

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/19 22:20:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1505985.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_SRR1505985 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1505985.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Dec 19 22:20:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1505985.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,745,778
Mapped reads	4,815,274 / 71.38%
Unmapped reads	1,930,504 / 28.62%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	263 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	428,816 / 6.36%
Duplication rate	6.93%
Clipped reads	805,068 / 11.93%

2.2. ACGT Content

Number/percentage of A's	65,049,292 / 29.14%
Number/percentage of C's	46,181,741 / 20.69%
Number/percentage of T's	65,073,983 / 29.15%
Number/percentage of G's	46,929,833 / 21.02%
Number/percentage of N's	865 / 0%
GC Percentage	41.71%

2.3. Coverage

Mean	0.0721

Standard Deviation	0.5742
--------------------	--------

2.4. Mapping Quality

Mean Mapping Quality	44.16
----------------------	-------

2.5. Mismatches and indels

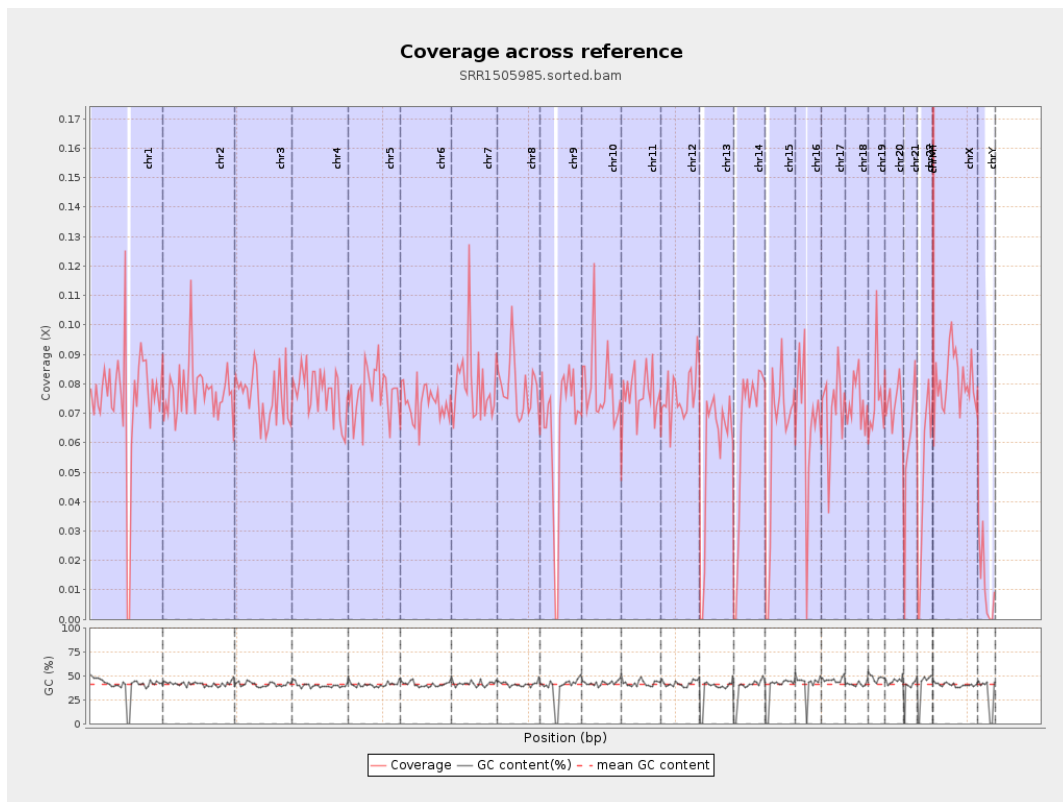
General error rate	0.5%
Mismatches	1,110,199
Insertions	10,399
Mapped reads with at least one insertion	0.22%
Deletions	30,763
Mapped reads with at least one deletion	0.64%
Homopolymer indels	44.86%

