

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/19 23:04:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1506011.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_SRR1506011 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1506011.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Dec 19 23:04:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1506011.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,670,563
Mapped reads	3,924,535 / 45.26%
Unmapped reads	4,746,028 / 54.74%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	167 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	275,270 / 3.17%
Duplication rate	5.42%
Clipped reads	550,308 / 6.35%

2.2. ACGT Content

Number/percentage of A's	54,277,028 / 29.64%
Number/percentage of C's	36,383,315 / 19.87%
Number/percentage of T's	54,573,368 / 29.8%
Number/percentage of G's	37,266,137 / 20.35%
Number/percentage of N's	613,092 / 0.33%
GC Percentage	40.22%

2.3. Coverage

Mean	0.0592

Standard Deviation	0.5103
--------------------	--------

2.4. Mapping Quality

Mean Mapping Quality	44.37
----------------------	-------

2.5. Mismatches and indels

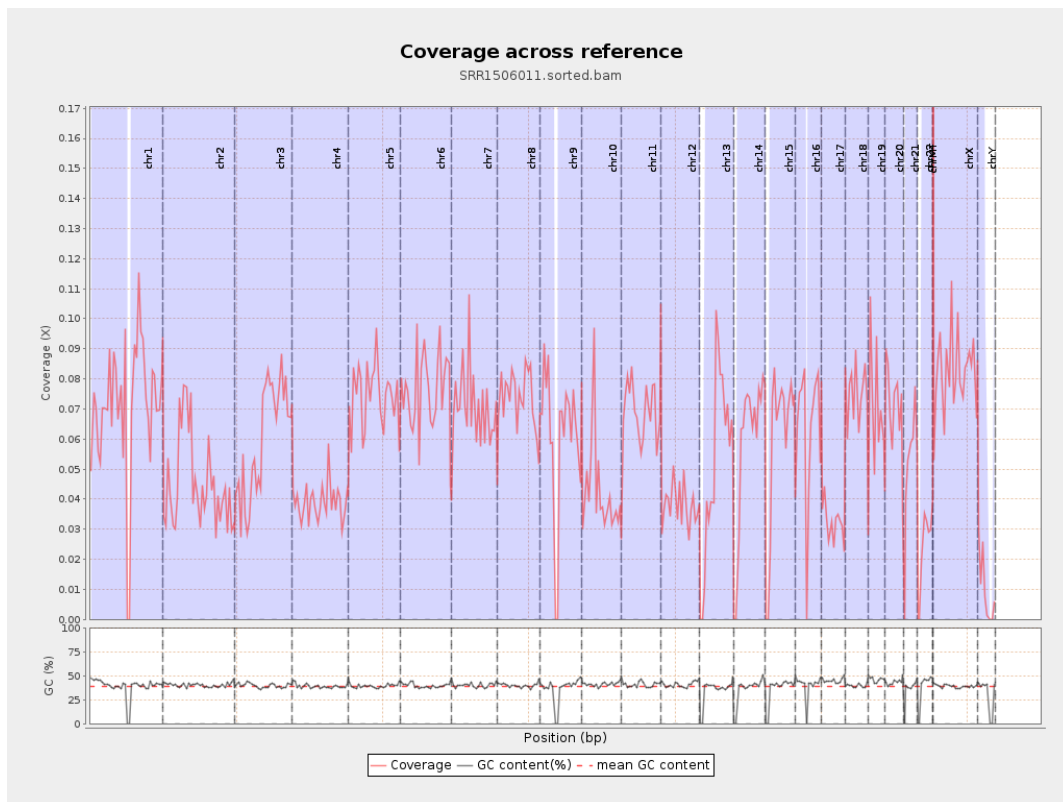
General error rate	0.81%
Mismatches	1,469,037
Insertions	8,285
Mapped reads with at least one insertion	0.21%
Deletions	27,739
Mapped reads with at least one deletion	0.7%
Homopolymer indels	46.63%

