

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 06:03:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237796.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_SRR6237796 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237796.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 06:03:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237796.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,512,355
Mapped reads	2,211,093 / 88.01%
Unmapped reads	301,262 / 11.99%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	23,554 / 0.94%
Read min/max/mean length	30 / 76 / 76.33
Duplicated reads (estimated)	255,593 / 10.17%
Duplication rate	8.44%
Clipped reads	887,120 / 35.31%

2.2. ACGT Content

Number/percentage of A's	41,648,672 / 27.83%
Number/percentage of C's	28,291,858 / 18.91%
Number/percentage of T's	46,548,272 / 31.11%
Number/percentage of G's	32,888,295 / 21.98%
Number/percentage of N's	257,504 / 0.17%
GC Percentage	40.89%

2.3. Coverage

Mean	0.0484

Standard Deviation	0.5414
--------------------	--------

2.4. Mapping Quality

Mean Mapping Quality	46.4
----------------------	------

2.5. Mismatches and indels

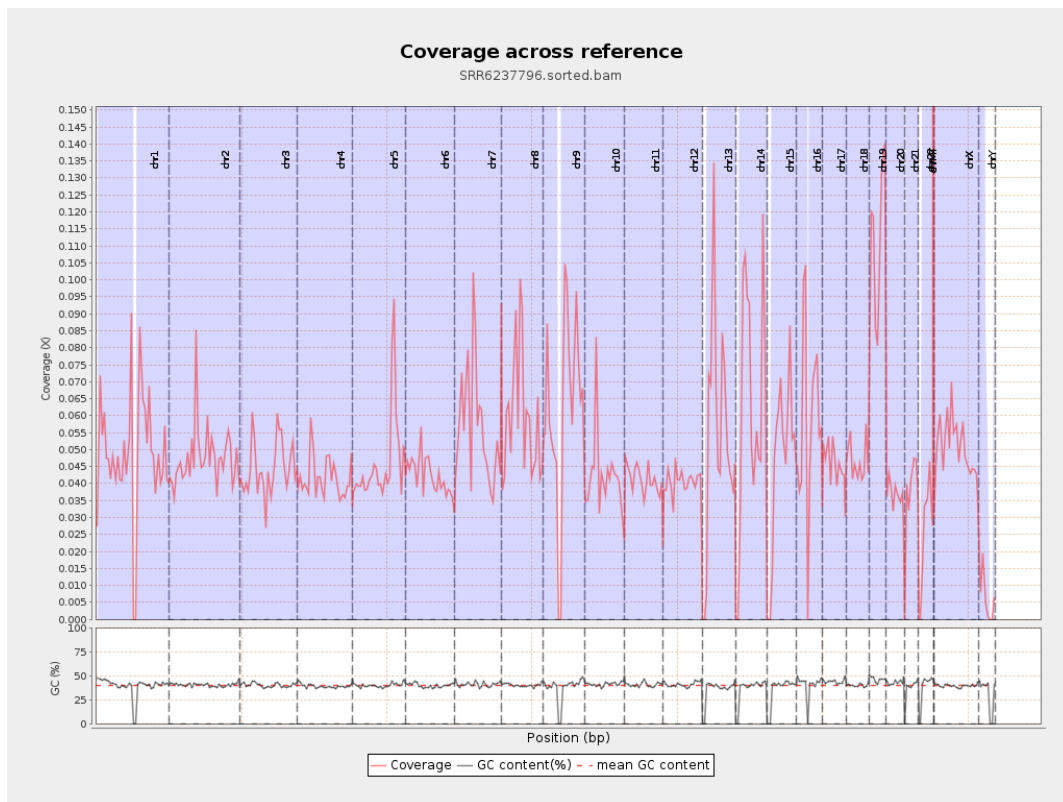
General error rate	0.84%
Mismatches	1,237,038
Insertions	10,807
Mapped reads with at least one insertion	0.48%
Deletions	35,626
Mapped reads with at least one deletion	1.6%
Homopolymer indels	47.56%

