

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 05:36:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818754.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_SRR1818754 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818754.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 05:36:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818754.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,206,587
Mapped reads	1,176,920 / 97.54%
Unmapped reads	29,667 / 2.46%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,095 / 0.75%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	498,305 / 41.3%
Duplication rate	35.96%
Clipped reads	1,174,161 / 97.31%

2.2. ACGT Content

Number/percentage of A's	22,852,431 / 28.55%
Number/percentage of C's	16,390,615 / 20.48%
Number/percentage of T's	22,535,534 / 28.16%
Number/percentage of G's	18,247,330 / 22.8%
Number/percentage of N's	4,454 / 0.01%
GC Percentage	43.28%

2.3. Coverage

Mean	0.0259

Standard Deviation	0.3432
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2.4. Mapping Quality

Mean Mapping Quality	48.03
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2.5. Mismatches and indels

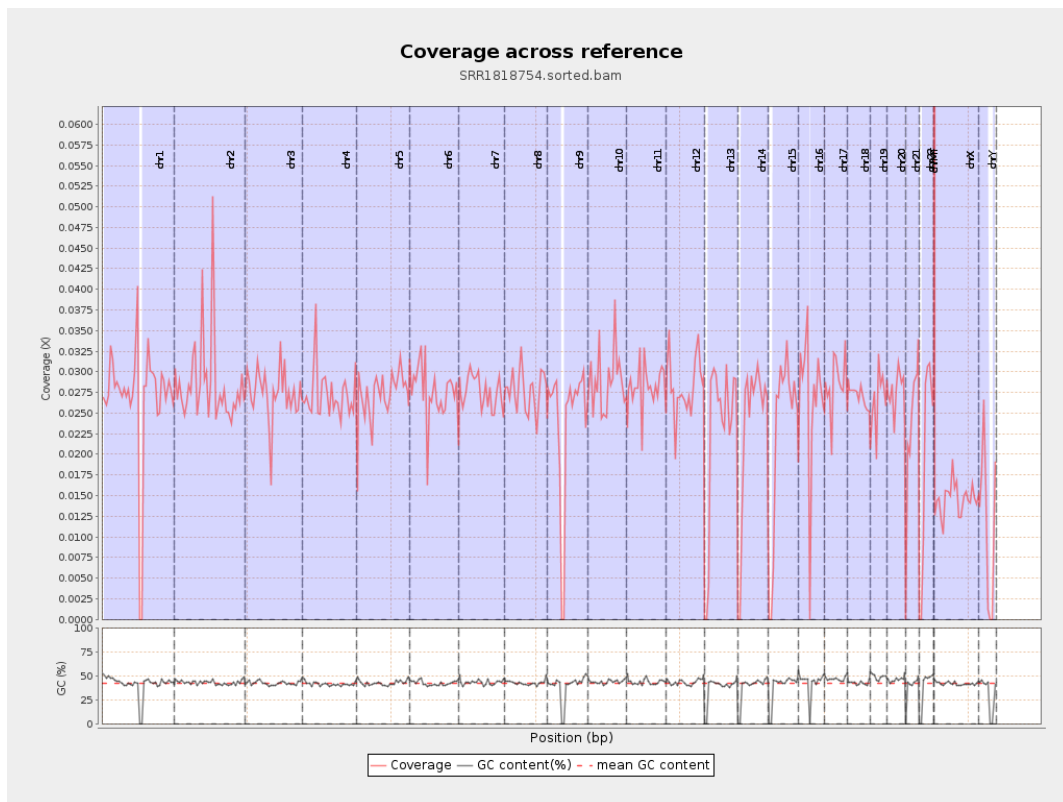
General error rate	0.51%
Mismatches	389,079
Insertions	11,093
Mapped reads with at least one insertion	0.93%
Deletions	20,608
Mapped reads with at least one deletion	1.73%
Homopolymer indels	38.39%

