

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 11:54:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008796.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_SRR6008796 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008796.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 11:54:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008796.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,749,772
Mapped reads	1,488,096 / 85.05%
Unmapped reads	261,676 / 14.95%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,219 / 0.41%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	65,033 / 3.72%
Duplication rate	3.44%
Clipped reads	757,678 / 43.3%

2.2. ACGT Content

Number/percentage of A's	25,674,459 / 26.67%
Number/percentage of C's	17,417,334 / 18.1%
Number/percentage of T's	30,764,356 / 31.96%
Number/percentage of G's	22,361,471 / 23.23%
Number/percentage of N's	34,417 / 0.04%
GC Percentage	41.33%

2.3. Coverage

Mean	0.0311

Standard Deviation	0.301
--------------------	-------

2.4. Mapping Quality

Mean Mapping Quality	45.8
----------------------	------

2.5. Mismatches and indels

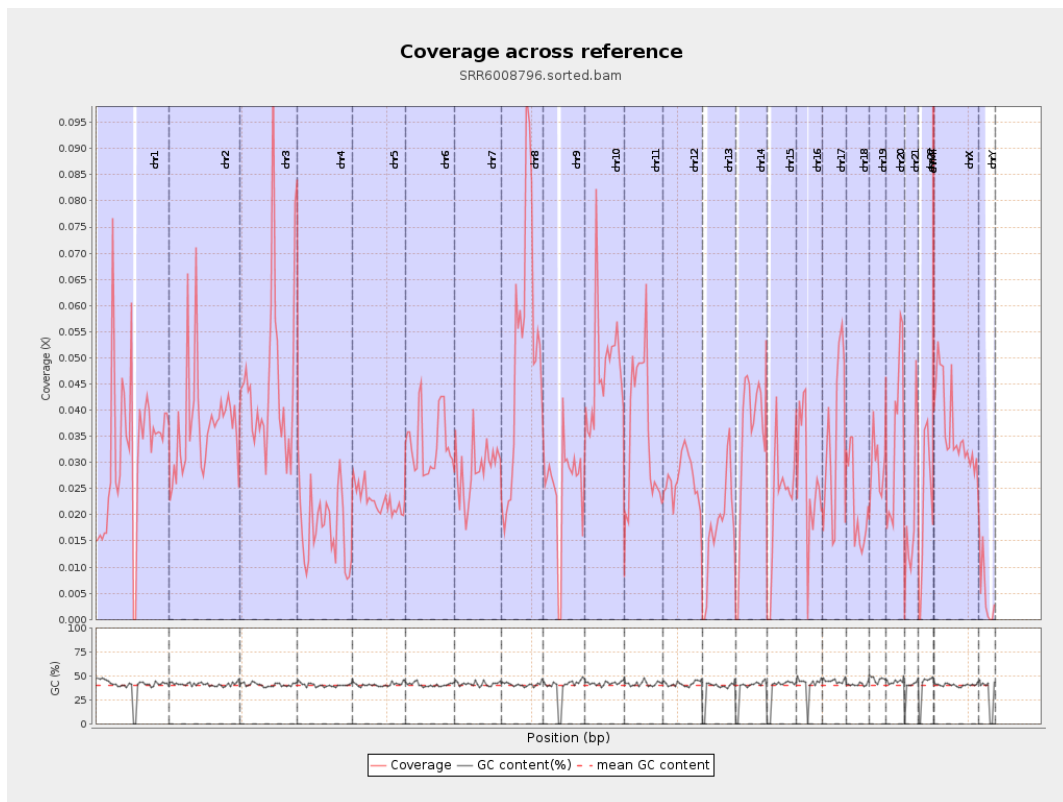
General error rate	0.82%
Mismatches	781,368
Insertions	6,183
Mapped reads with at least one insertion	0.41%
Deletions	27,816
Mapped reads with at least one deletion	1.85%
Homopolymer indels	44.52%