2.6. Chromosome stats

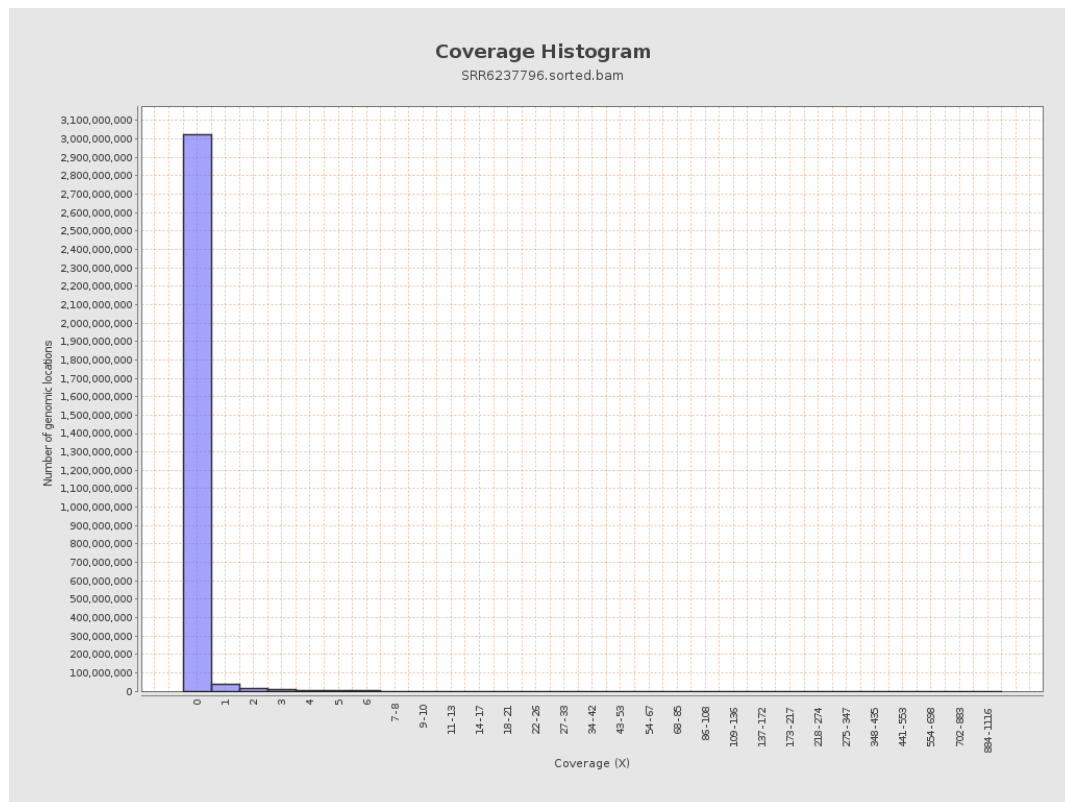
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	12116697	0.0486	1.0412
chr2	243199373	11547839	0.0475	0.5343
chr3	198022430	8840036	0.0446	0.3791
chr4	191154276	7945466	0.0416	0.3723
chr5	180915260	8363629	0.0462	0.3816
chr6	171115067	7216078	0.0422	0.4008
chr7	159138663	9046271	0.0568	0.6502

chr8	146364022	8642842	0.0591	0.5733
chr9	141213431	8884164	0.0629	0.5333
chr10	135534747	5709969	0.0421	0.5192
chr11	135006516	5511695	0.0408	0.4125
chr12	133851895	5396725	0.0403	0.36
chr13	115169878	6060529	0.0526	0.4094
chr14	107349540	6740721	0.0628	0.4699
chr15	102531392	4849126	0.0473	0.391
chr16	90354753	5336291	0.0591	0.4658
chr17	81195210	3709630	0.0457	0.4023
chr18	78077248	3644662	0.0467	0.7966
chr19	59128983	6445917	0.109	0.823
chr20	63025520	2322929	0.0369	0.3465
chr21	48129895	1777431	0.0369	0.3469
chr22	51304566	1308149	0.0255	0.2719
chrMT	16571	43557	2.6285	3.1544
chrX	155270560	7849584	0.0506	0.4108
chrY	59373566	387334	0.0065	0.1622