2.6. Chromosome stats

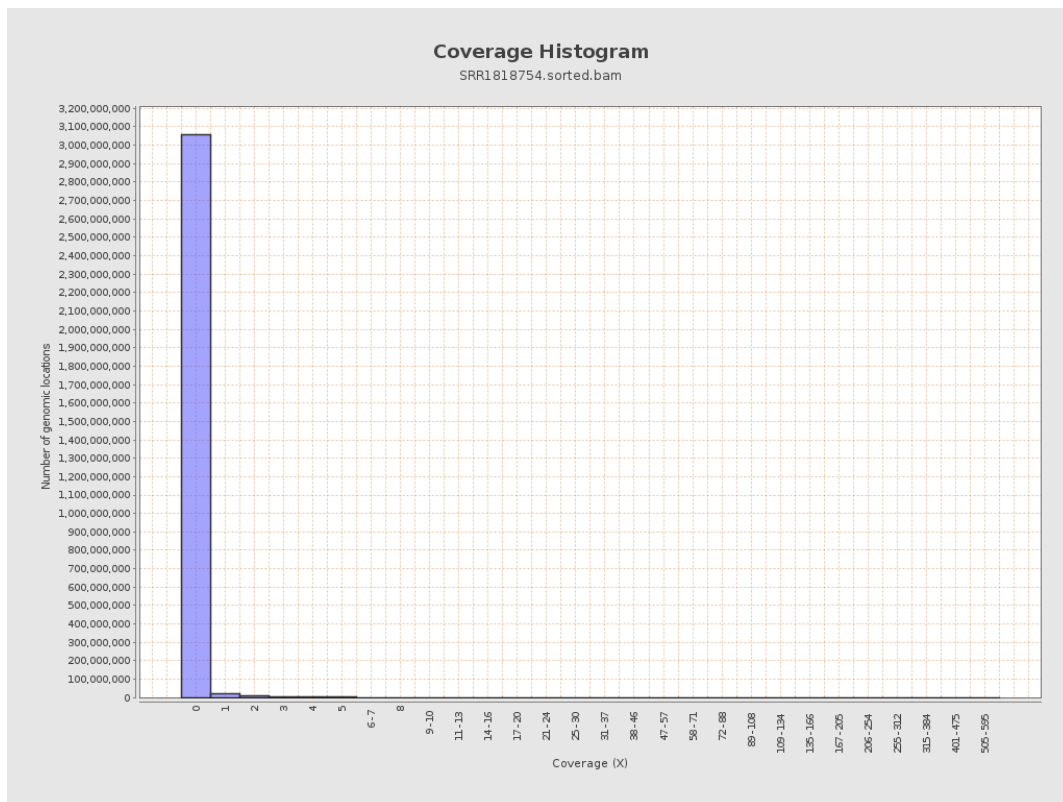
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	6703699	0.0269	0.4406
chr2	243199373	6926544	0.0285	0.5048
chr3	198022430	5433348	0.0274	0.2926
chr4	191154276	5217512	0.0273	0.3081
chr5	180915260	5003033	0.0277	0.2977
chr6	171115067	4716152	0.0276	0.3092
chr7	159138663	4397930	0.0276	0.3261

chr8	146364022	4066629	0.0278	0.3146
chr9	141213431	3379209	0.0239	0.2948
chr10	135534747	3915688	0.0289	0.3696
chr11	135006516	3829376	0.0284	0.3103
chr12	133851895	3764820	0.0281	0.3084
chr13	115169878	2597464	0.0226	0.2648
chr14	107349540	2488870	0.0232	0.2841
chr15	102531392	2338915	0.0228	0.2691
chr16	90354753	2381396	0.0264	0.3939
chr17	81195210	2310443	0.0285	0.3092
chr18	78077248	2115341	0.0271	0.3556
chr19	59128983	1574949	0.0266	0.3987
chr20	63025520	1737278	0.0276	0.3078
chr21	48129895	1134116	0.0236	0.2872
chr22	51304566	1034152	0.0202	0.2728
chrMT	16571	37490	2.2624	3.6177
chrX	155270560	2266423	0.0146	0.2211
chrY	59373566	692577	0.0117	0.4495