2.6. Chromosome stats

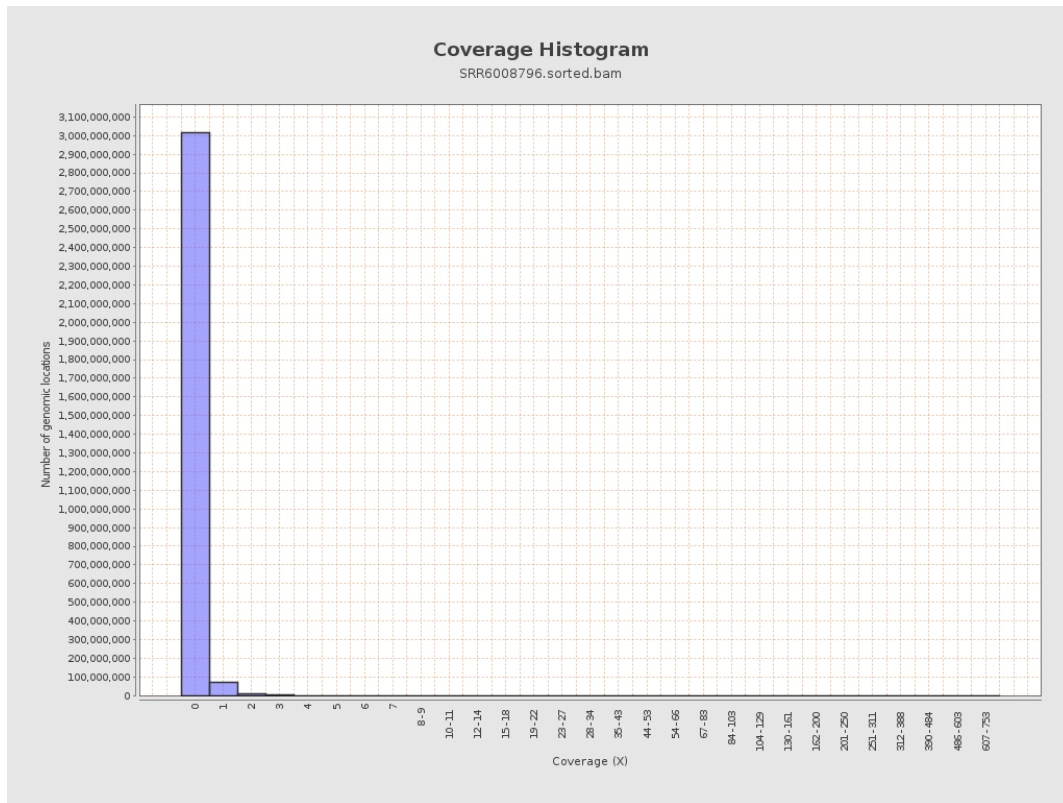
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	7924998	0.0318	0.5734
chr2	243199373	9020001	0.0371	0.3485
chr3	198022430	8921919	0.0451	0.2468
chr4	191154276	3297960	0.0173	0.1604
chr5	180915260	4113884	0.0227	0.1713
chr6	171115067	5742740	0.0336	0.2461
chr7	159138663	4553182	0.0286	0.251

chr8	146364022	7345219	0.0502	0.3064
chr9	141213431	3562929	0.0252	0.2757
chr10	135534747	6447397	0.0476	0.4099
chr11	135006516	4837111	0.0358	0.3135
chr12	133851895	3597555	0.0269	0.1884
chr13	115169878	2009057	0.0174	0.1465
chr14	107349540	3684009	0.0343	0.2127
chr15	102531392	2346682	0.0229	0.1694
chr16	90354753	2455864	0.0272	0.2173
chr17	81195210	2758177	0.034	0.2801
chr18	78077248	1692677	0.0217	0.437
chr19	59128983	1780885	0.0301	0.3843
chr20	63025520	2168027	0.0344	0.2118
chr21	48129895	983668	0.0204	0.1746
chr22	51304566	1110138	0.0216	0.1633
chrMT	16571	6321	0.3814	0.6487
chrX	155270560	5651198	0.0364	0.2452
chrY	59373566	288765	0.0049	0.1457

