

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/01 19:09:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524483.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_SRR10524483 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524483.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 01 19:09:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524483.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,276,625
Mapped reads	1,186,754 / 92.96%
Unmapped reads	89,871 / 7.04%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,655 / 0.21%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	44,831 / 3.51%
Duplication rate	2.98%
Clipped reads	1,188,189 / 93.07%

2.2. ACGT Content

Number/percentage of A's	17,826,705 / 25.7%
Number/percentage of C's	12,909,432 / 18.61%
Number/percentage of T's	21,008,008 / 30.29%
Number/percentage of G's	17,608,256 / 25.39%
Number/percentage of N's	1,437 / 0%
GC Percentage	44%

2.3. Coverage

Mean	0.0224

Standard Deviation	0.2141
--------------------	--------

2.4. Mapping Quality

Mean Mapping Quality	46.06
----------------------	-------

2.5. Mismatches and indels

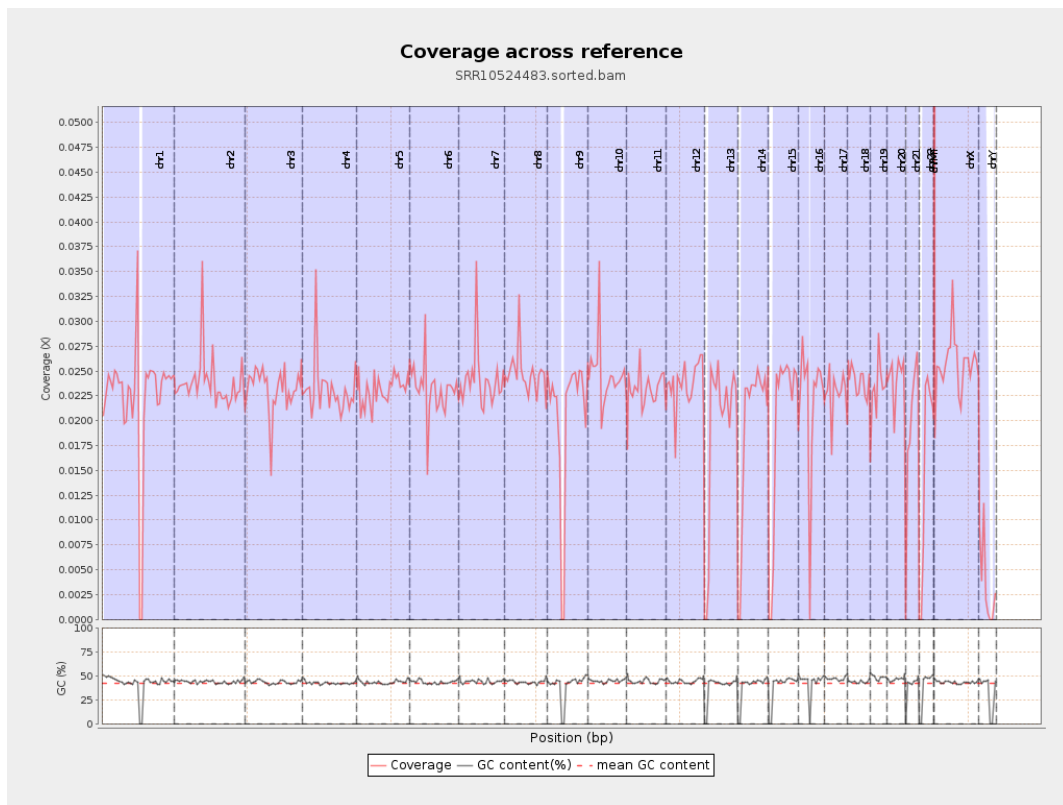
General error rate	0.46%
Mismatches	313,325
Insertions	3,885
Mapped reads with at least one insertion	0.33%
Deletions	12,155
Mapped reads with at least one deletion	1.02%
Homopolymer indels	43.03%