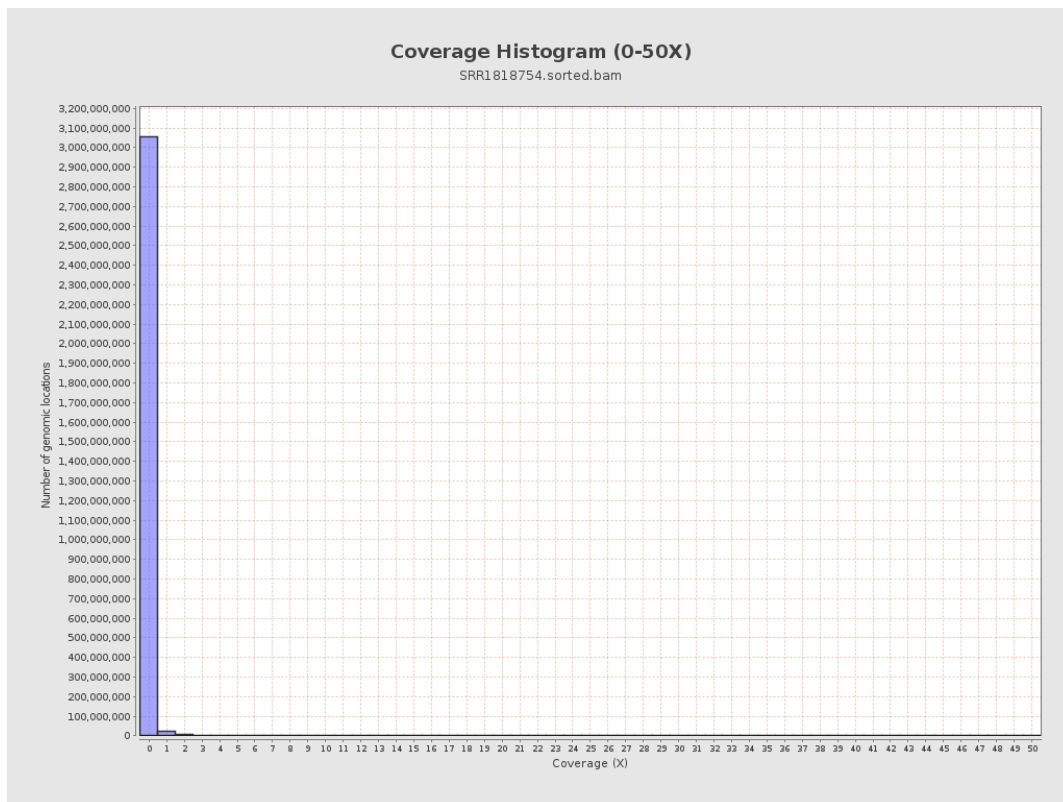
3. Results : Coverage across reference



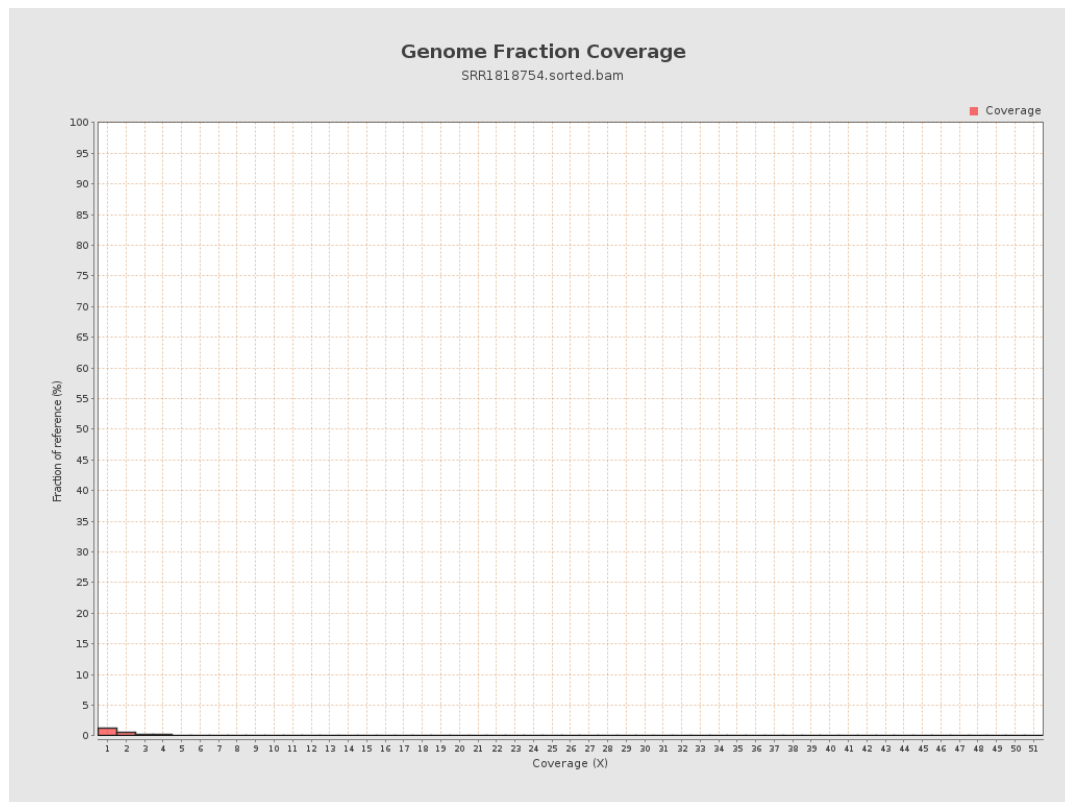
