

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 01:06:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9717018.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_SRR9717018 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9717018.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 01:06:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9717018.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,085,930
Mapped reads	1,026,225 / 94.5%
Unmapped reads	59,705 / 5.5%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	23,747 / 2.19%
Read min/max/mean length	30 / 101 / 101.8
Duplicated reads (estimated)	33,118 / 3.05%
Duplication rate	2.44%
Clipped reads	1,047,938 / 96.5%

2.2. ACGT Content

Number/percentage of A's	20,042,858 / 25.17%
Number/percentage of C's	16,778,557 / 21.07%
Number/percentage of T's	23,405,230 / 29.39%
Number/percentage of G's	19,408,496 / 24.37%
Number/percentage of N's	3,044 / 0%
GC Percentage	45.44%

2.3. Coverage

Mean	0.0257

Standard Deviation	0.2234
--------------------	--------

2.4. Mapping Quality

Mean Mapping Quality	46.66
----------------------	-------

2.5. Mismatches and indels

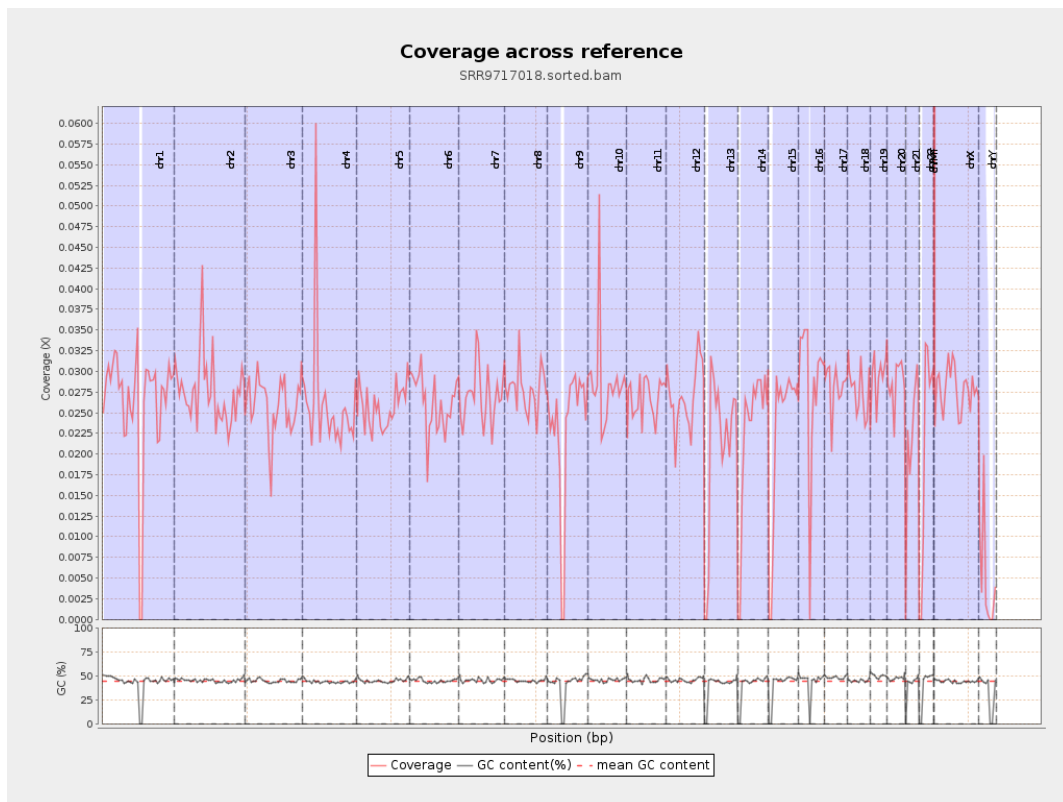
General error rate	0.68%
Mismatches	522,193
Insertions	7,182
Mapped reads with at least one insertion	0.69%
Deletions	15,675
Mapped reads with at least one deletion	1.5%
Homopolymer indels	38.55%

