

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 16:02:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1819020.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_SRR1819020 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1819020.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 16:02:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1819020.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,598,826
Mapped reads	1,575,644 / 98.55%
Unmapped reads	23,182 / 1.45%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	23,048 / 1.44%
Read min/max/mean length	30 / 101 / 101.55
Duplicated reads (estimated)	618,884 / 38.71%
Duplication rate	31.82%
Clipped reads	1,581,351 / 98.91%

2.2. ACGT Content

Number/percentage of A's	40,788,683 / 27.99%
Number/percentage of C's	30,187,629 / 20.71%
Number/percentage of T's	42,310,747 / 29.03%
Number/percentage of G's	32,446,419 / 22.26%
Number/percentage of N's	6,661 / 0%
GC Percentage	42.98%

2.3. Coverage

Mean	0.0471

Standard Deviation	0.6151
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2.4. Mapping Quality

Mean Mapping Quality	49.16
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2.5. Mismatches and indels

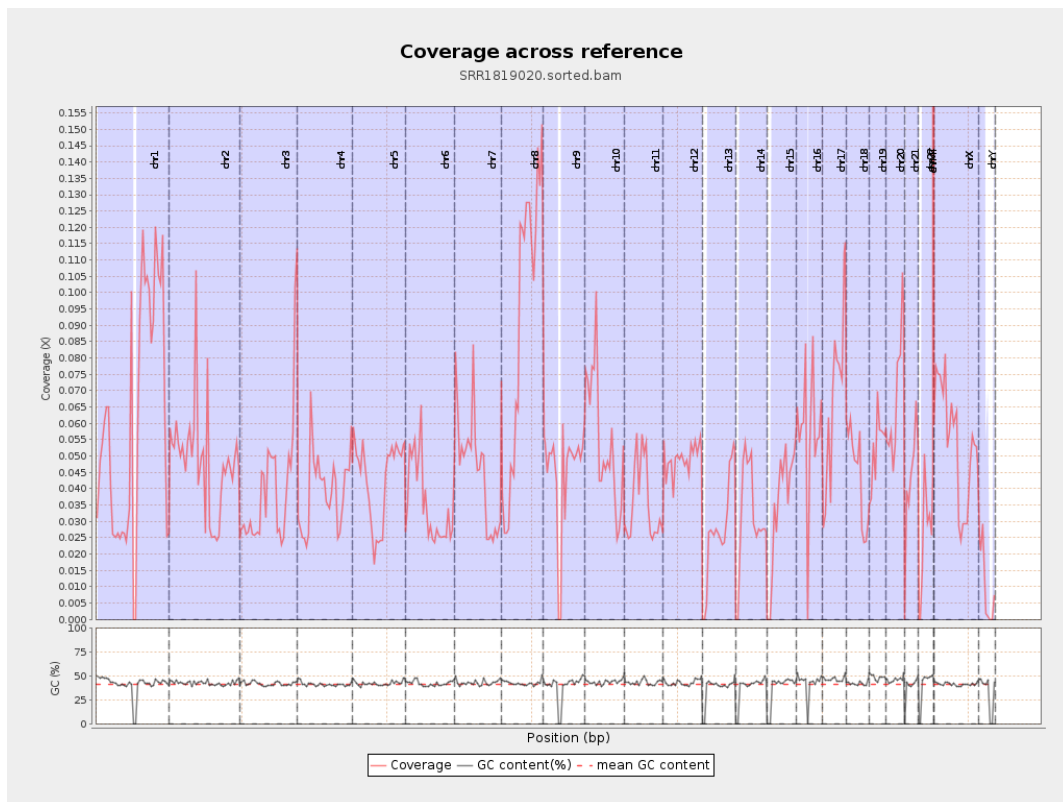
General error rate	0.67%
Mismatches	917,653
Insertions	23,359
Mapped reads with at least one insertion	1.44%
Deletions	46,868
Mapped reads with at least one deletion	2.9%
Homopolymer indels	41.01%