2.6. Chromosome stats

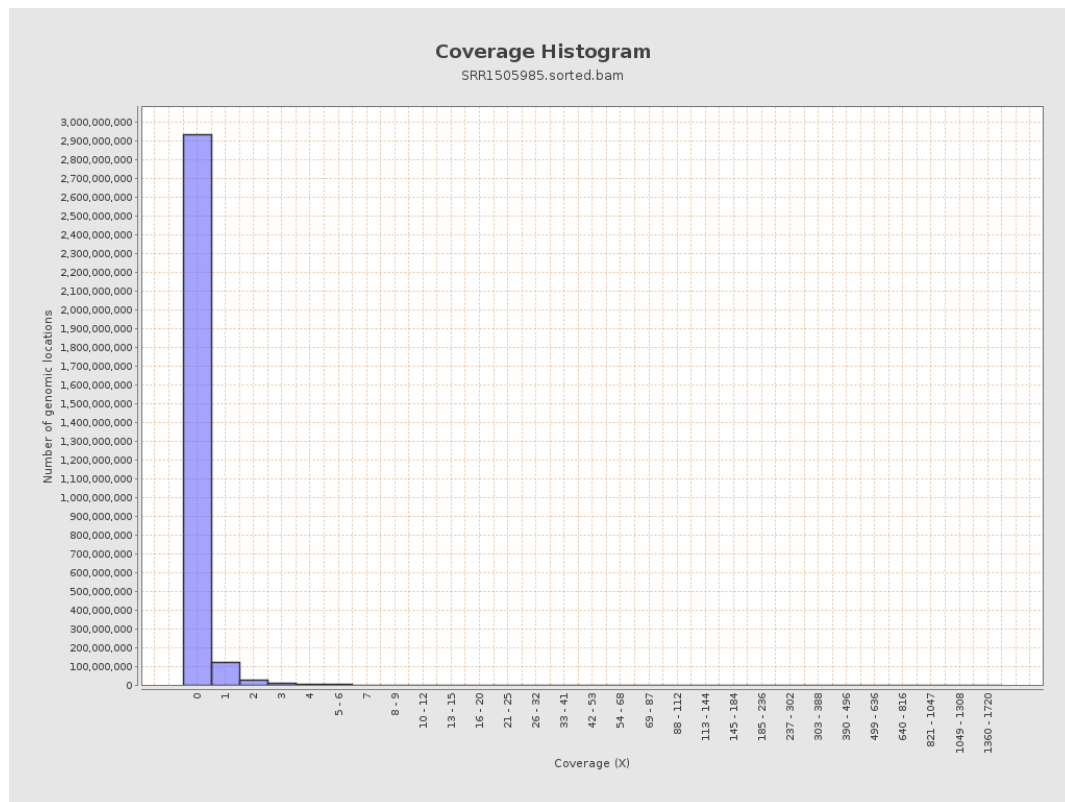
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	18527911	0.0743	1.0757
chr2	243199373	18844569	0.0775	0.5017
chr3	198022430	14984460	0.0757	0.364
chr4	191154276	14734982	0.0771	0.382
chr5	180915260	13915138	0.0769	0.3725
chr6	171115067	12557469	0.0734	0.4221
chr7	159138663	12681172	0.0797	0.7384

chr8	146364022	11453157	0.0783	0.9766
chr9	141213431	9221564	0.0653	0.4455
chr10	135534747	10627947	0.0784	0.5716
chr11	135006516	10308756	0.0764	0.5025
chr12	133851895	10228823	0.0764	0.3968
chr13	115169878	6576134	0.0571	0.3133
chr14	107349540	6965284	0.0649	0.4374
chr15	102531392	6192856	0.0604	0.3227
chr16	90354753	6032351	0.0668	0.3785
chr17	81195210	5886747	0.0725	0.3987
chr18	78077248	5737847	0.0735	0.8297
chr19	59128983	4462695	0.0755	0.7589
chr20	63025520	4646092	0.0737	0.3782
chr21	48129895	2870368	0.0596	0.3564
chr22	51304566	2510277	0.0489	0.2941
chrMT	16571	41968	2.5326	2.5481
chrX	155270560	12568792	0.0809	0.4318
chrY	59373566	700584	0.0118	0.1962