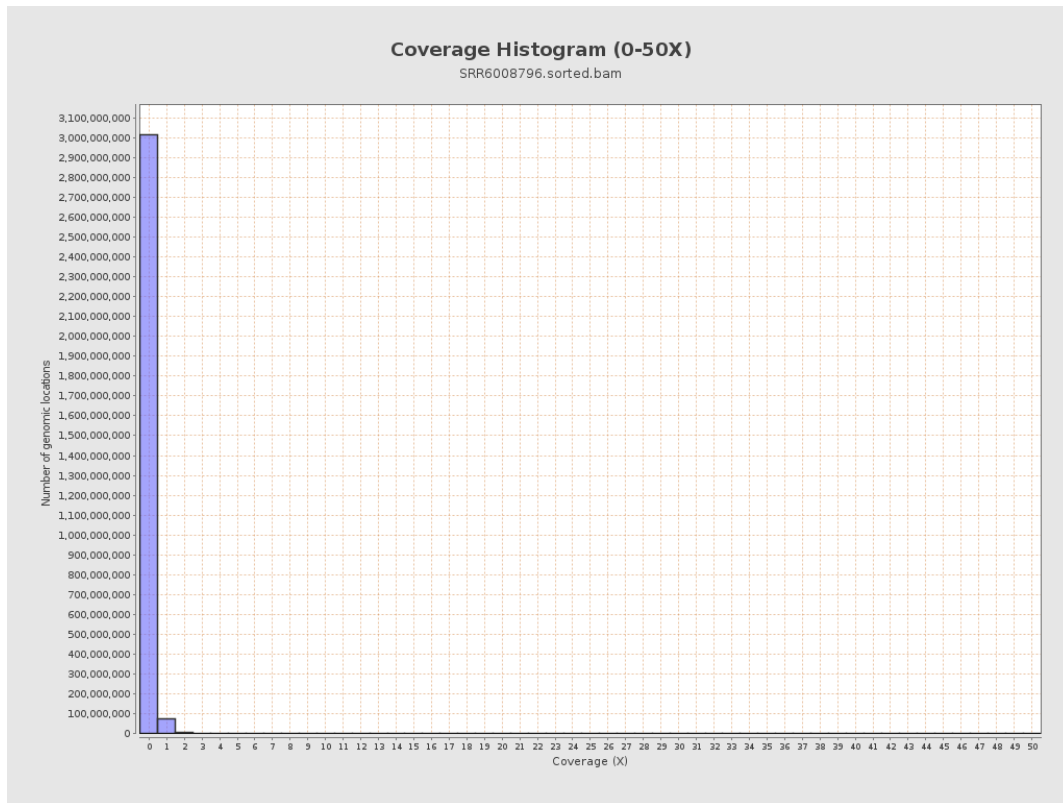
3. Results : Coverage across reference



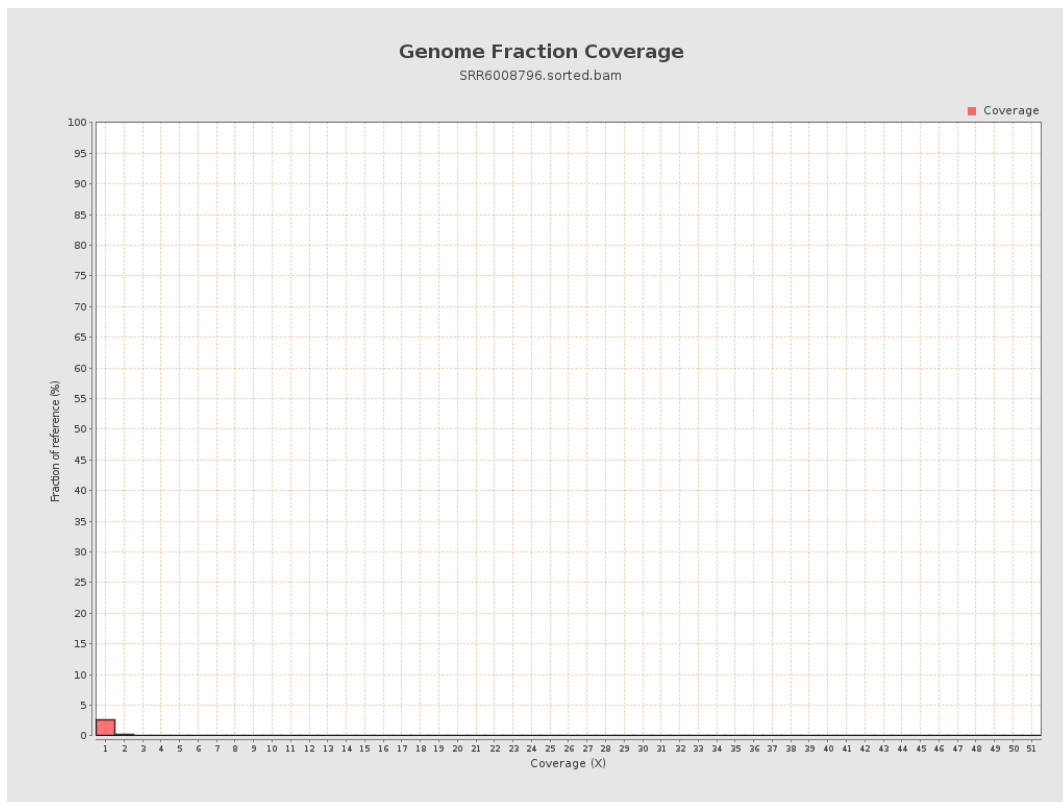