2.6. Chromosome stats

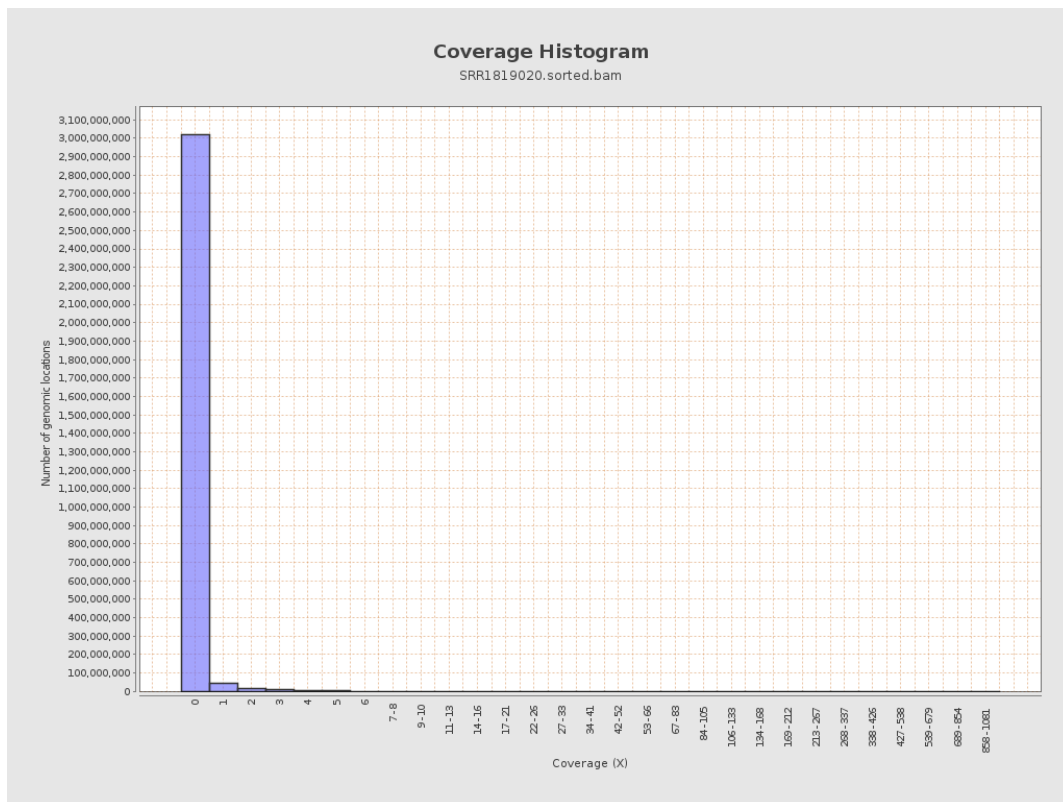
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	15265831	0.0612	1.0748
chr2	243199373	11790730	0.0485	0.9198
chr3	198022430	7718048	0.039	0.3354
chr4	191154276	7502500	0.0392	0.4063
chr5	180915260	7735426	0.0428	0.3714
chr6	171115067	6056158	0.0354	0.3878
chr7	159138663	7239644	0.0455	0.7356

chr8	146364022	13178022	0.09	0.557
chr9	141213431	6254634	0.0443	0.5555
chr10	135534747	7339615	0.0542	0.7552
chr11	135006516	4854140	0.036	0.3759
chr12	133851895	6590145	0.0492	0.3946
chr13	115169878	3164066	0.0275	0.2821
chr14	107349540	3410025	0.0318	0.3222
chr15	102531392	3581262	0.0349	0.3277
chr16	90354753	5171245	0.0572	0.7883
chr17	81195210	5554417	0.0684	0.5191
chr18	78077248	3461259	0.0443	0.6306
chr19	59128983	3132211	0.053	0.8832
chr20	63025520	4301070	0.0682	0.4882
chr21	48129895	2095505	0.0435	0.3952
chr22	51304566	1277710	0.0249	0.3025
chrMT	16571	137316	8.2865	7.2891
chrX	155270560	8422543	0.0542	0.4529
chrY	59373566	596320	0.01	0.7386

