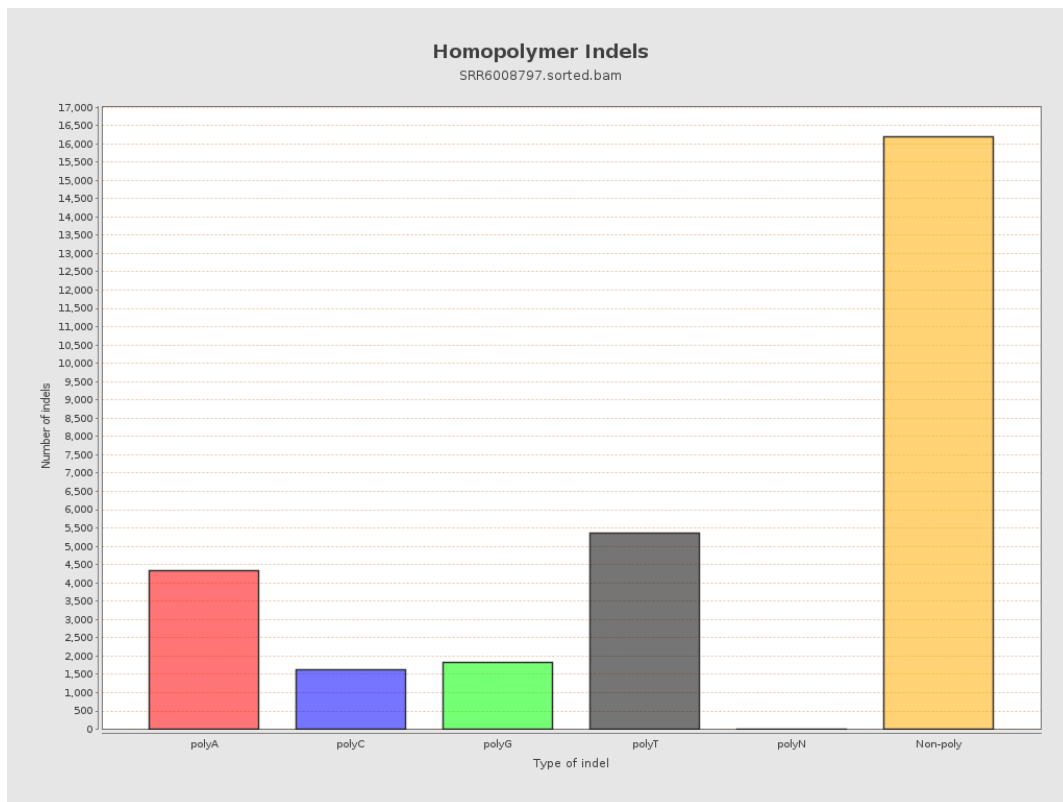
9. Results : Mapped Reads GC-content Distribution



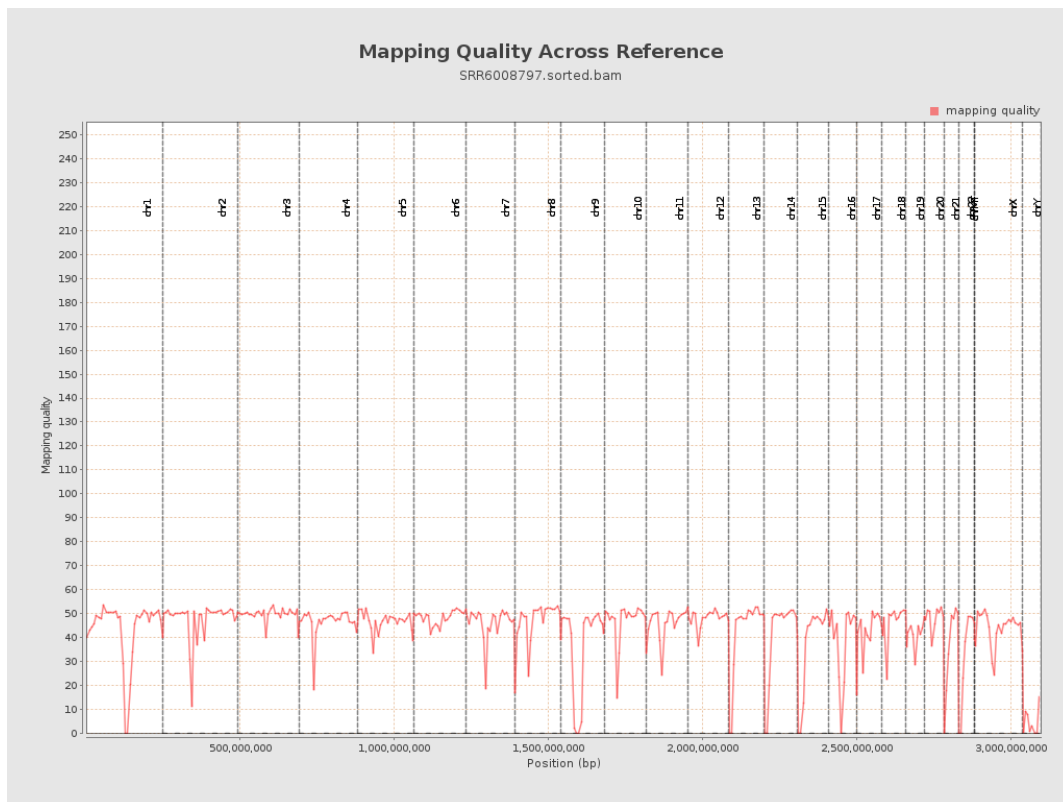
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