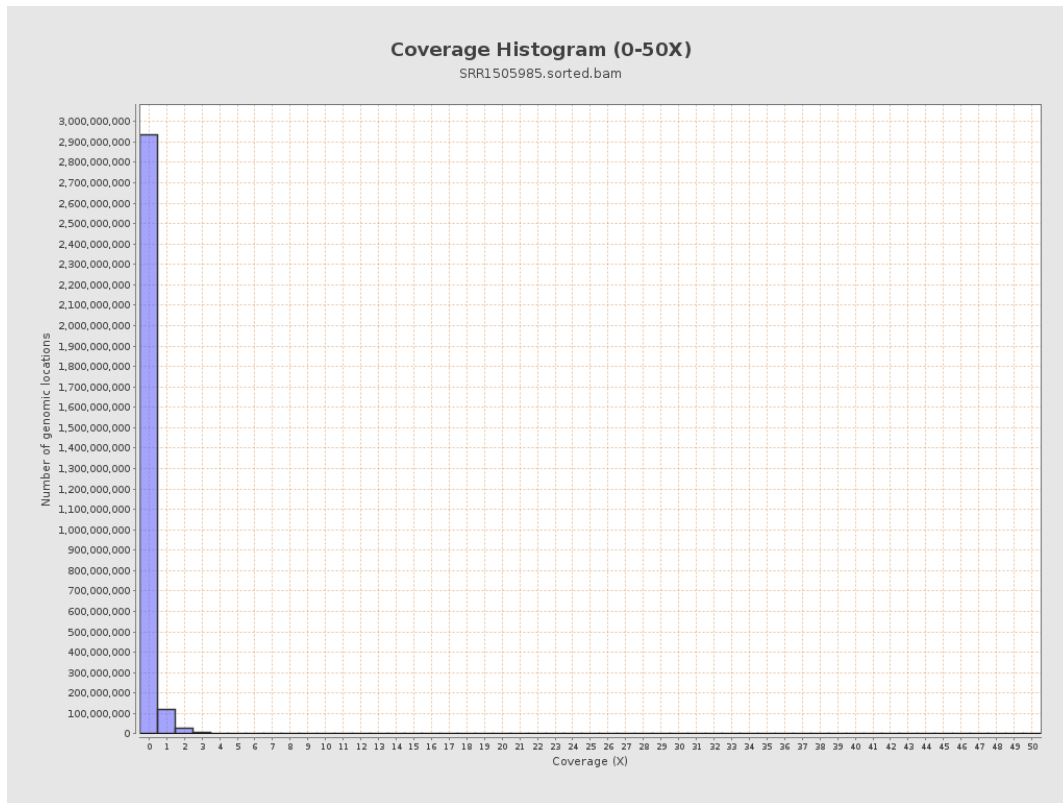
3. Results : Coverage across reference



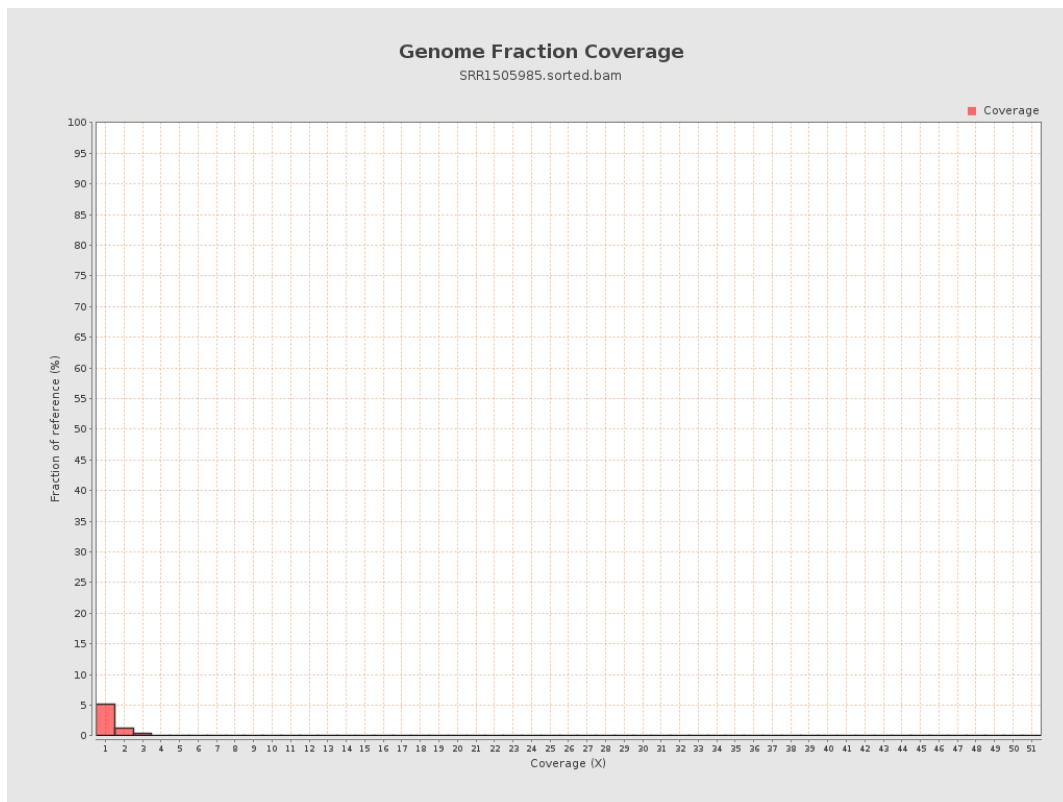