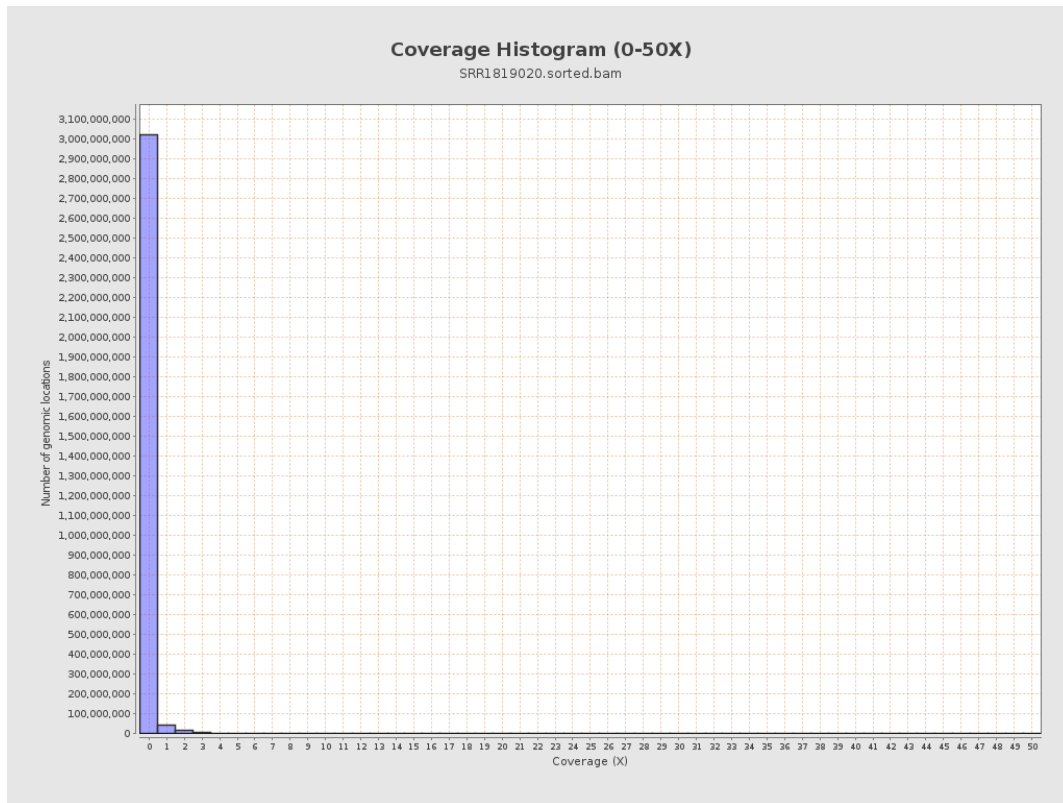
3. Results : Coverage across reference



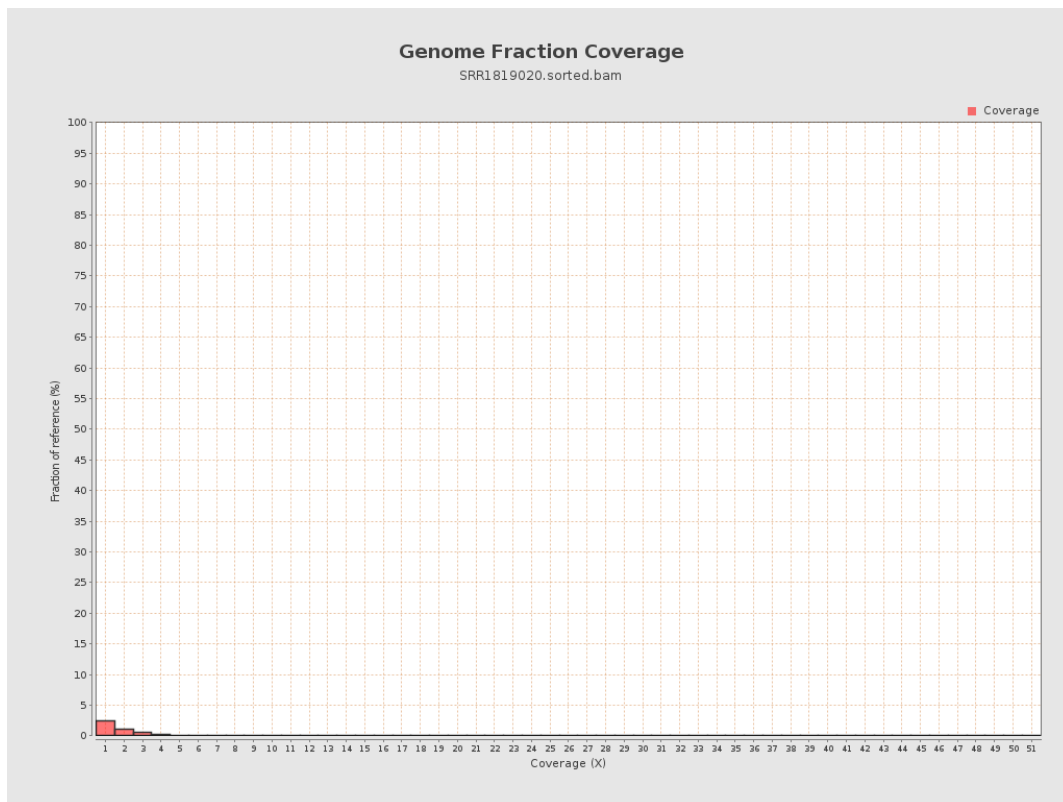