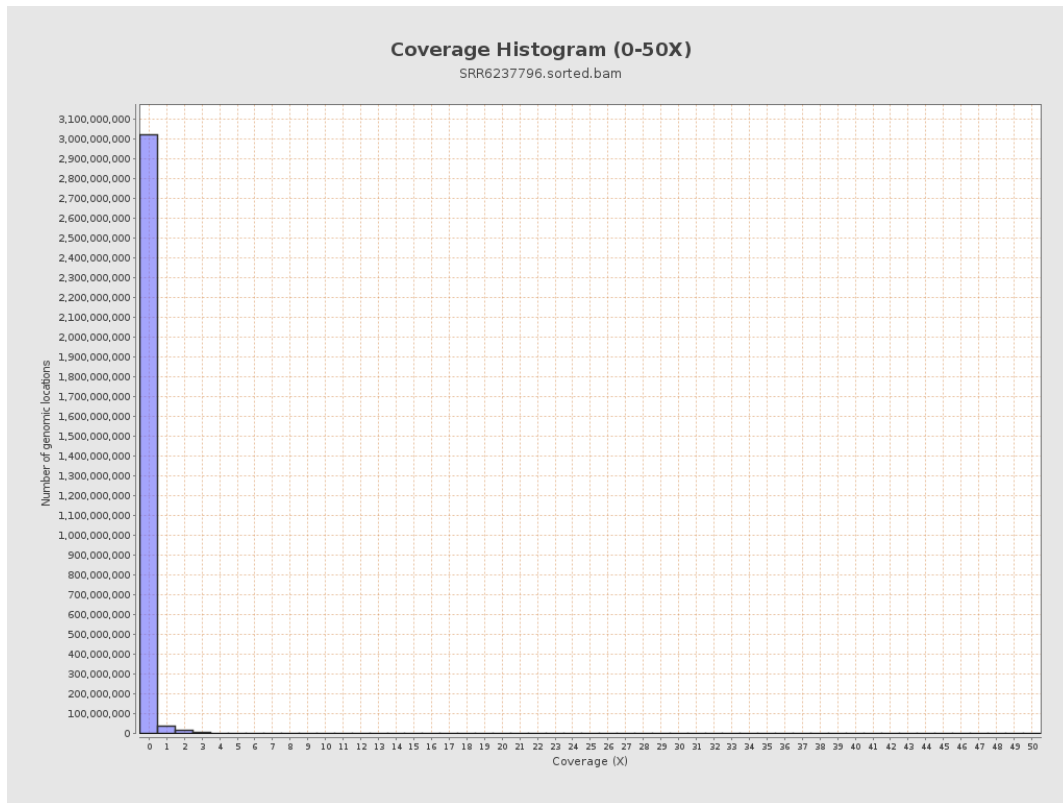
3. Results : Coverage across reference



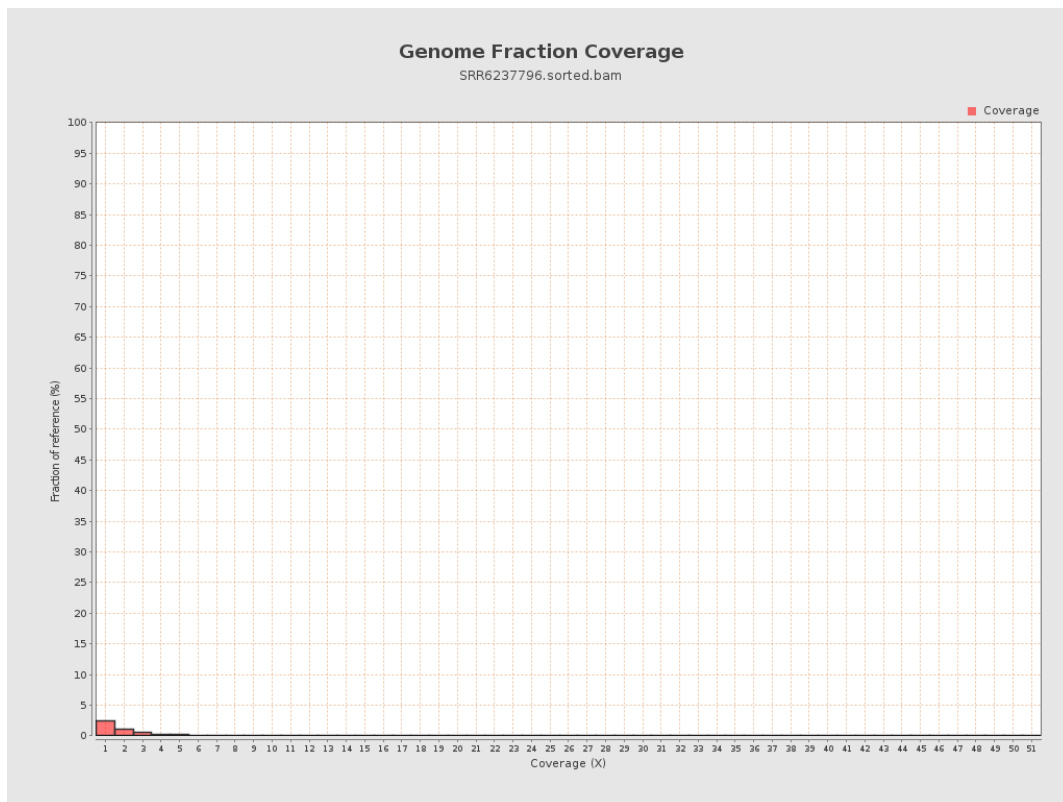