2.6. Chromosome stats

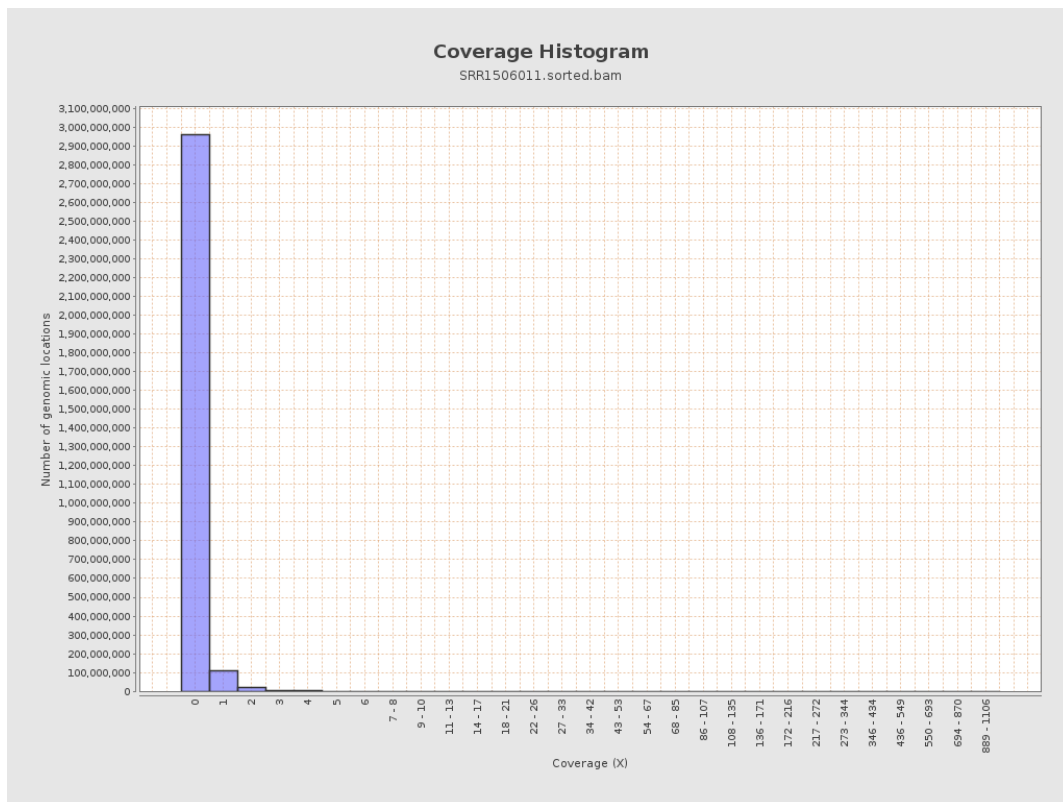
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	17664919	0.0709	0.9034
chr2	243199373	11020679	0.0453	0.3993
chr3	198022430	11733533	0.0593	0.3123
chr4	191154276	7466066	0.0391	0.2591
chr5	180915260	13412538	0.0741	0.354
chr6	171115067	13082709	0.0765	0.4827
chr7	159138663	11167480	0.0702	0.6242

chr8	146364022	10698555	0.0731	0.6732
chr9	141213431	8608151	0.061	0.4239
chr10	135534747	5693849	0.042	0.5379
chr11	135006516	9306677	0.0689	0.4017
chr12	133851895	5061352	0.0378	0.2772
chr13	115169878	6161245	0.0535	0.295
chr14	107349540	6278721	0.0585	0.9117
chr15	102531392	5990280	0.0584	0.3079
chr16	90354753	5590164	0.0619	0.3643
chr17	81195210	2635280	0.0325	0.2495
chr18	78077248	5869445	0.0752	0.7416
chr19	59128983	4130081	0.0698	0.7339
chr20	63025520	4496733	0.0713	0.3552
chr21	48129895	2512149	0.0522	0.3135
chr22	51304566	1205488	0.0235	0.1903
chrMT	16571	8792	0.5306	0.9702
chrX	155270560	12794060	0.0824	0.4129
chrY	59373566	562918	0.0095	0.1679