4. Results : Coverage Histogram



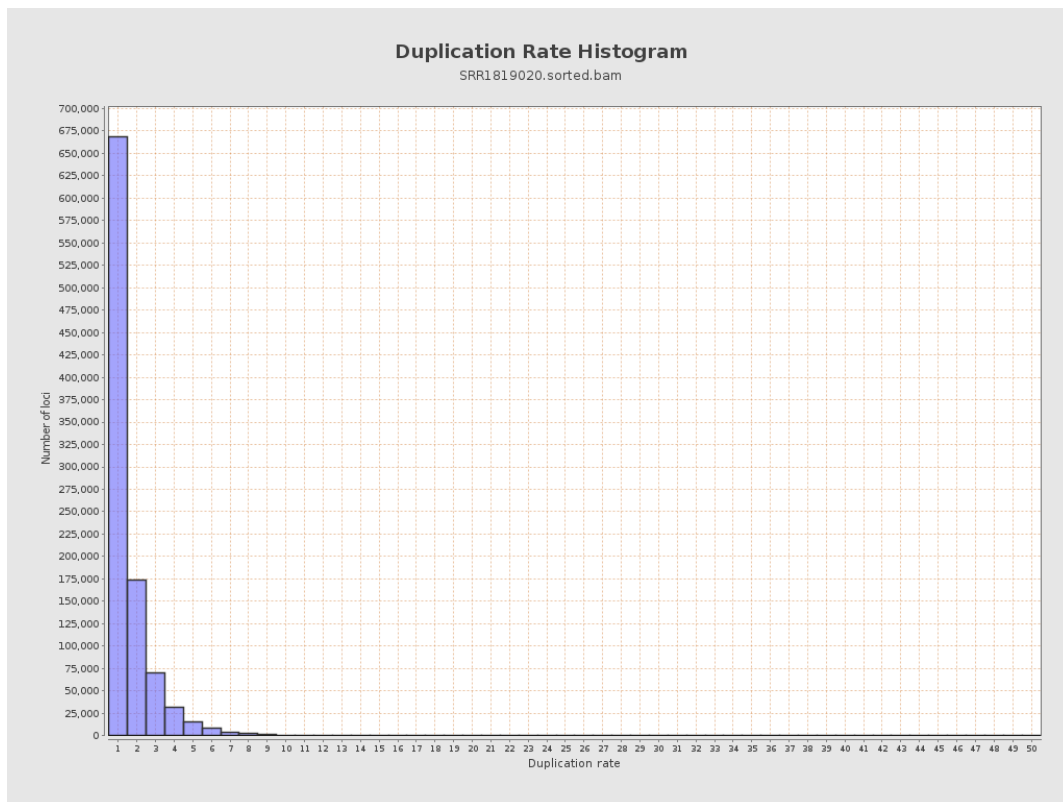
5. Results : Coverage Histogram (0-50X)