2.6. Chromosome stats

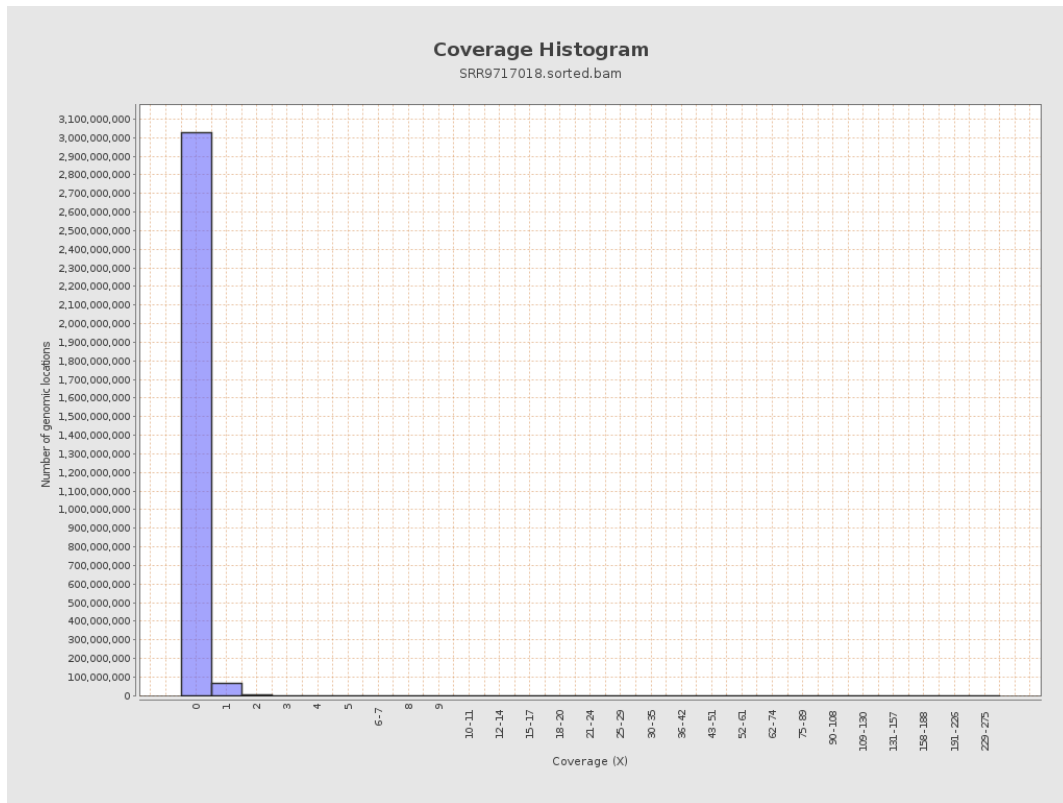
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	6555176	0.0263	0.2866
chr2	243199373	6698909	0.0275	0.256
chr3	198022430	5138140	0.0259	0.1757
chr4	191154276	4986234	0.0261	0.2399
chr5	180915260	4680222	0.0259	0.1763
chr6	171115067	4485877	0.0262	0.1812
chr7	159138663	4288311	0.0269	0.2619

chr8	146364022	4063858	0.0278	0.2351
chr9	141213431	3242339	0.023	0.1986
chr10	135534747	3891461	0.0287	0.3078
chr11	135006516	3618236	0.0268	0.2307
chr12	133851895	3599534	0.0269	0.1812
chr13	115169878	2400311	0.0208	0.1577
chr14	107349540	2422396	0.0226	0.177
chr15	102531392	2310482	0.0225	0.164
chr16	90354753	2534226	0.028	0.1983
chr17	81195210	2284030	0.0281	0.2032
chr18	78077248	2148274	0.0275	0.3035
chr19	59128983	1740252	0.0294	0.2362
chr20	63025520	1795533	0.0285	0.1927
chr21	48129895	1060329	0.022	0.2111
chr22	51304566	1102379	0.0215	0.1637
chrMT	16571	19309	1.1652	1.3471
chrX	155270560	4317922	0.0278	0.1951
chrY	59373566	287293	0.0048	0.2063