4. Results : Coverage Histogram



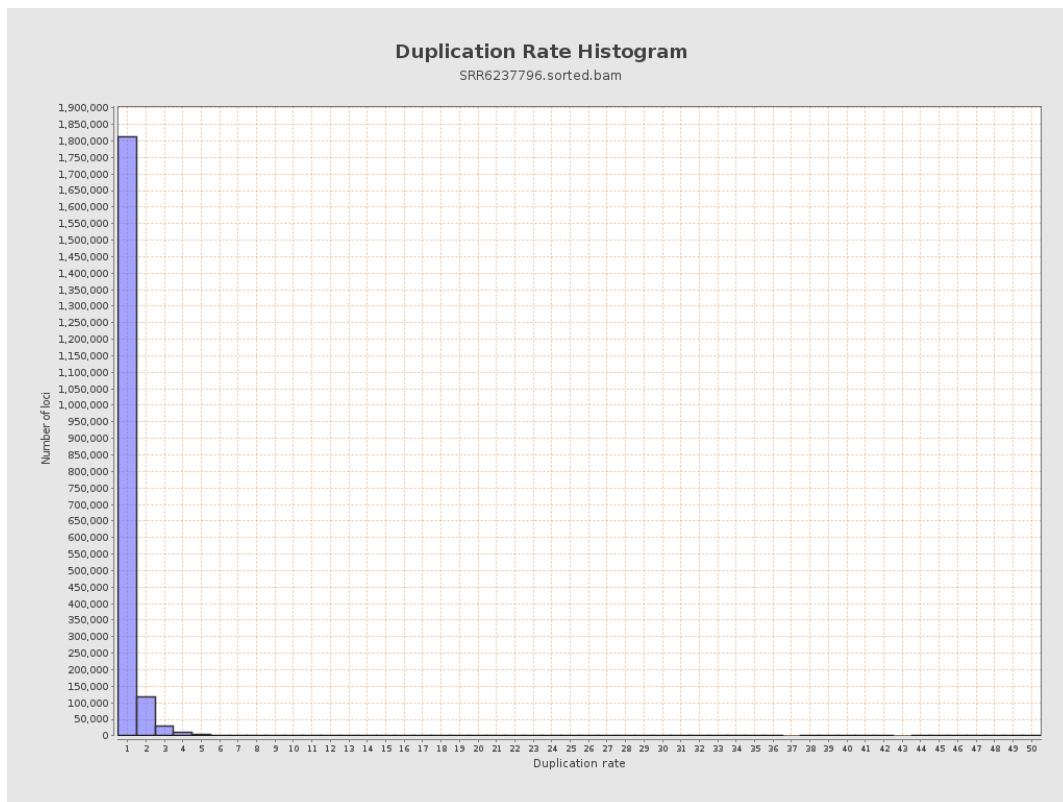
5. Results : Coverage Histogram (0-50X)