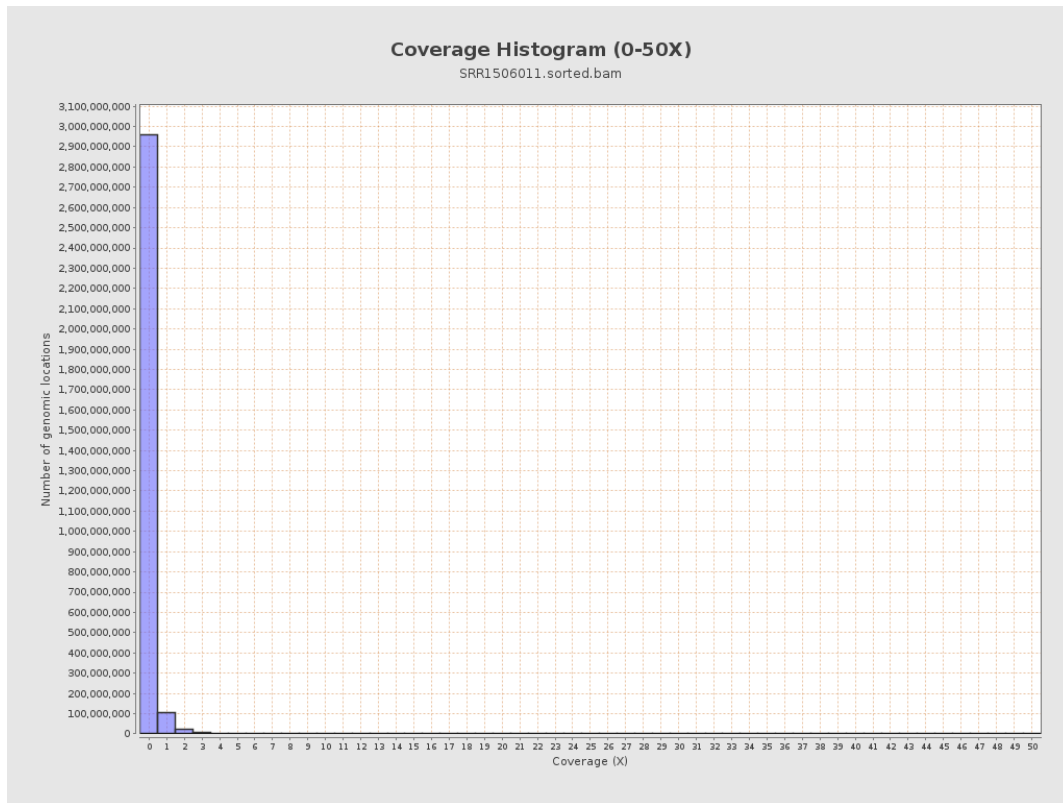
3. Results : Coverage across reference



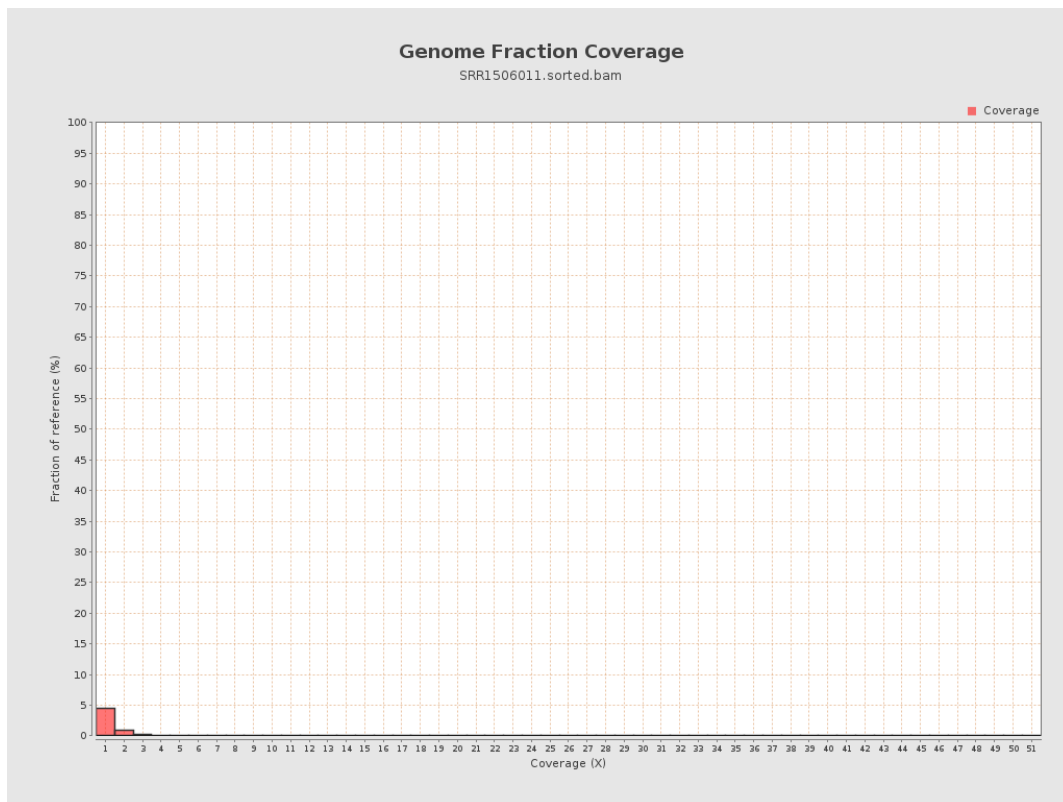