2.6. Chromosome stats

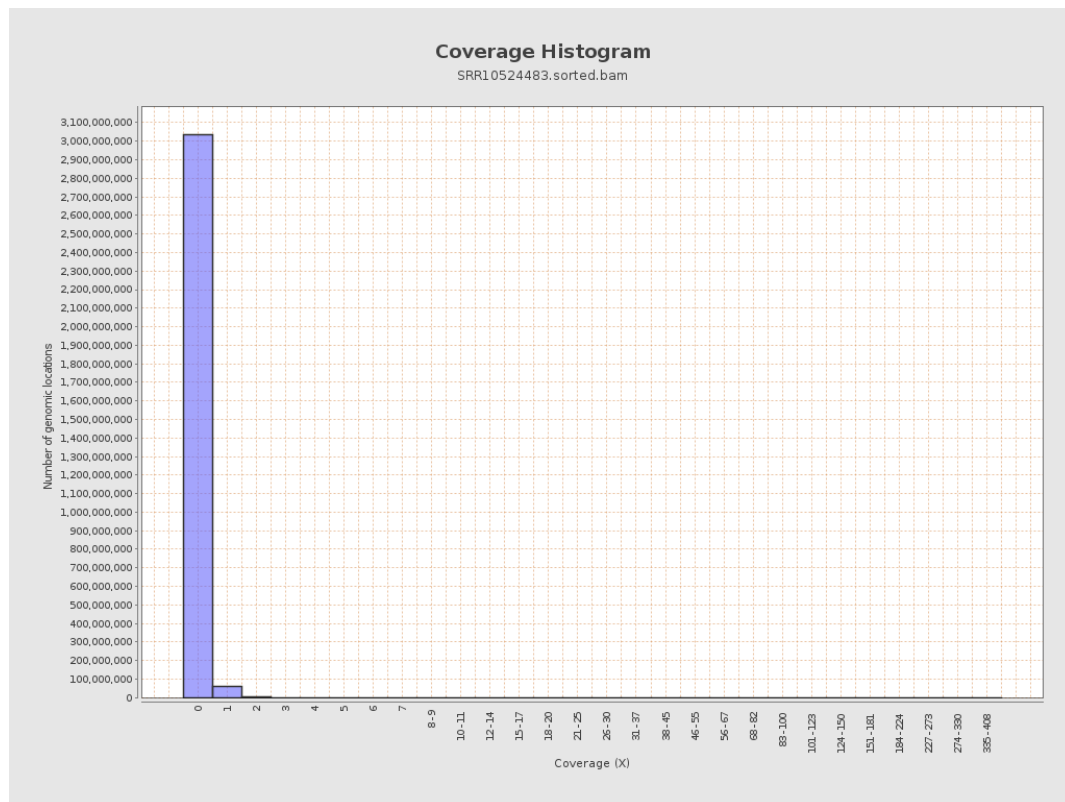
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	5560229	0.0223	0.3557
chr2	243199373	5793076	0.0238	0.2406
chr3	198022430	4595198	0.0232	0.1666
chr4	191154276	4419691	0.0231	0.1786
chr5	180915260	4188706	0.0232	0.1651
chr6	171115067	3957966	0.0231	0.1888
chr7	159138663	3841354	0.0241	0.2814

chr8	146364022	3620332	0.0247	0.2112
chr9	141213431	2878189	0.0204	0.1874
chr10	135534747	3338607	0.0246	0.2064
chr11	135006516	3141478	0.0233	0.2143
chr12	133851895	3173790	0.0237	0.168
chr13	115169878	2207337	0.0192	0.151
chr14	107349540	2088580	0.0195	0.1536
chr15	102531392	2014651	0.0196	0.1547
chr16	90354753	1961217	0.0217	0.1671
chr17	81195210	1848700	0.0228	0.1717
chr18	78077248	1866993	0.0239	0.3006
chr19	59128983	1388512	0.0235	0.2562
chr20	63025520	1520151	0.0241	0.1711
chr21	48129895	947739	0.0197	0.161
chr22	51304566	815174	0.0159	0.1371
chrMT	16571	4754	0.2869	0.6089
chrX	155270560	3994188	0.0257	0.1898
chrY	59373566	208077	0.0035	0.1006