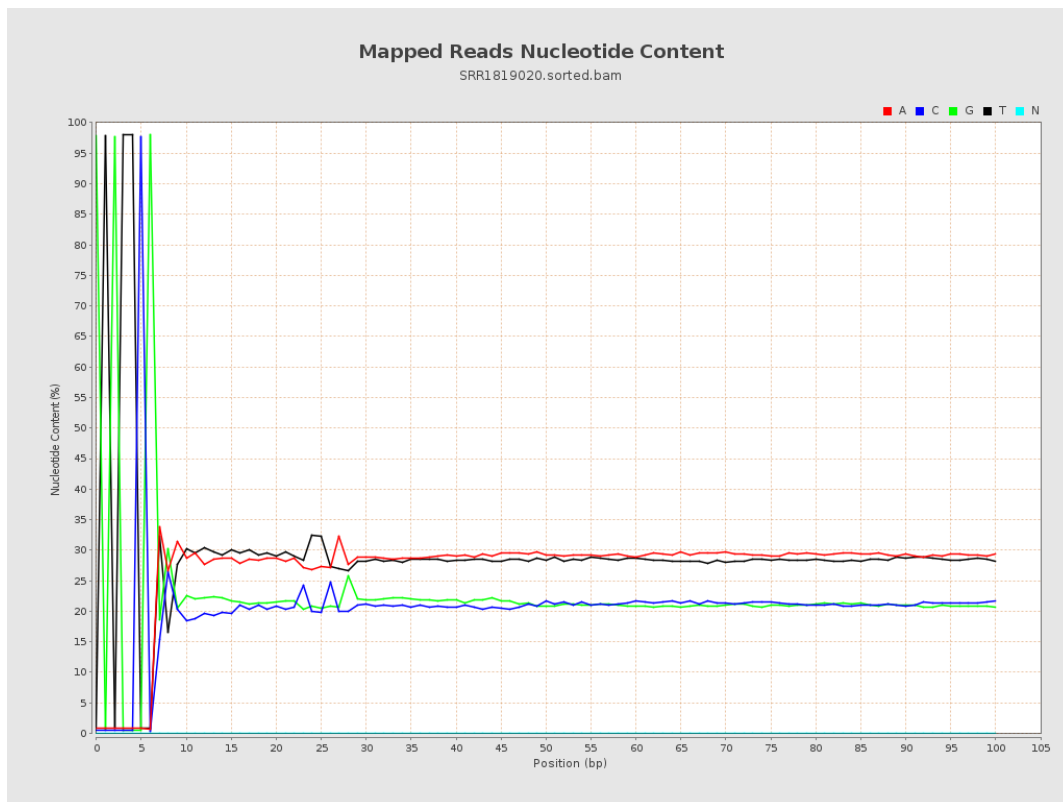
6. Results : Genome Fraction Coverage



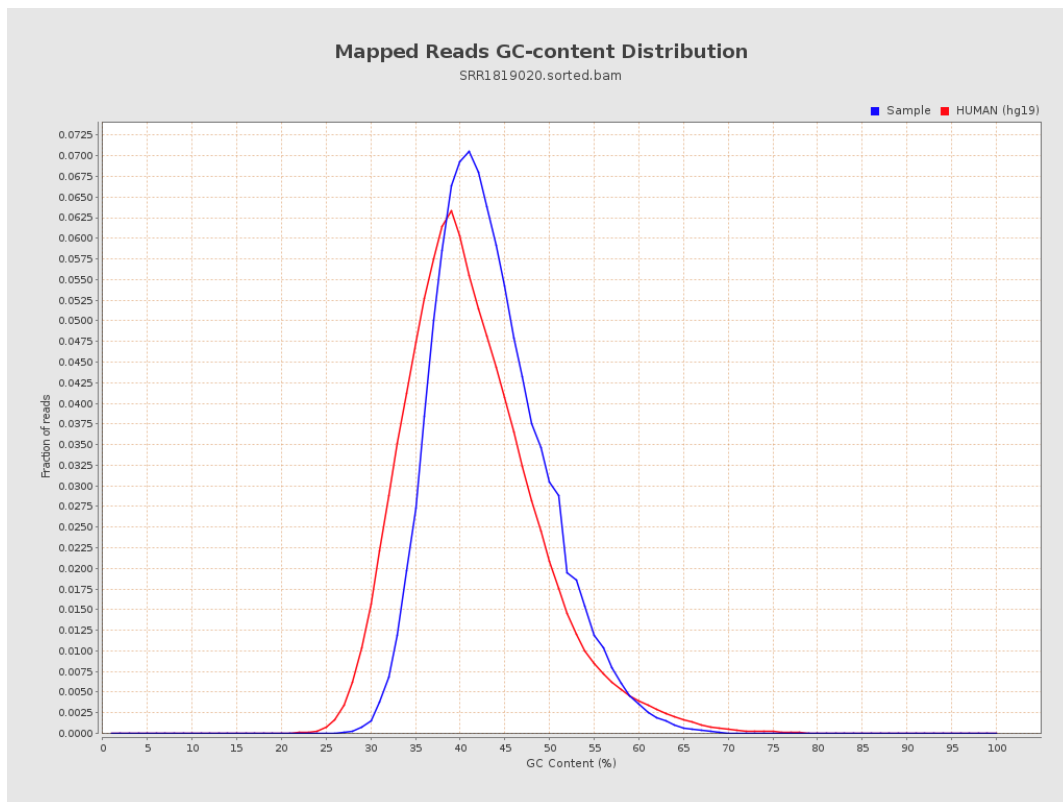