4. Results : Coverage Histogram



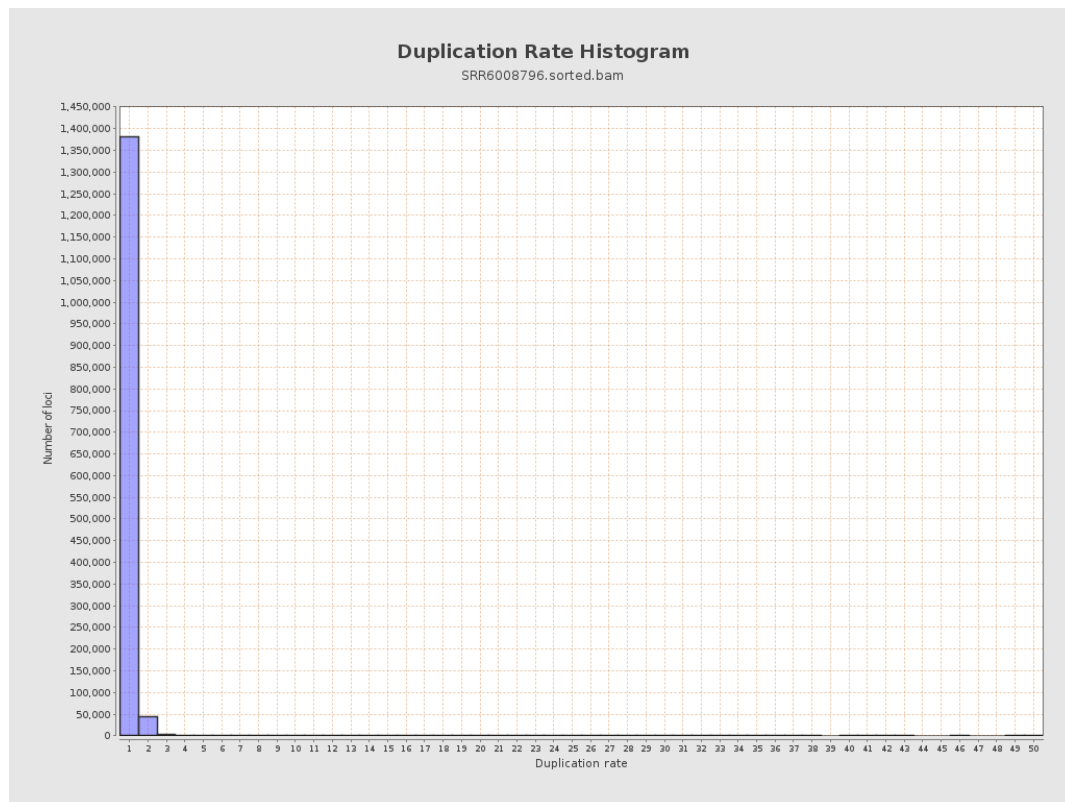
5. Results : Coverage Histogram (0-50X)