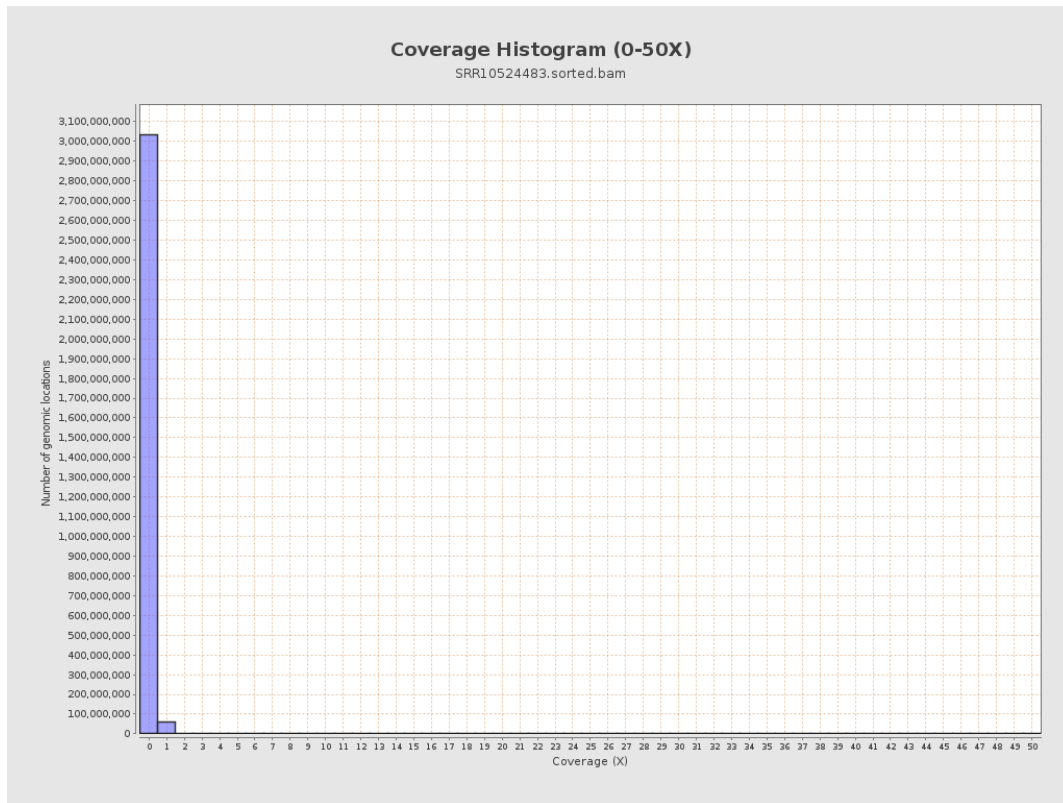
3. Results : Coverage across reference



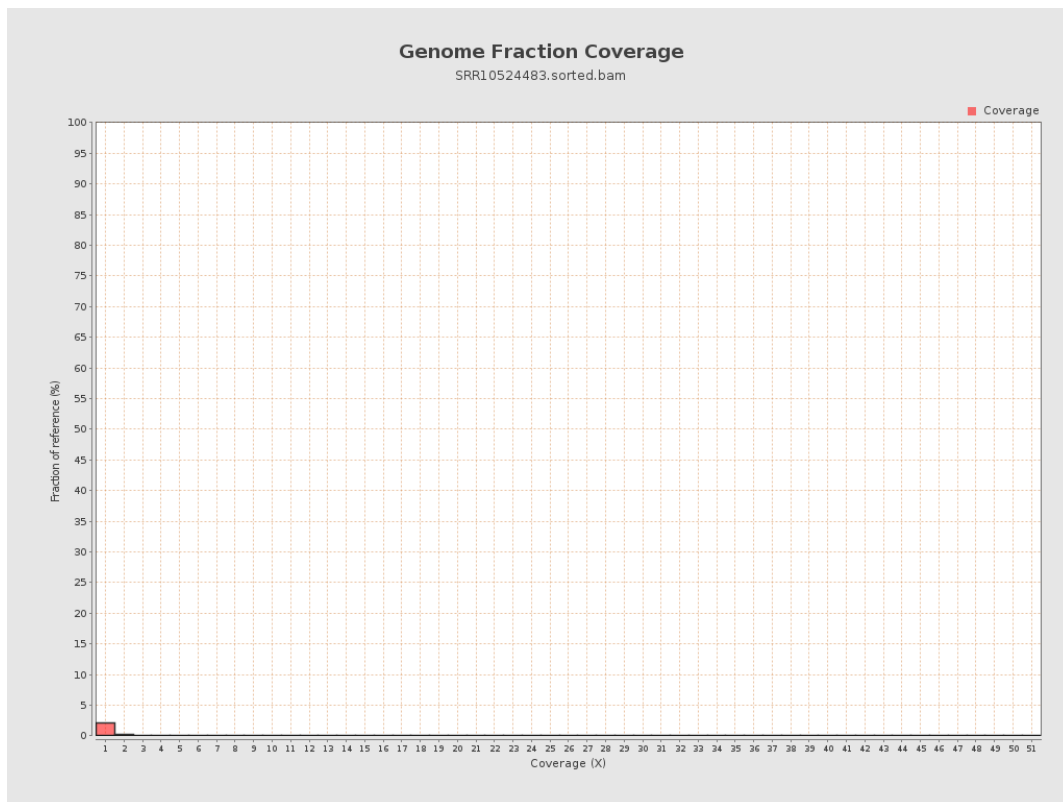