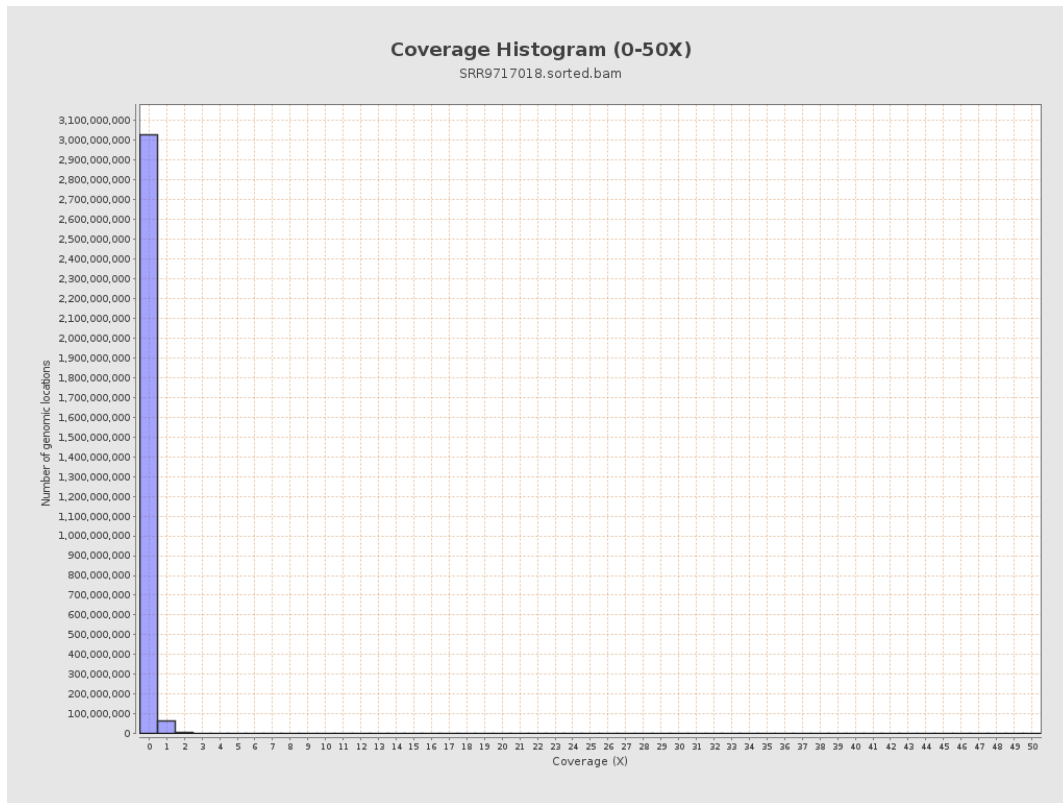
3. Results : Coverage across reference



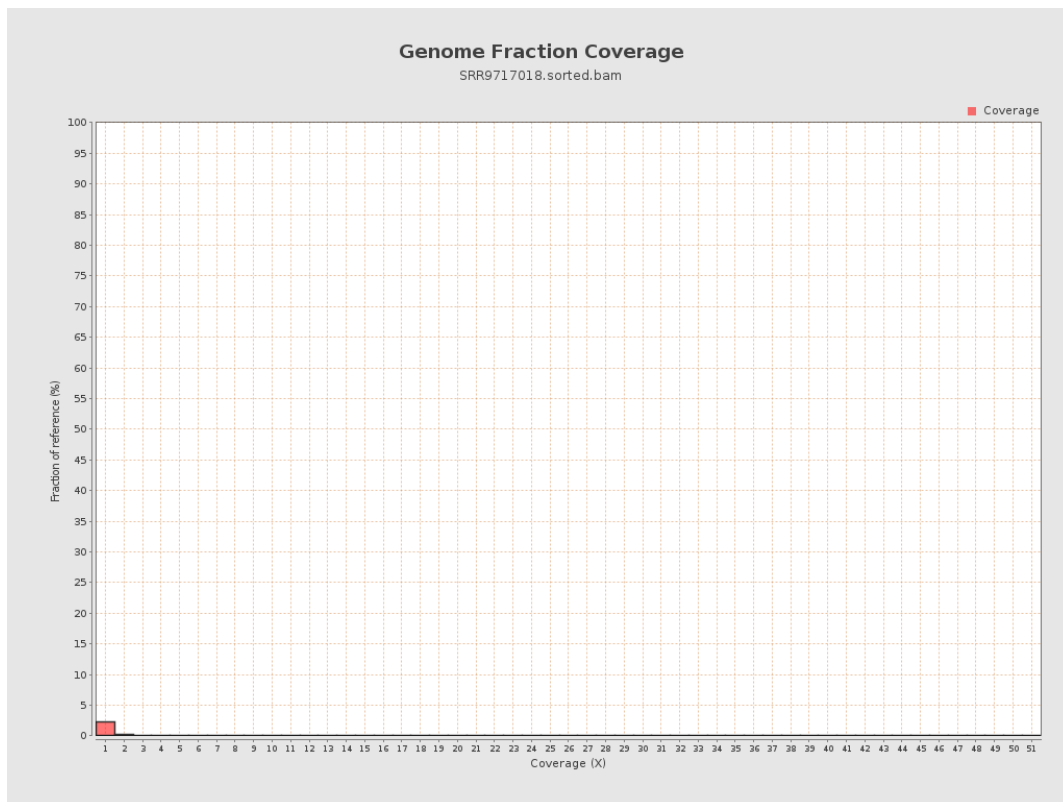