4. Results : Coverage Histogram



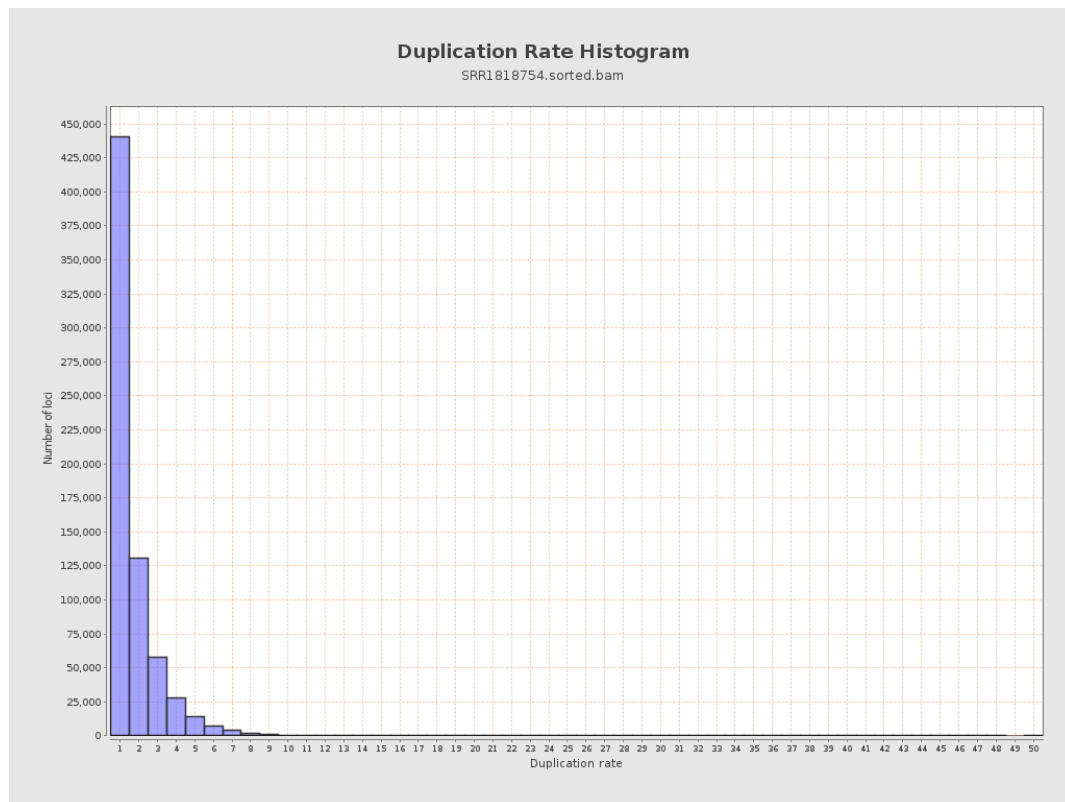
5. Results : Coverage Histogram (0-50X)