4. Results : Coverage Histogram



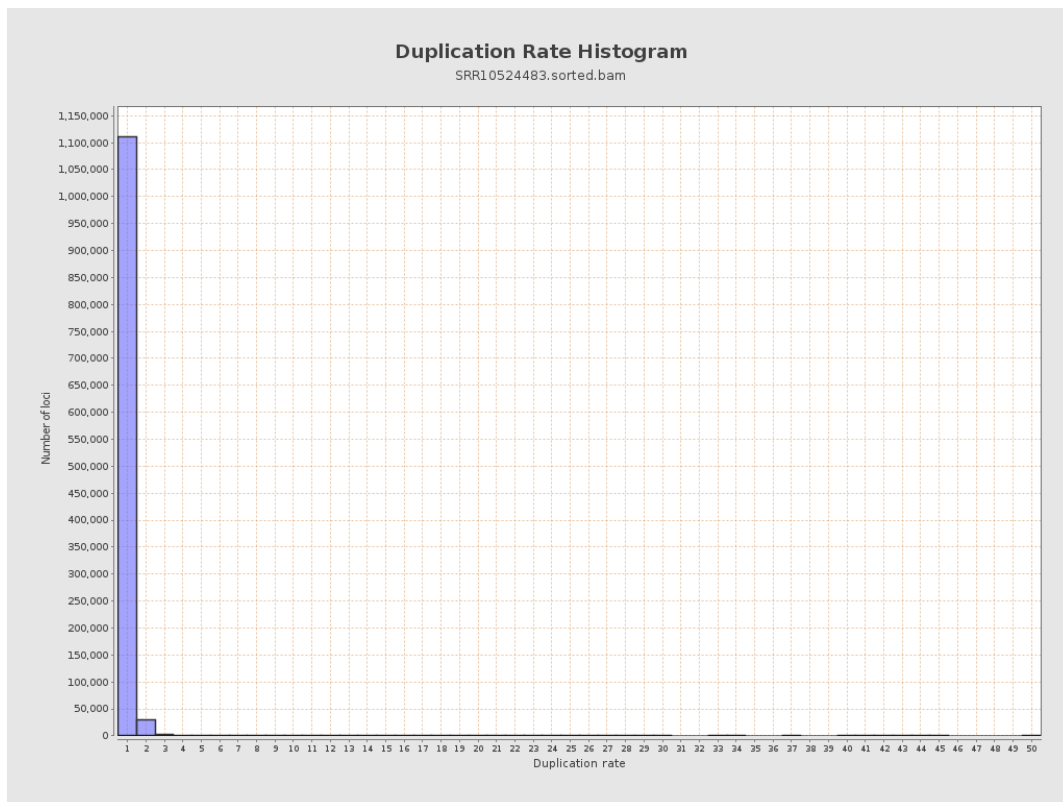
5. Results : Coverage Histogram (0-50X)