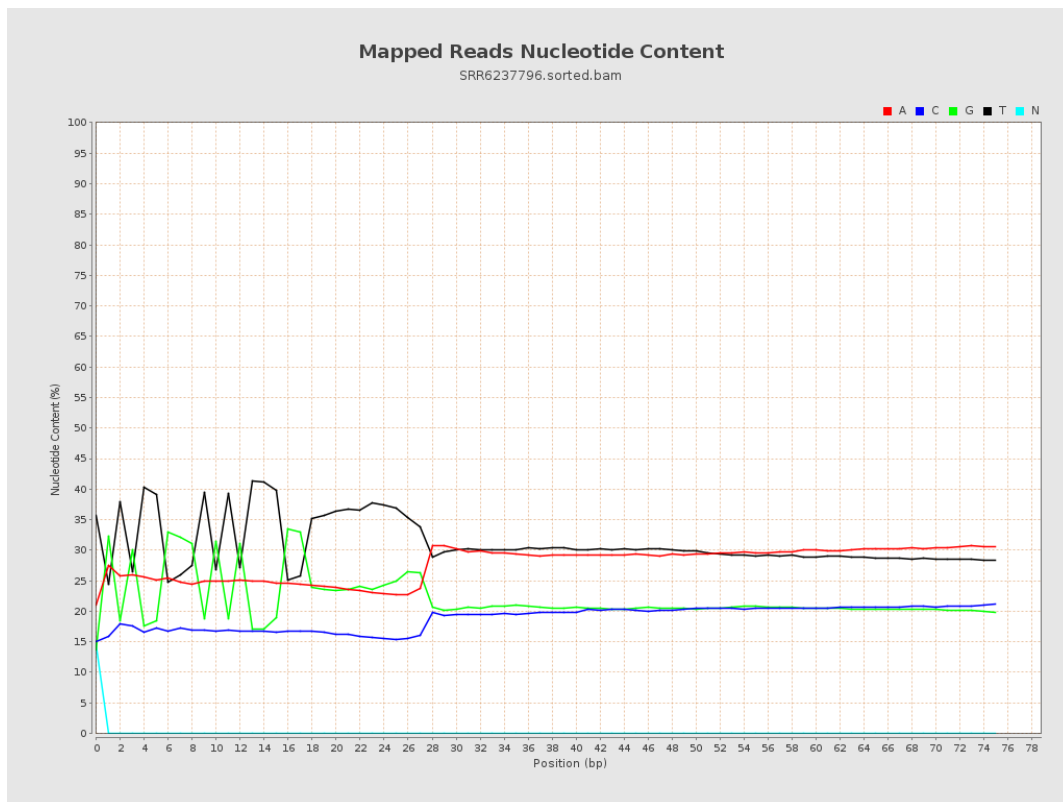
6. Results : Genome Fraction Coverage



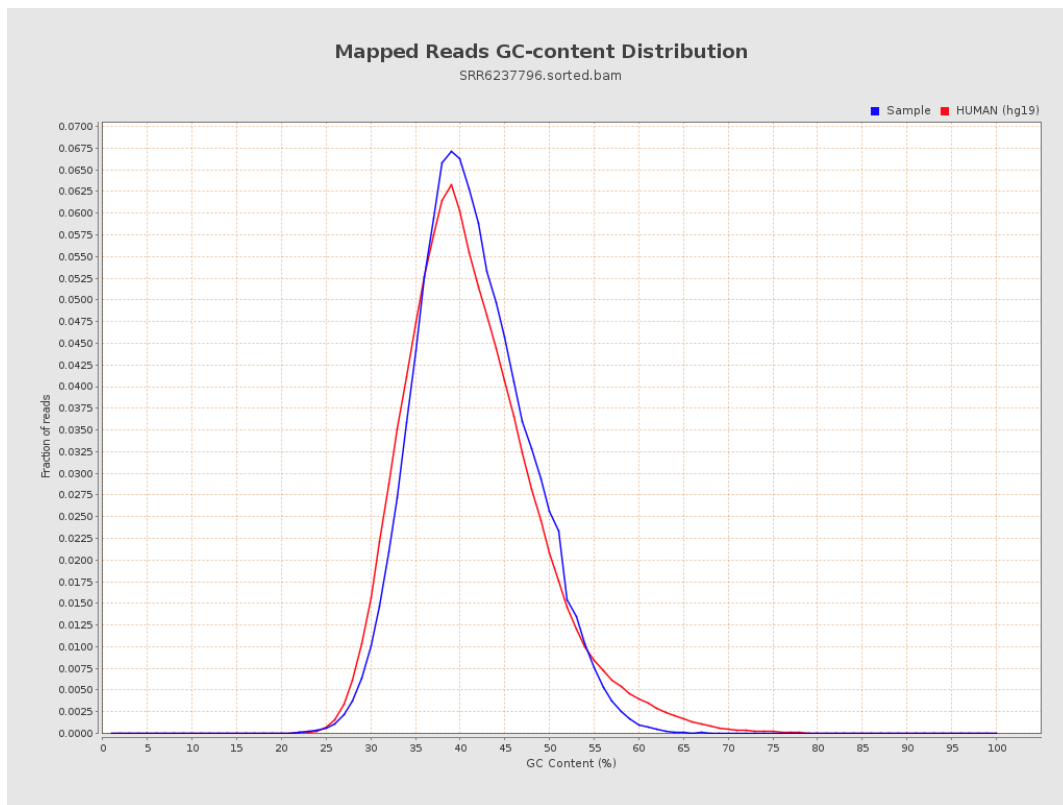