4. Results : Coverage Histogram



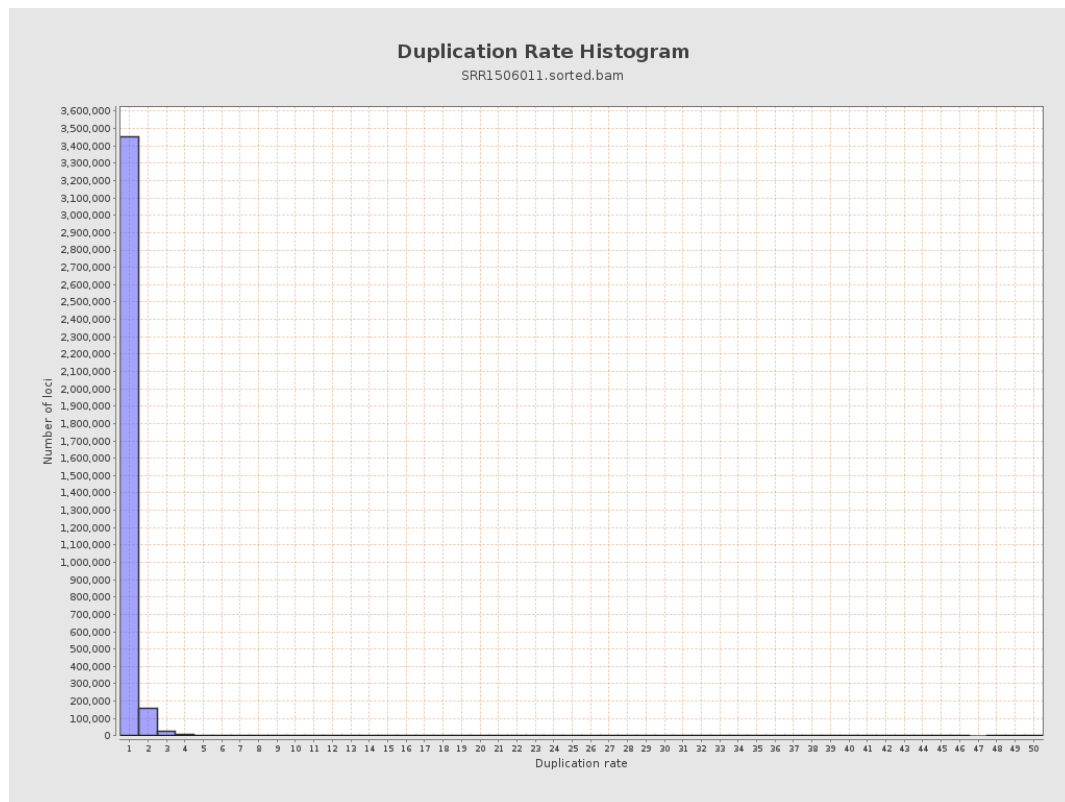
5. Results : Coverage Histogram (0-50X)