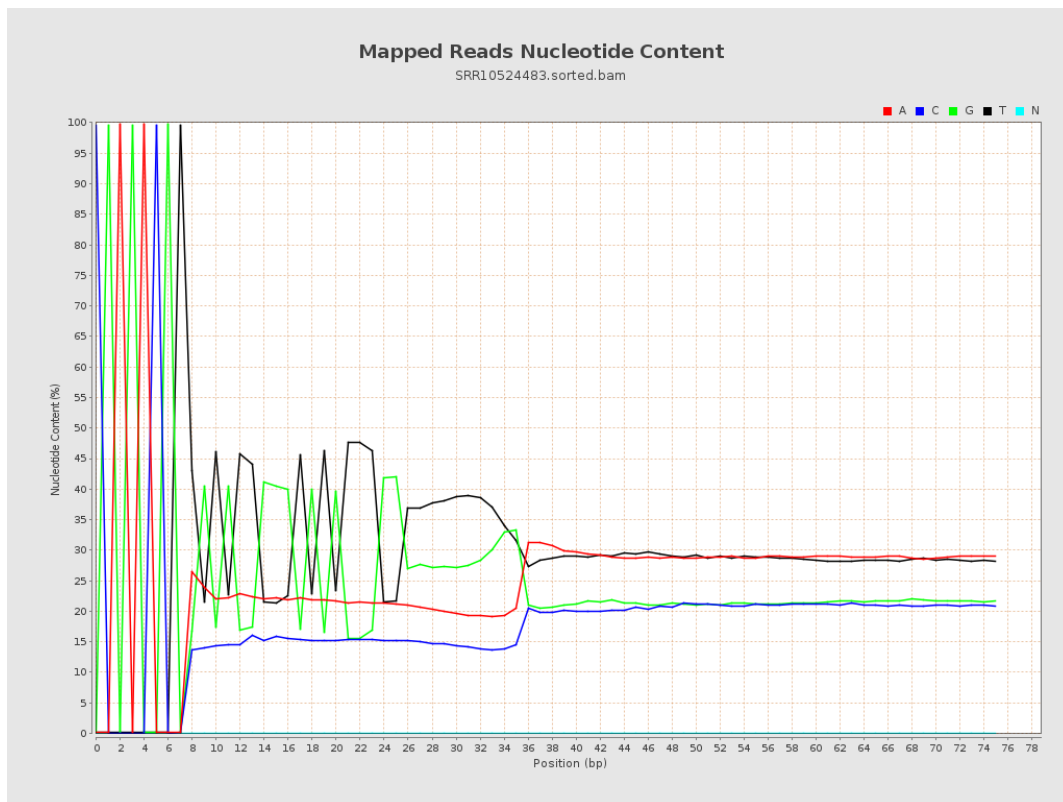
6. Results : Genome Fraction Coverage



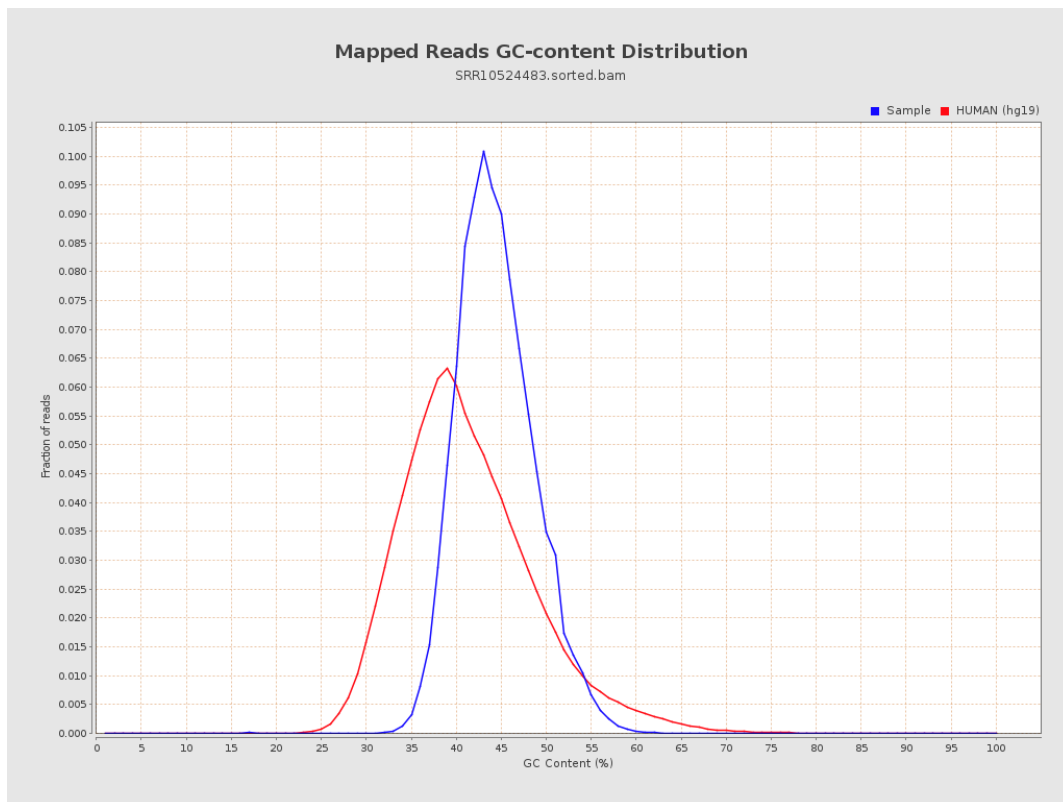