7. Results : Duplication Rate Histogram



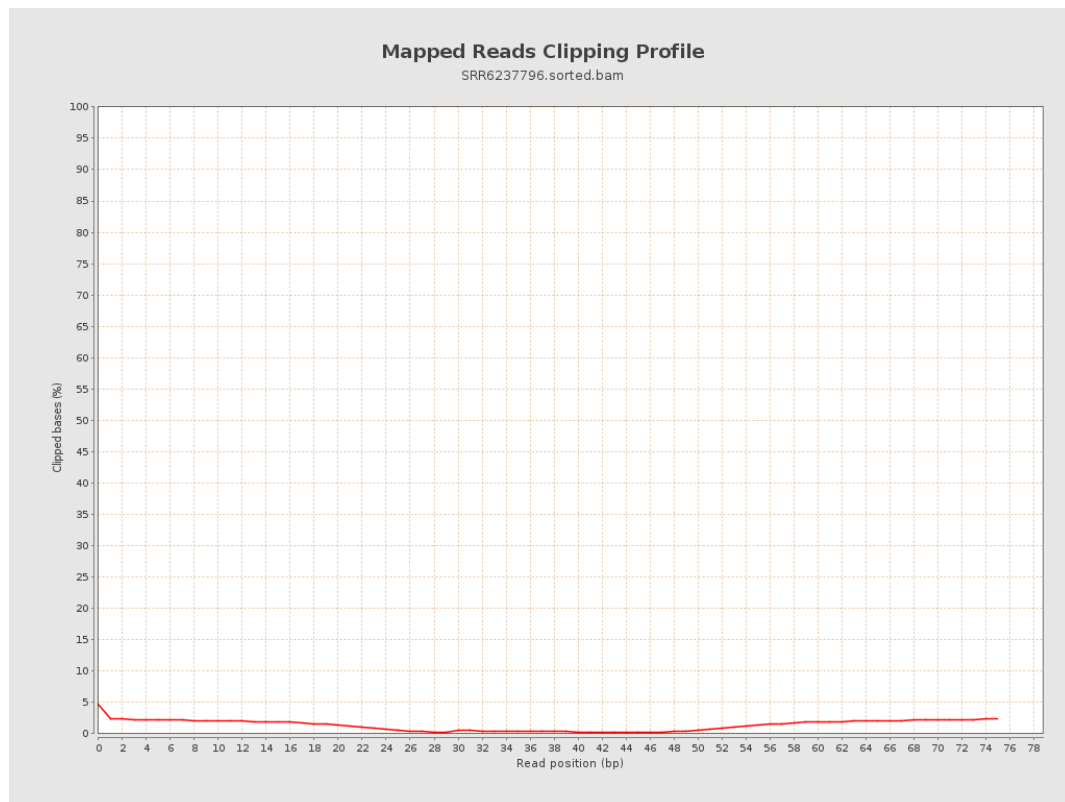
8. Results : Mapped Reads Nucleotide Content