7. Results : Duplication Rate Histogram



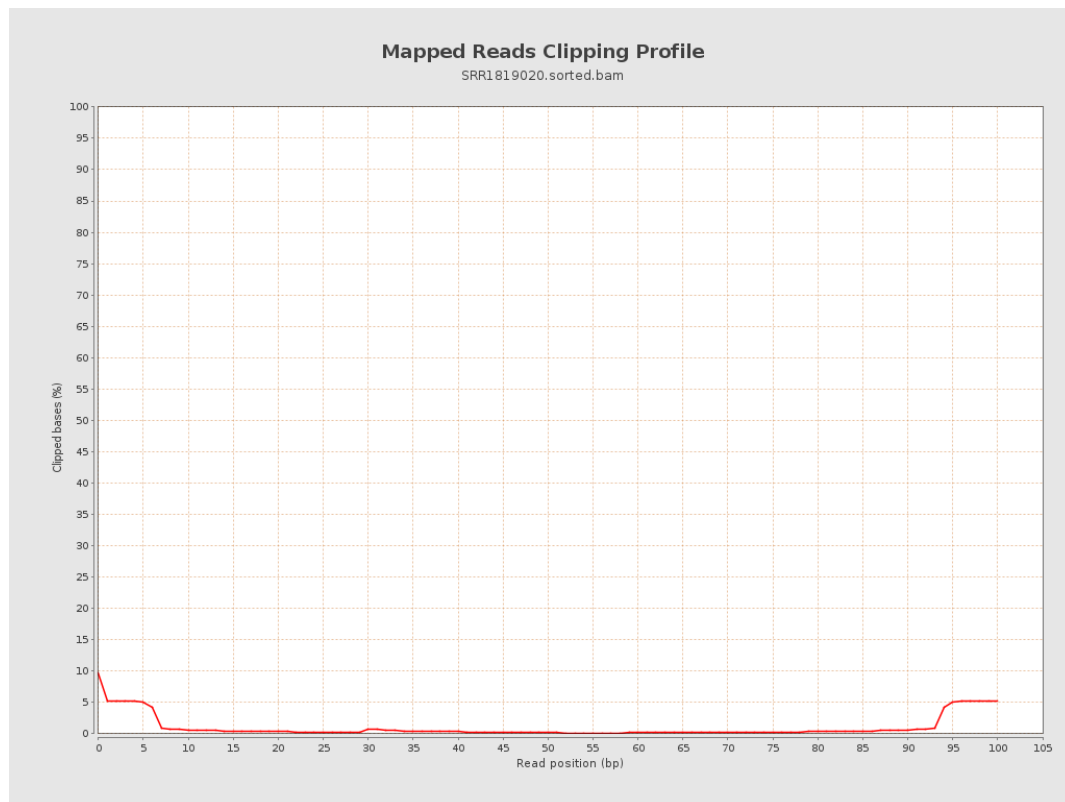
8. Results : Mapped Reads Nucleotide Content