7. Results : Duplication Rate Histogram



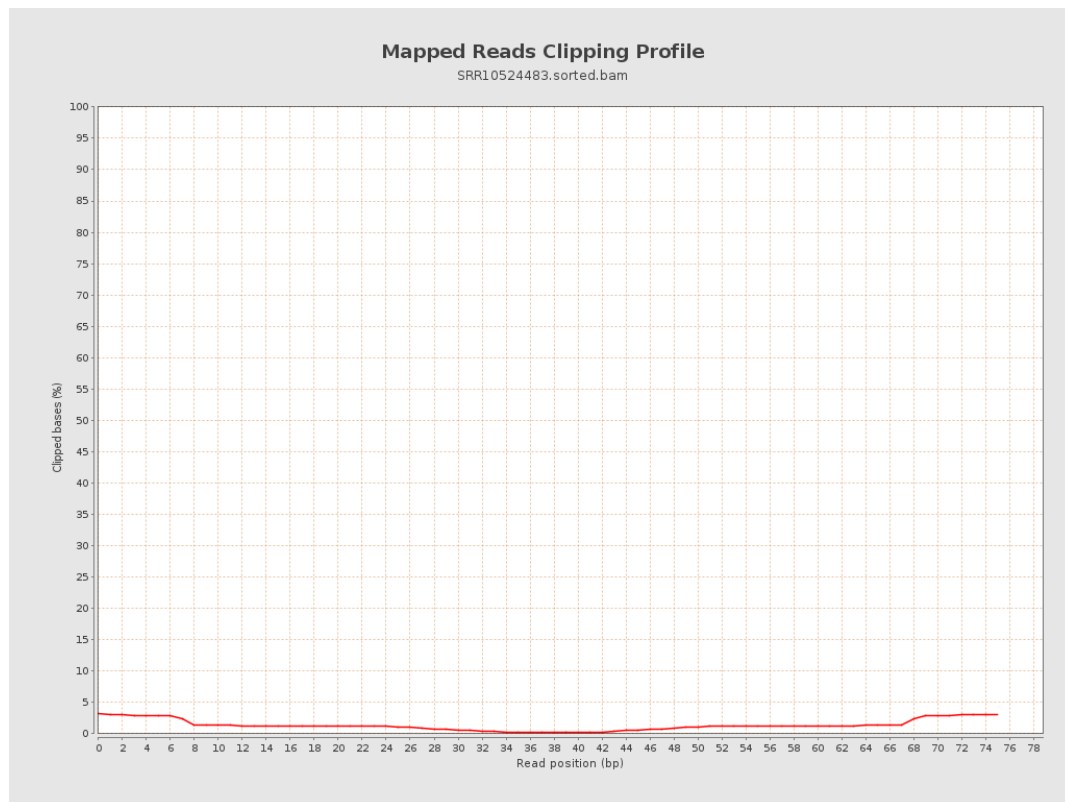
8. Results : Mapped Reads Nucleotide Content