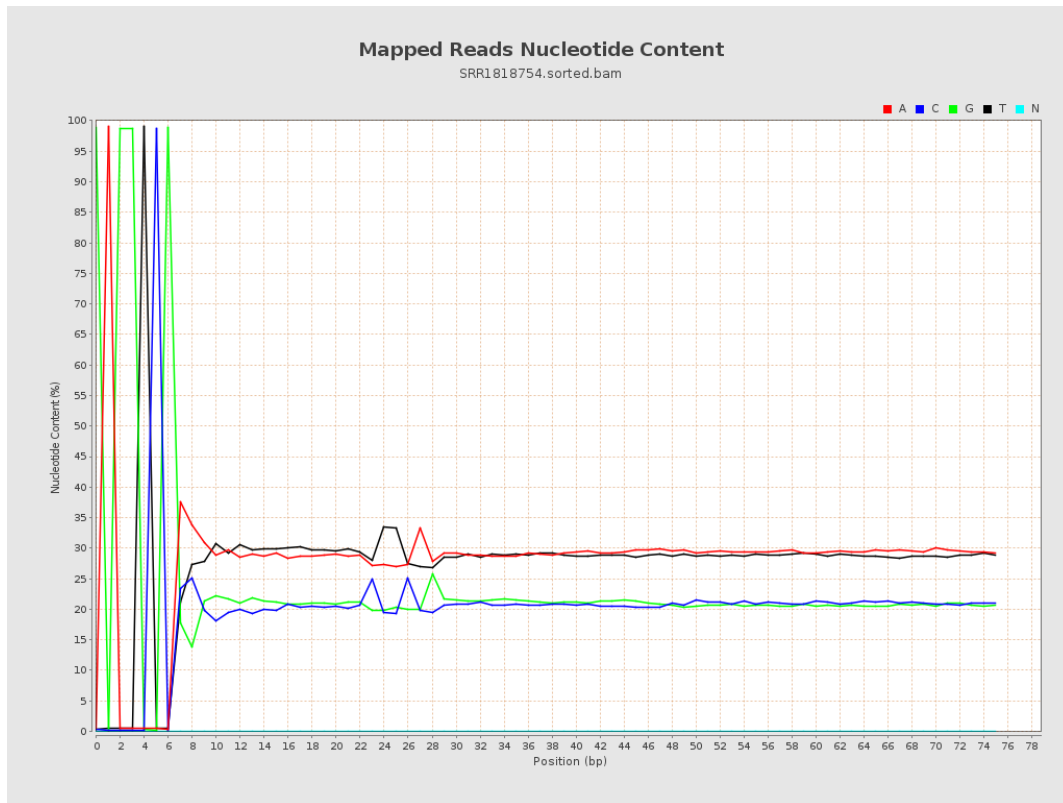
6. Results : Genome Fraction Coverage



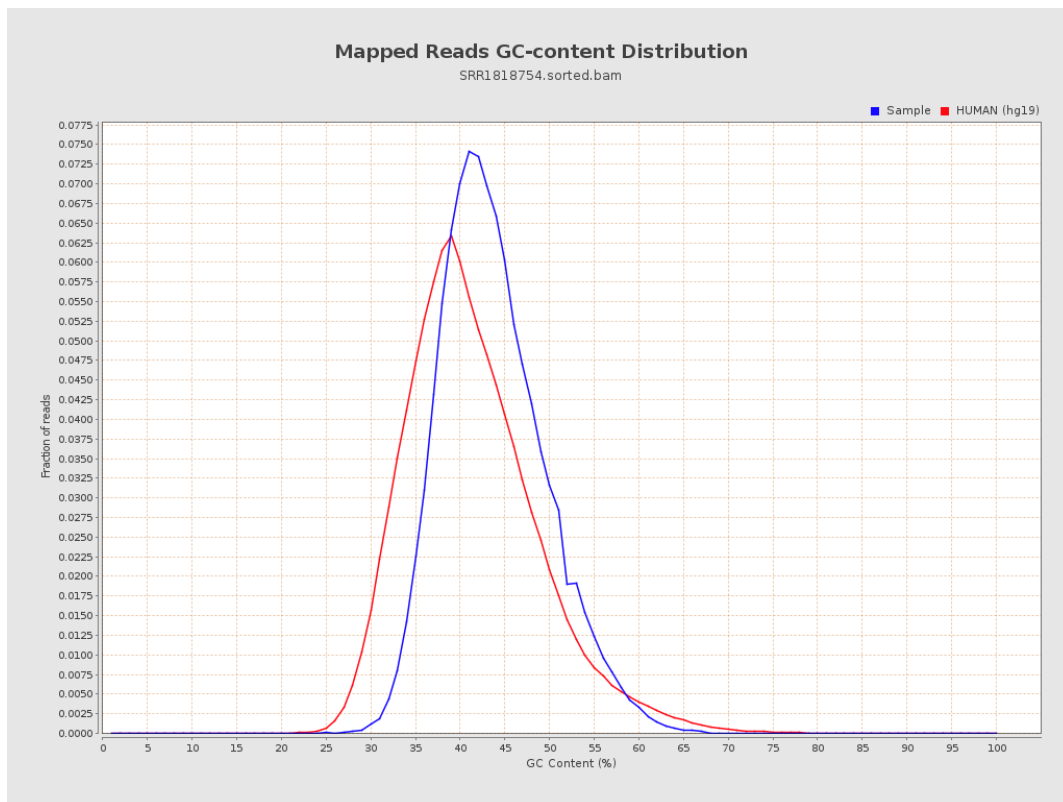