4. Results : Coverage Histogram



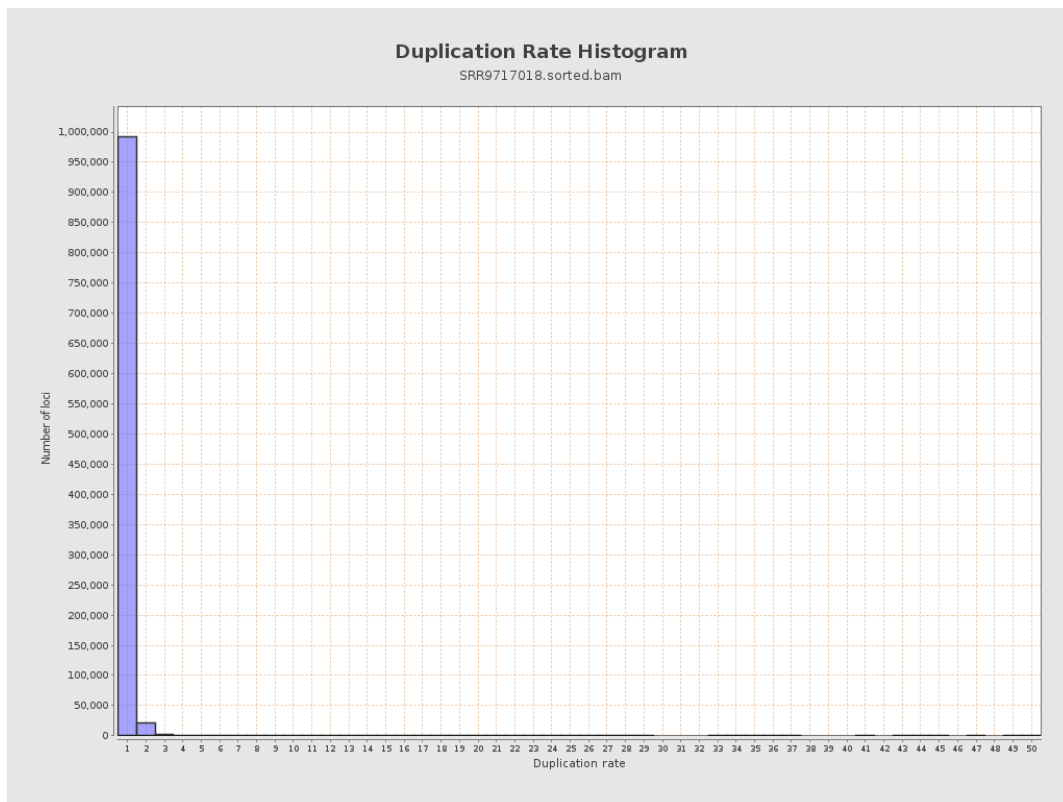
5. Results : Coverage Histogram (0-50X)