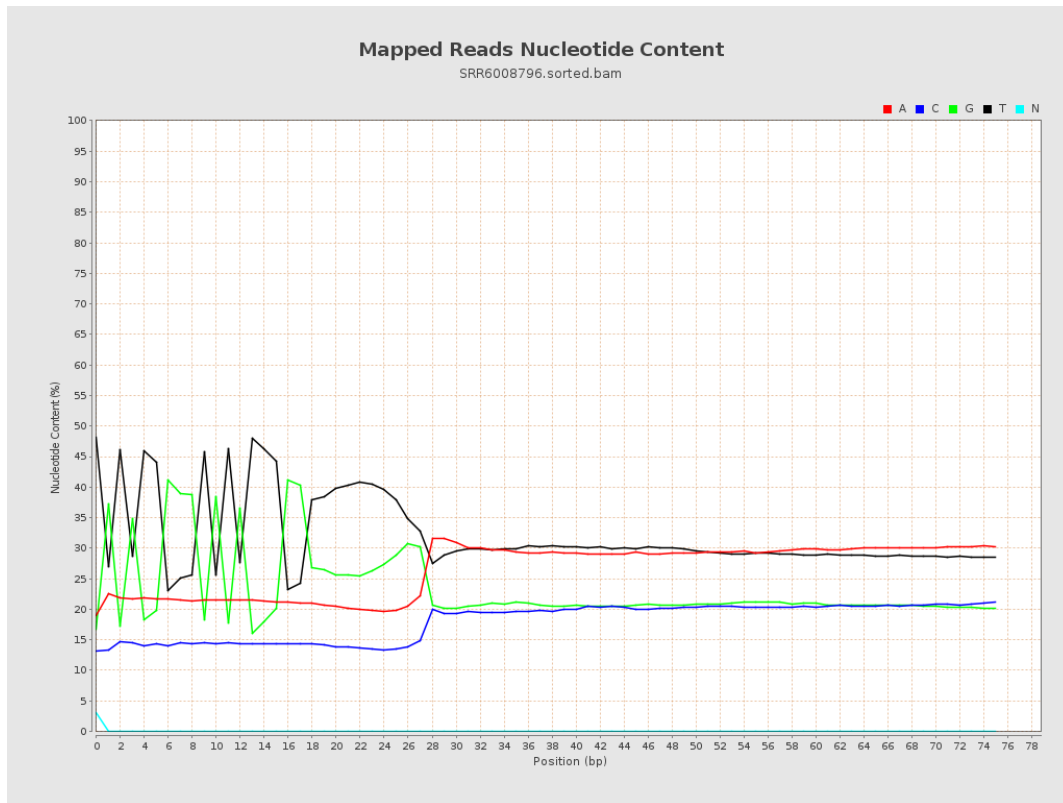
6. Results : Genome Fraction Coverage



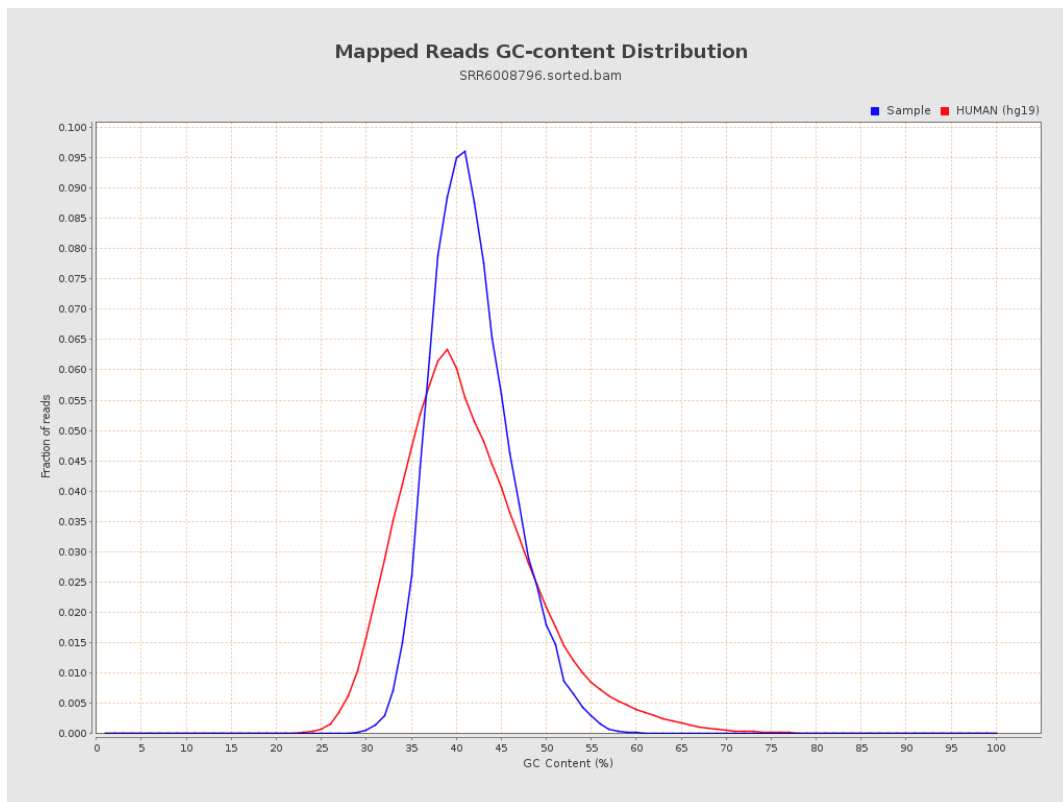