4. Results : Coverage Histogram



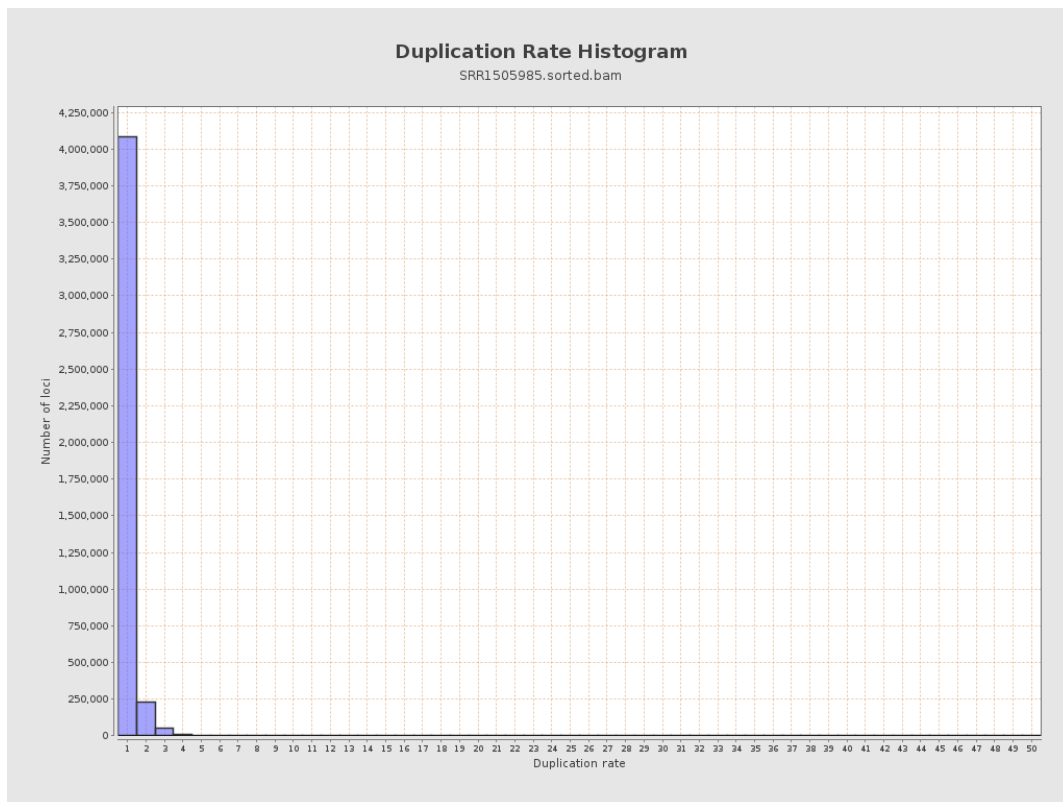
5. Results : Coverage Histogram (0-50X)