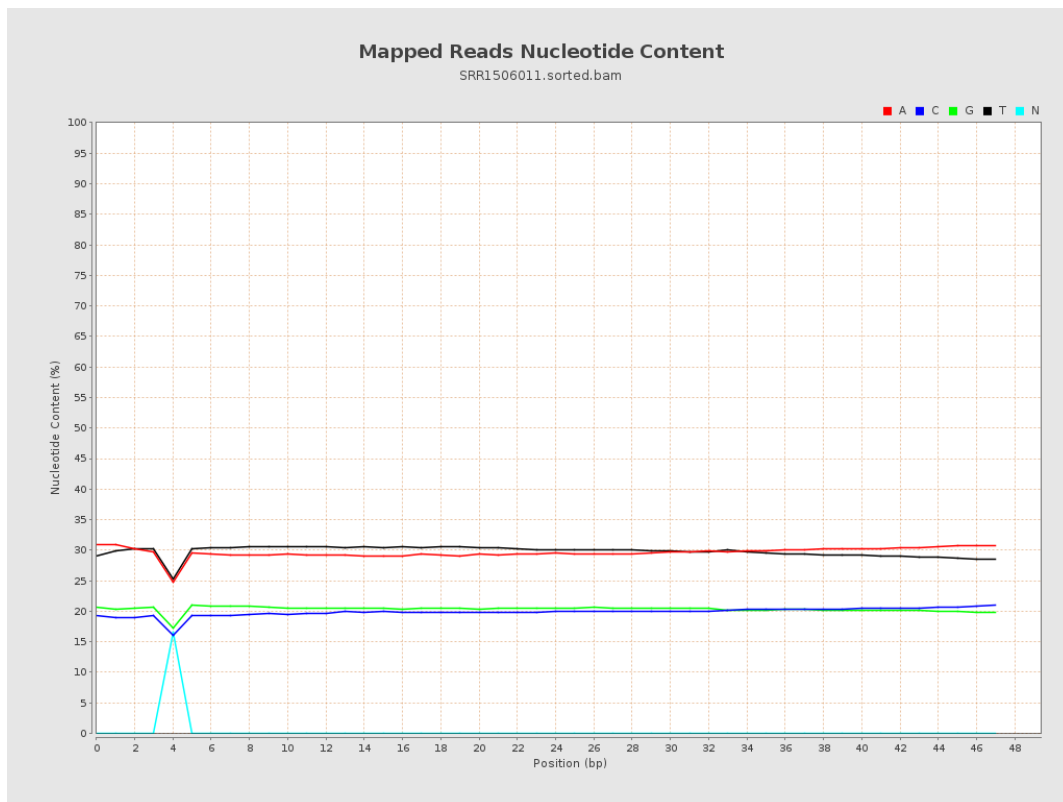
6. Results : Genome Fraction Coverage



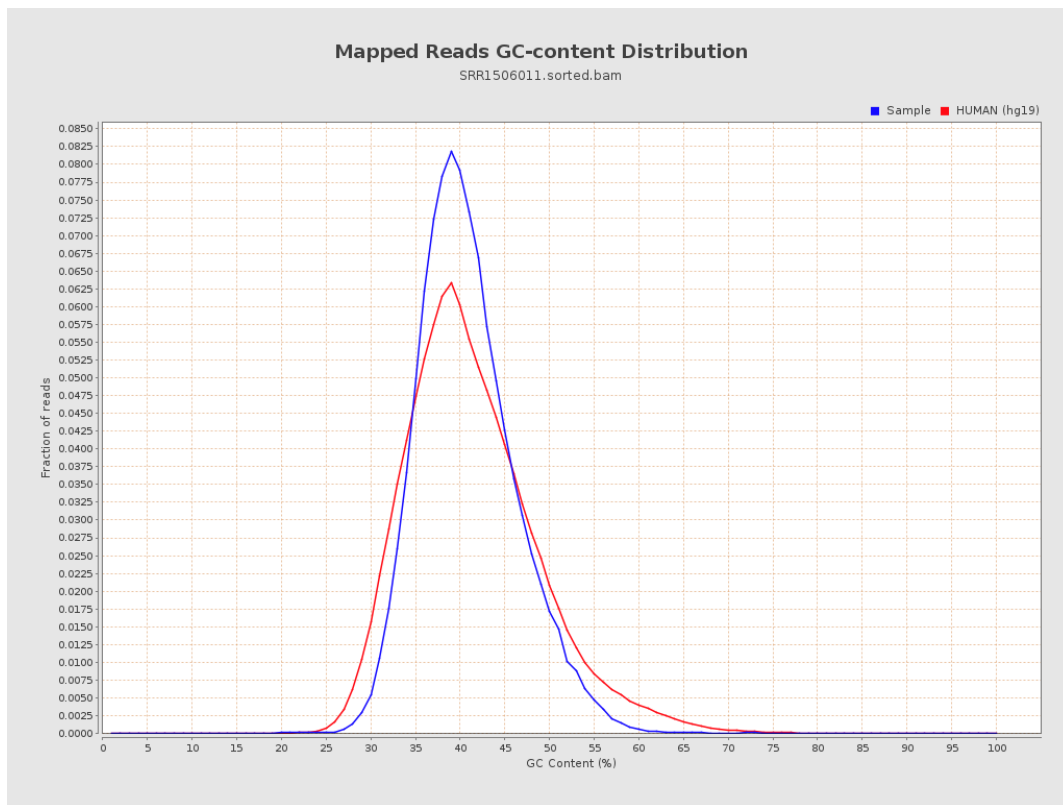