7. Results : Duplication Rate Histogram



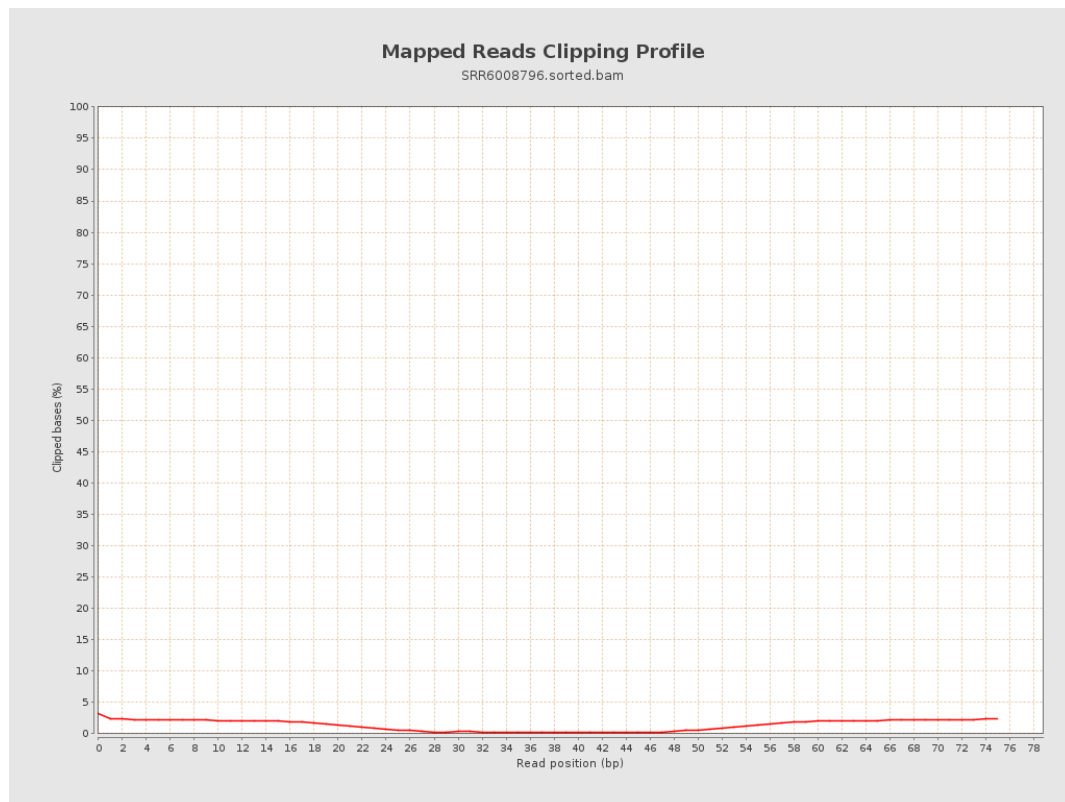
8. Results : Mapped Reads Nucleotide Content