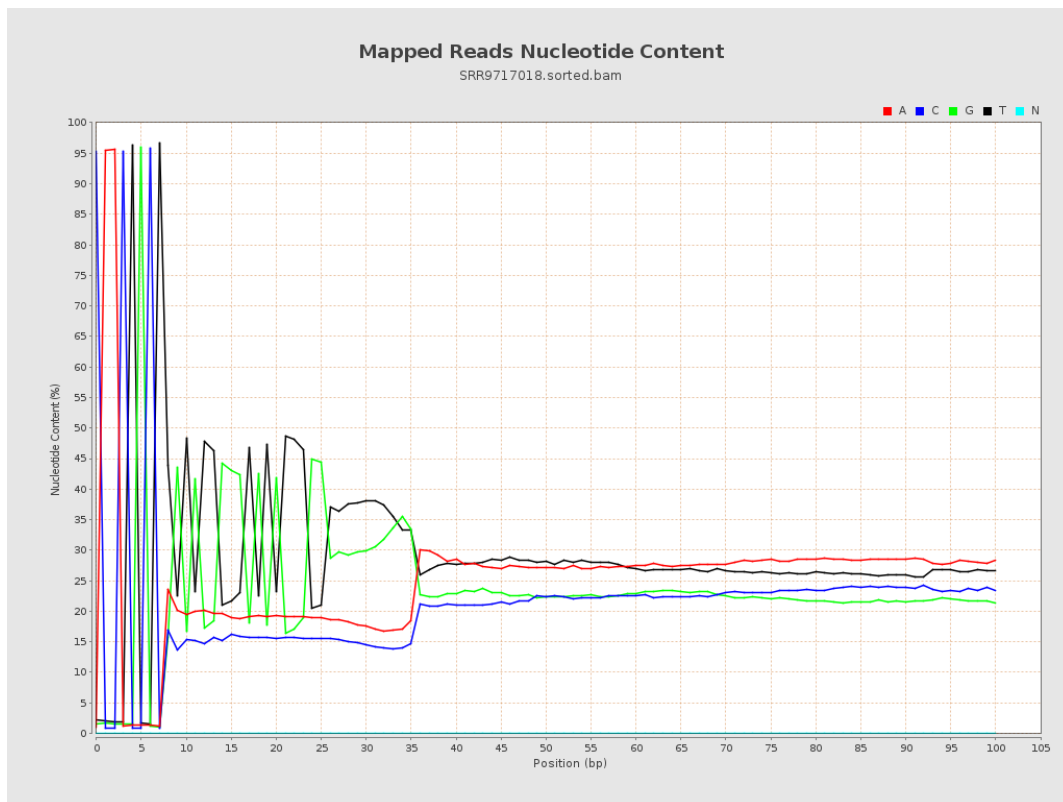
6. Results : Genome Fraction Coverage



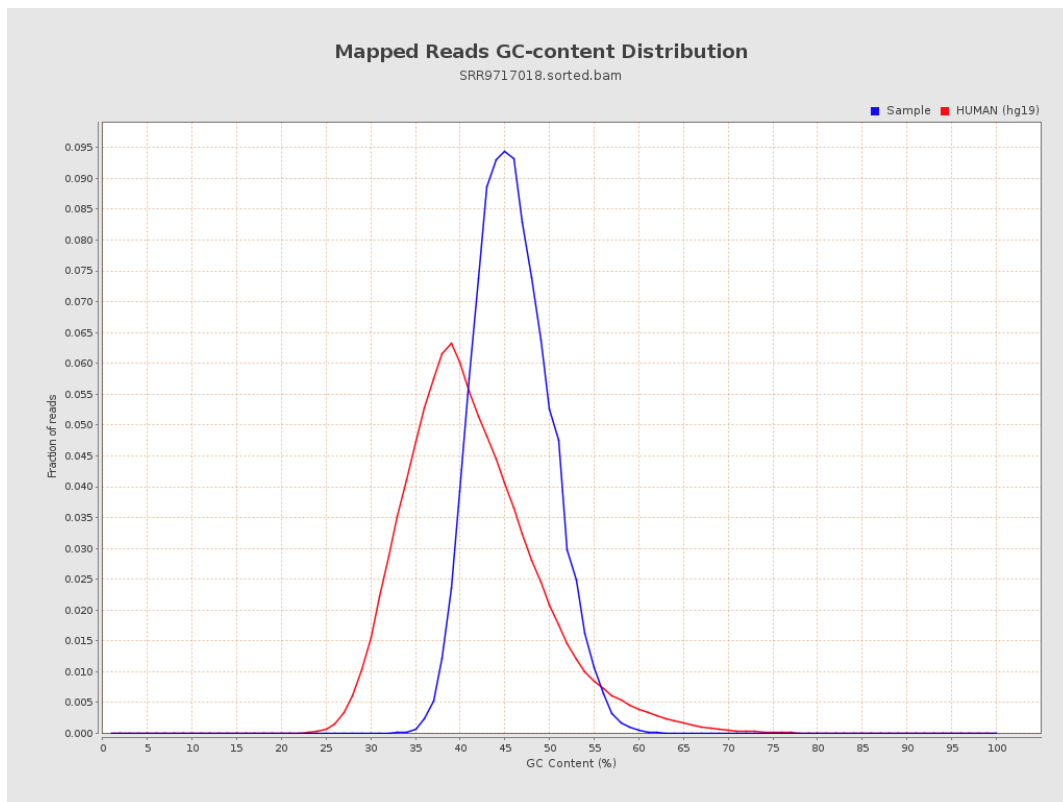