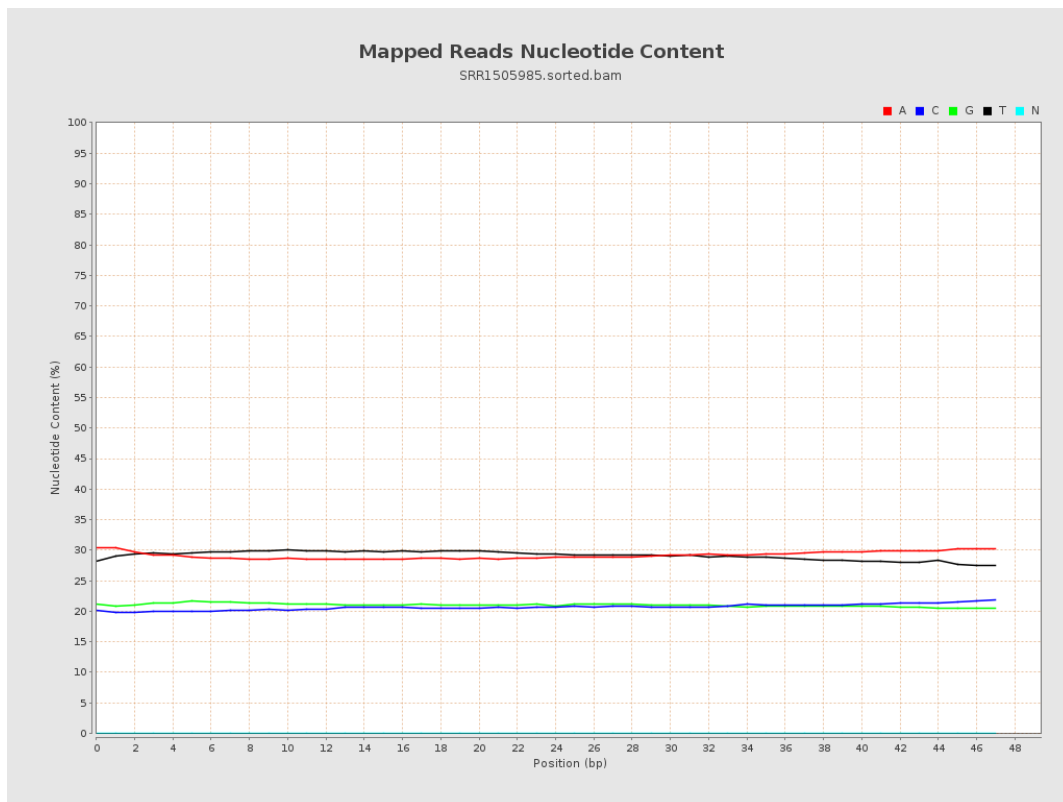
6. Results : Genome Fraction Coverage



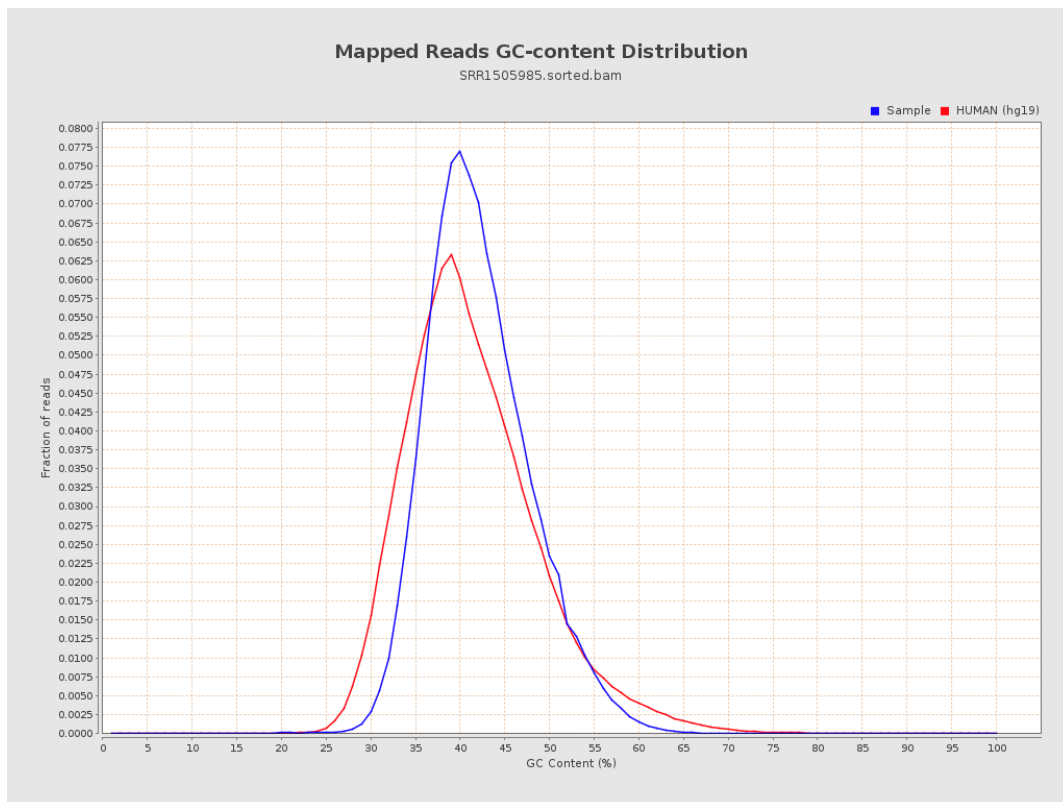