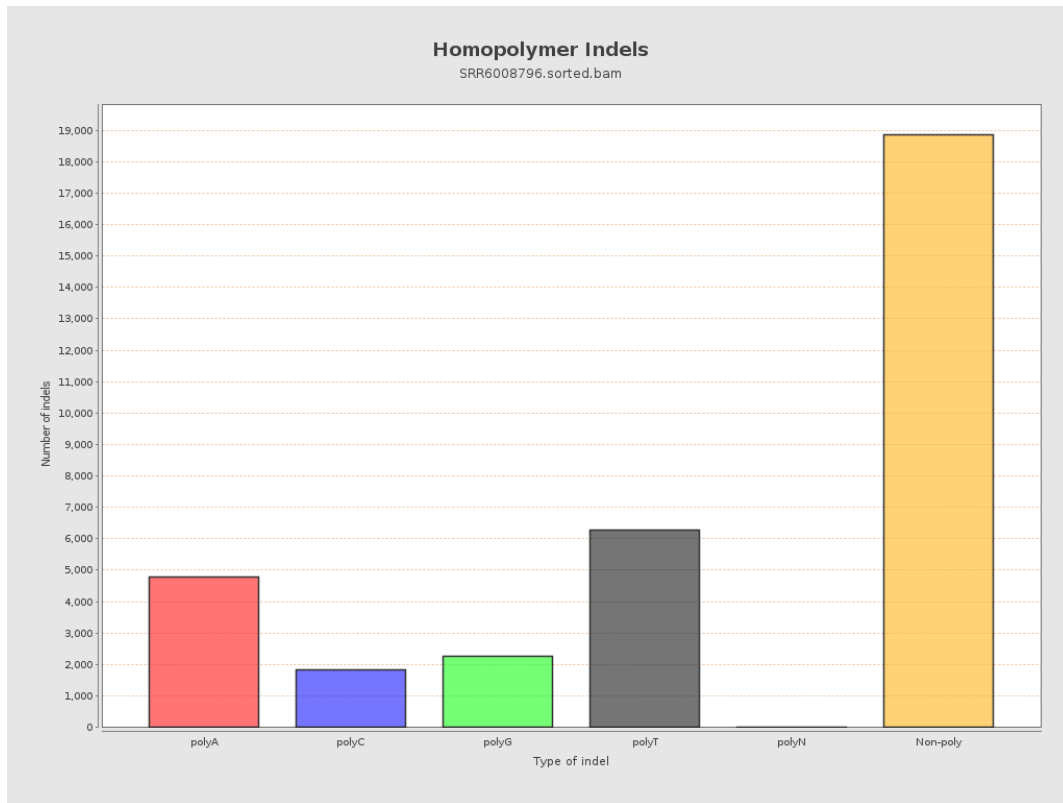
9. Results : Mapped Reads GC-content Distribution



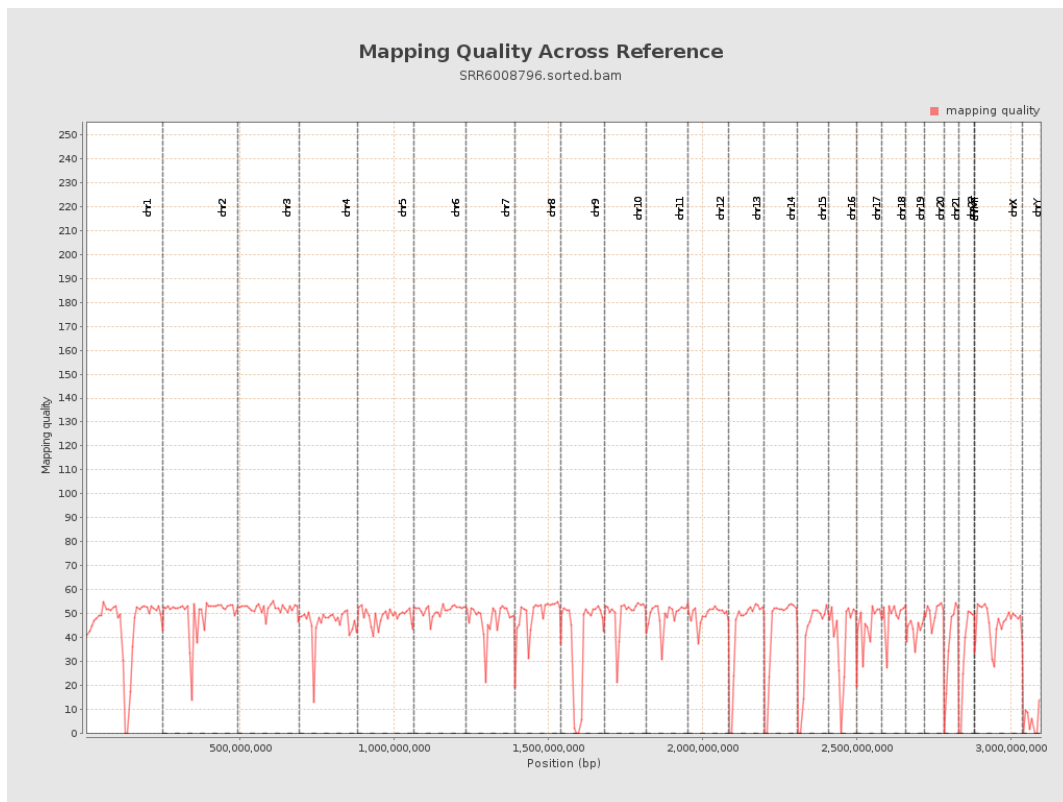
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