7. Results : Duplication Rate Histogram



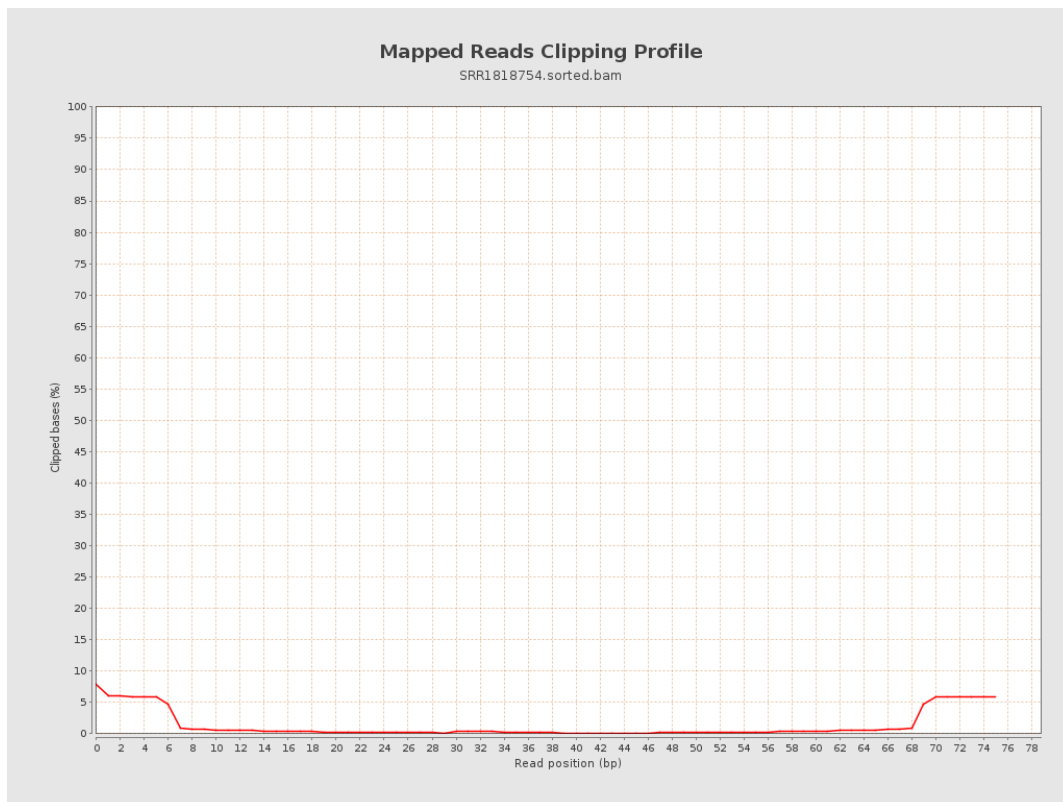
8. Results : Mapped Reads Nucleotide Content