7. Results : Duplication Rate Histogram



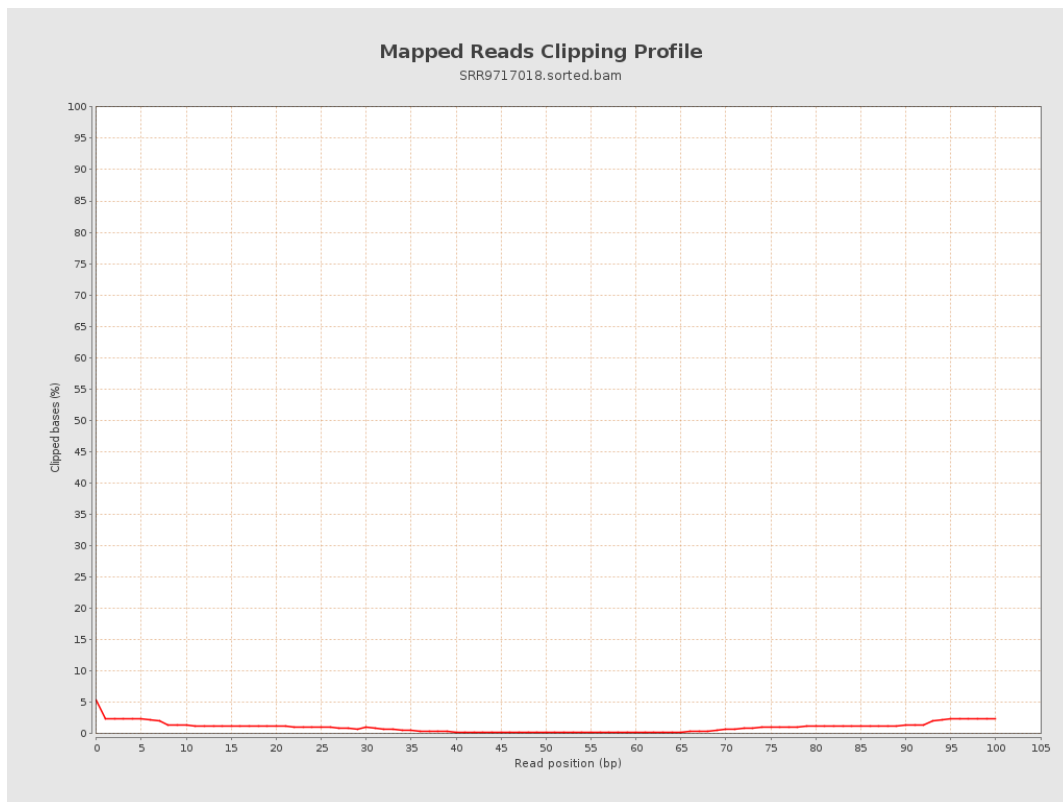
8. Results : Mapped Reads Nucleotide Content