7. Results : Duplication Rate Histogram



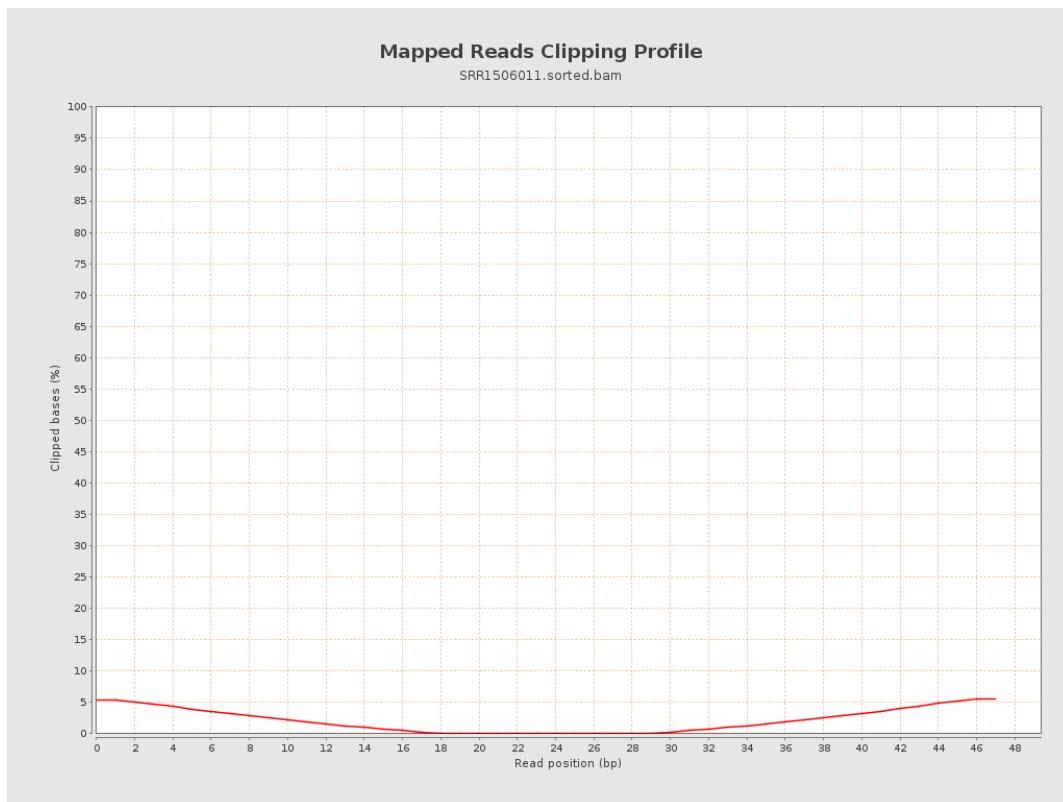
8. Results : Mapped Reads Nucleotide Content