7. Results : Duplication Rate Histogram



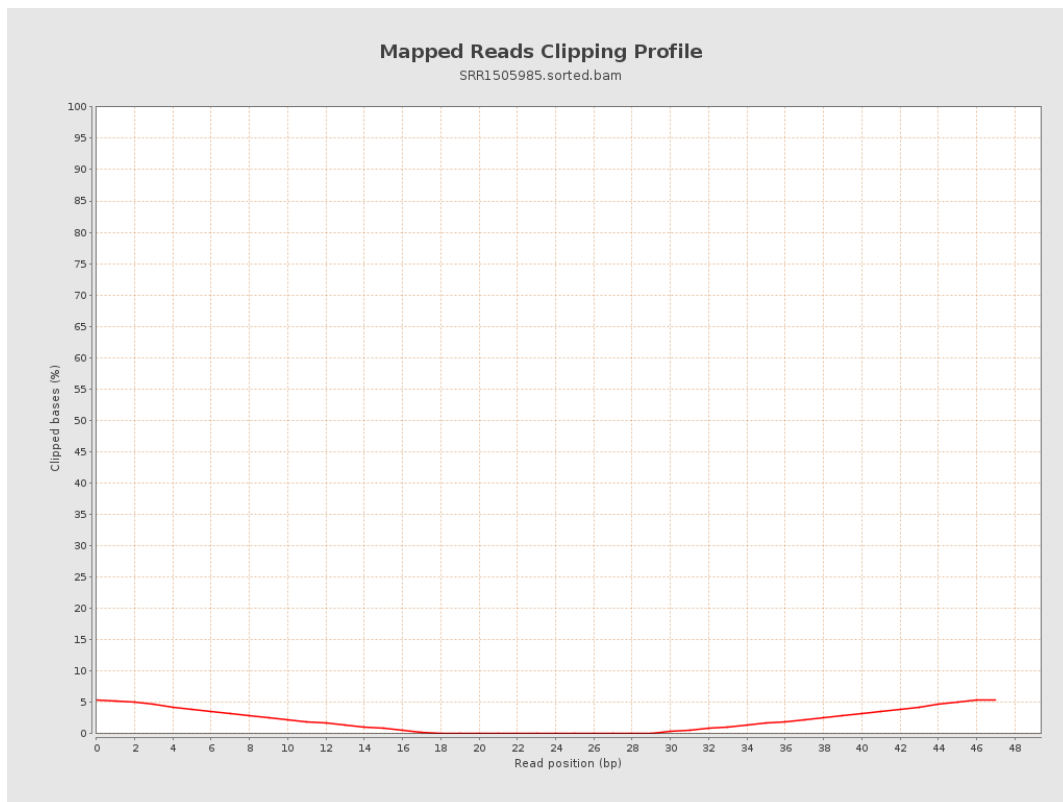
8. Results : Mapped Reads Nucleotide Content