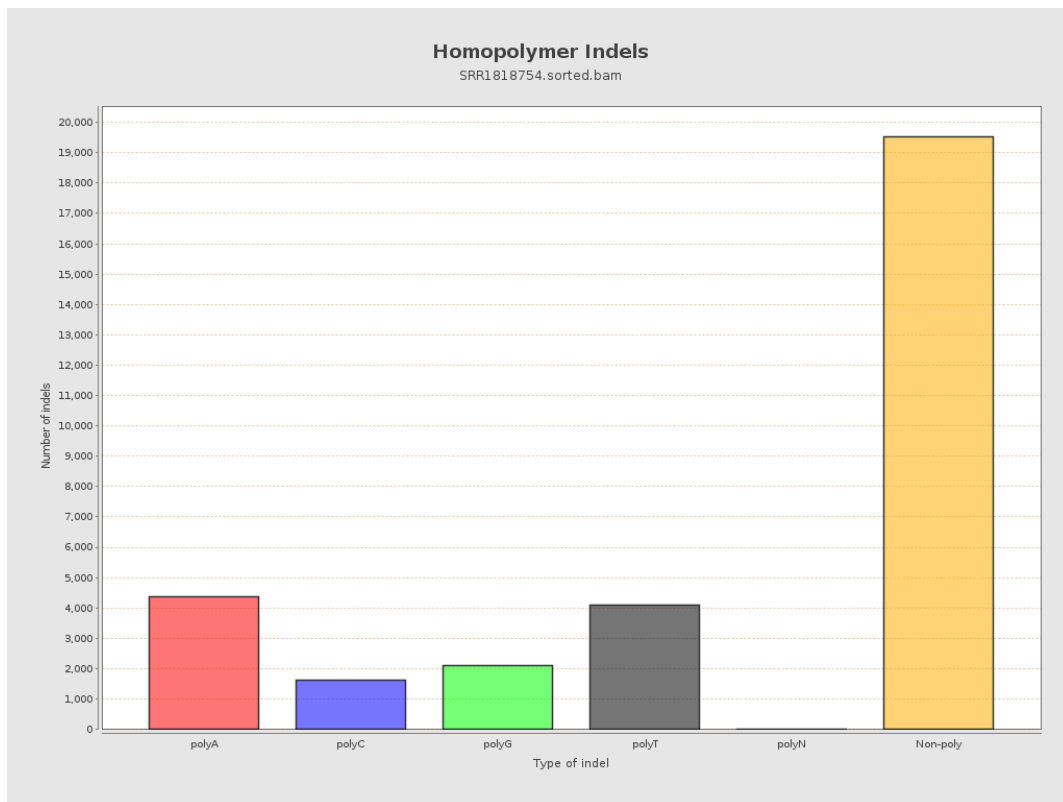
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