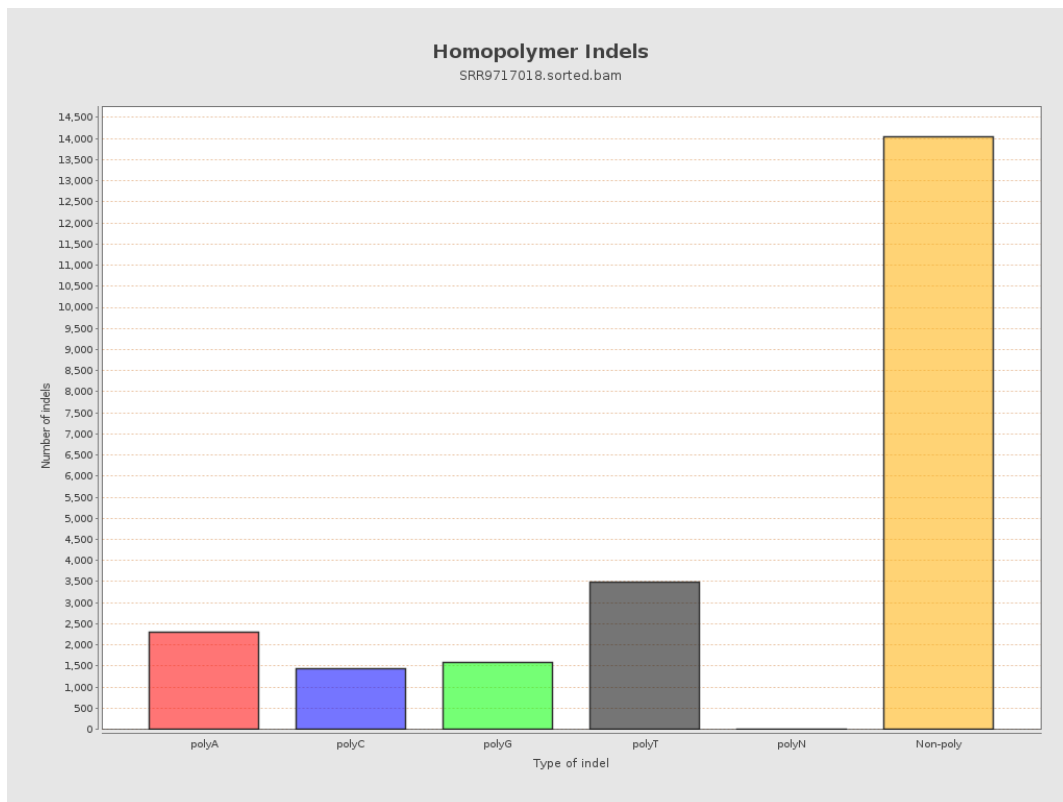
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