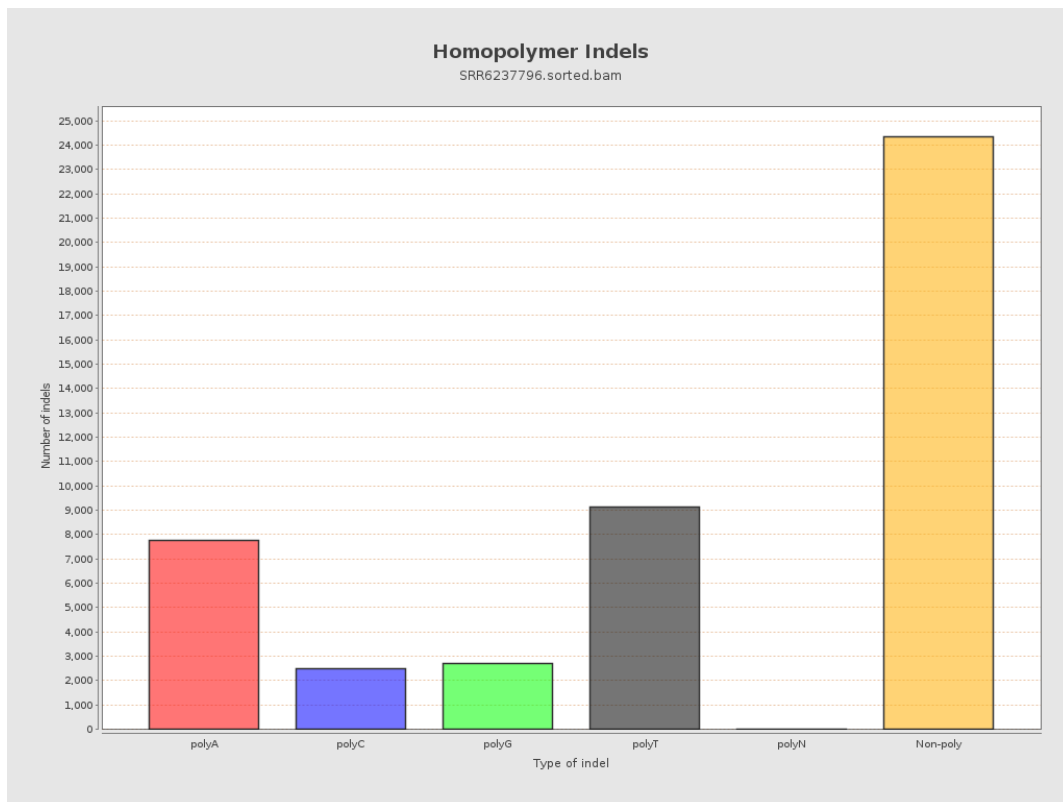
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