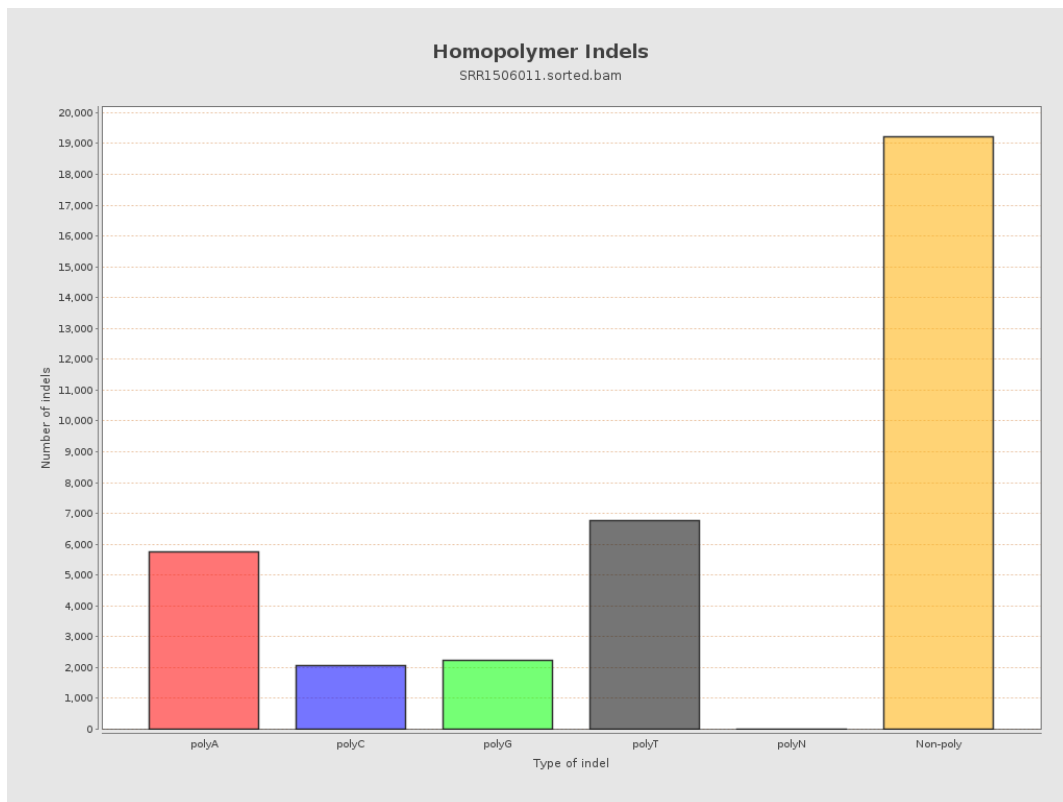
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