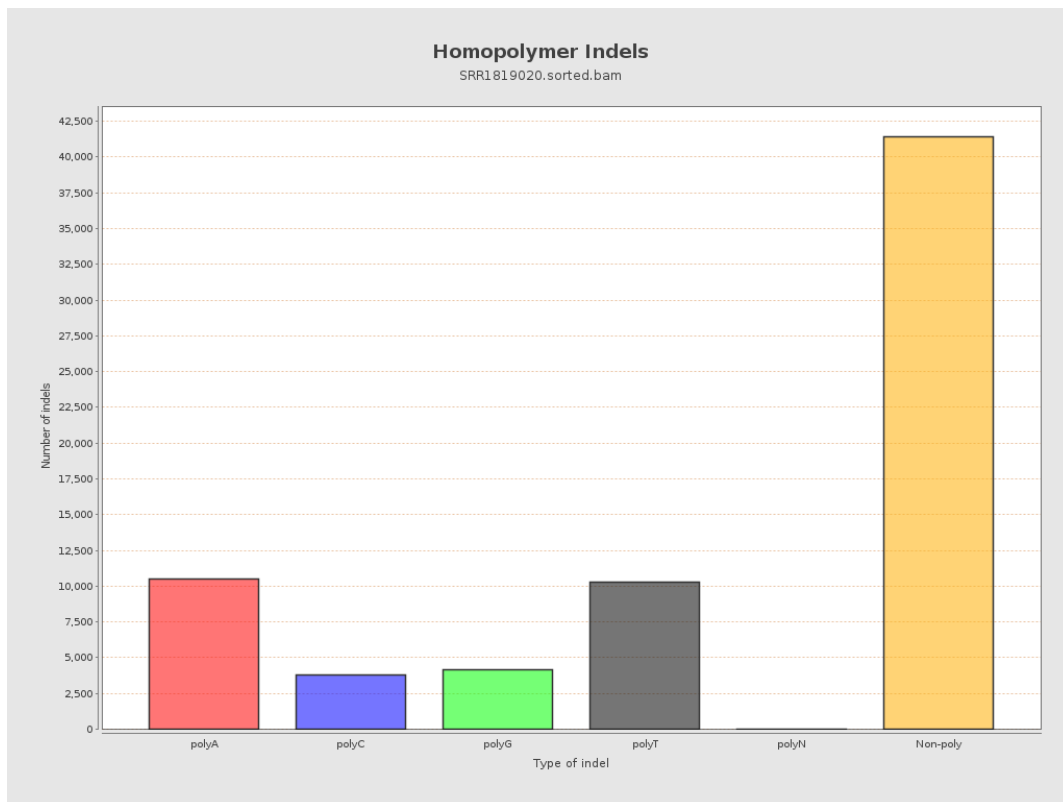
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