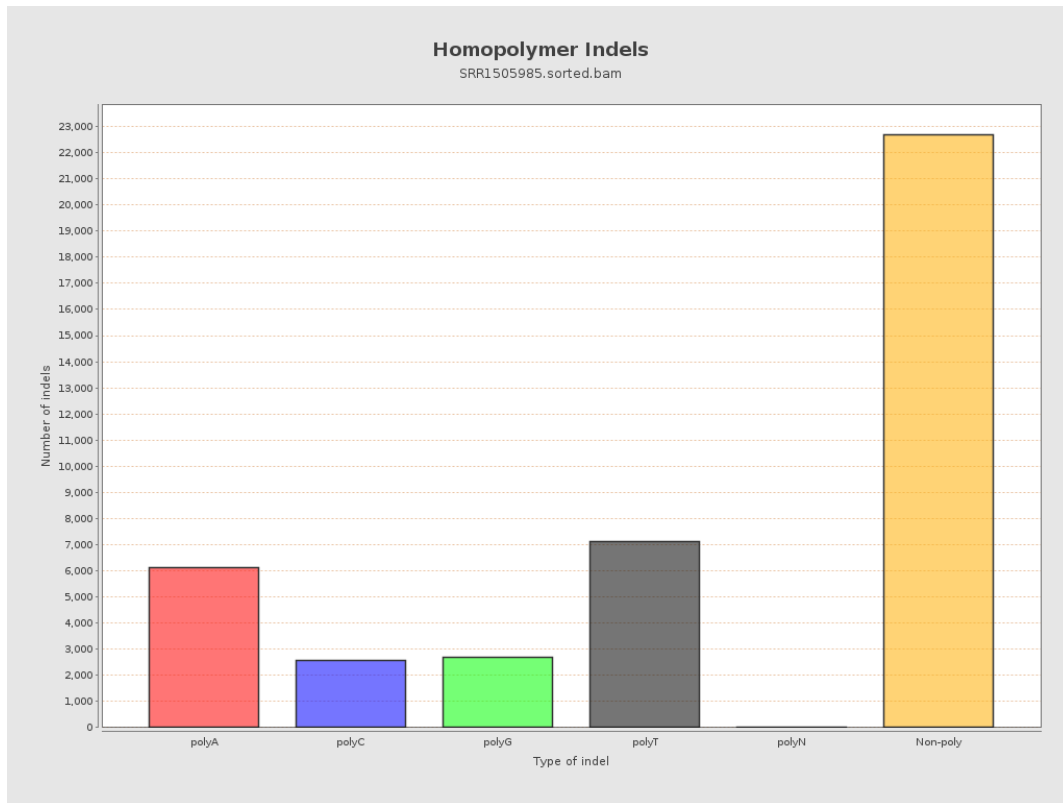
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