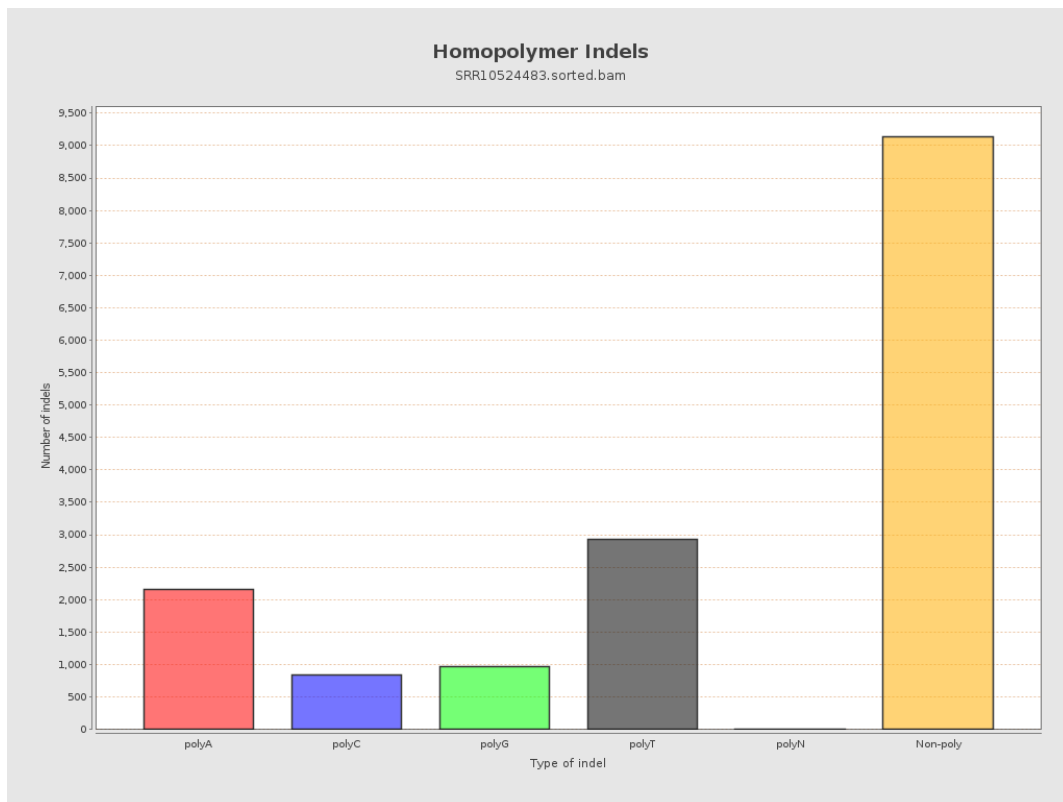
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

