

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 03:54:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818746.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_SRR1818746 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818746.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 03:54:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818746.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,097,754
Mapped reads	3,022,810 / 97.58%
Unmapped reads	74,944 / 2.42%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,827 / 0.64%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	1,544,491 / 49.86%
Duplication rate	43.65%
Clipped reads	3,011,596 / 97.22%

2.2. ACGT Content

Number/percentage of A's	57,558,107 / 27.98%
Number/percentage of C's	43,082,718 / 20.94%
Number/percentage of T's	59,892,625 / 29.11%
Number/percentage of G's	45,193,589 / 21.97%
Number/percentage of N's	12,743 / 0.01%
GC Percentage	42.91%

2.3. Coverage

Mean	0.0665

Standard Deviation	0.8099
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2.4. Mapping Quality

Mean Mapping Quality	47.53
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2.5. Mismatches and indels

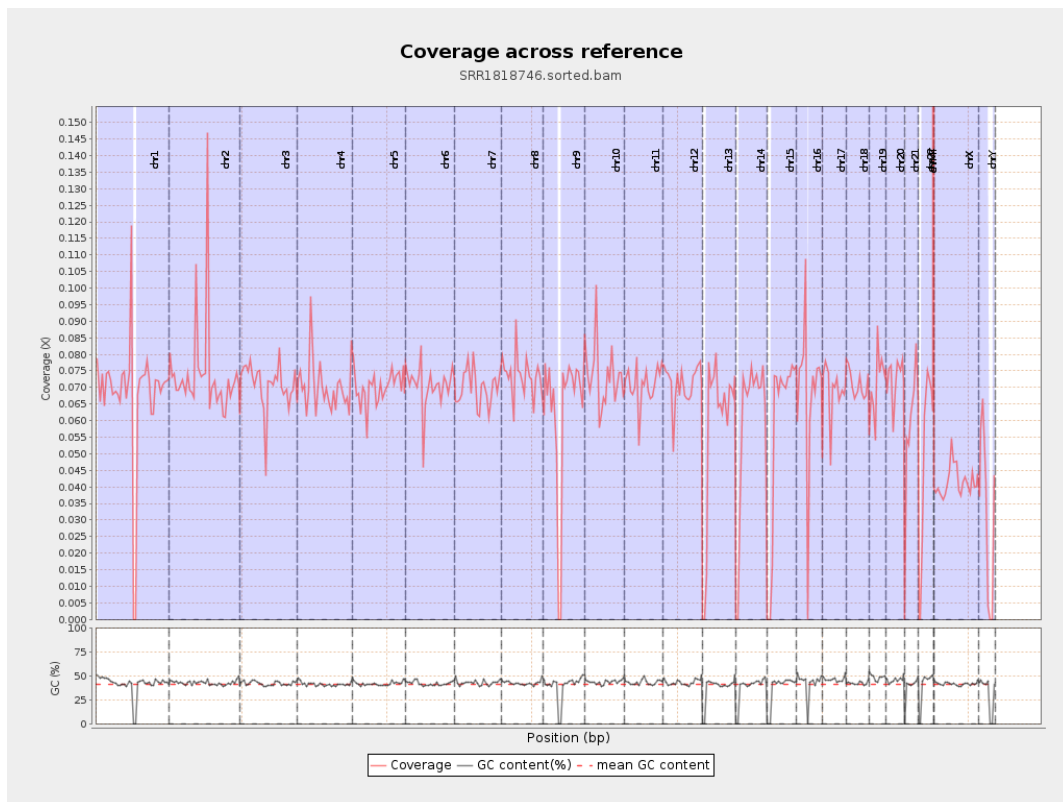
General error rate	0.54%
Mismatches	1,049,916
Insertions	24,989
Mapped reads with at least one insertion	0.81%
Deletions	51,516
Mapped reads with at least one deletion	1.69%
Homopolymer indels	39.35%

2.6. Chromosome stats

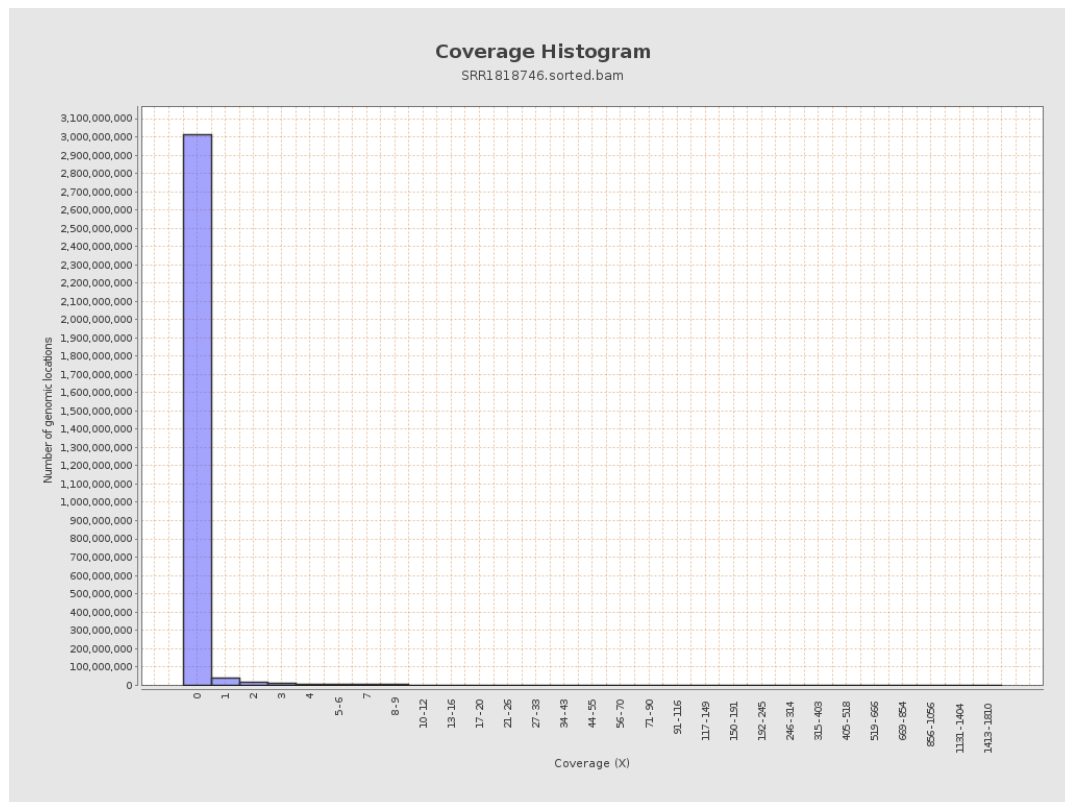
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	16931956	0.0679	1.302
chr2	243199373	17969677	0.0739	1.3135
chr3	198022430	14010293	0.0708	0.5463
chr4	191154276	13396614	0.0701	0.6267
chr5	180915260	12664370	0.07	0.5614
chr6	171115067	12098597	0.0707	0.6097
chr7	159138663	11120598	0.0699	0.6653

chr8	146364022	10752472	0.0735	0.6636
chr9	141213431	8833763	0.0626	0.6631
chr10	135534747	9885121	0.0729	0.8384
chr11	135006516	9569517	0.0709	0.6263
chr12	133851895	9471821	0.0708	0.5801
chr13	115169878	6655298	0.0578	0.5014
chr14	107349540	6372159	0.0594	0.5848
chr15	102531392	5973983	0.0583	0.5102
chr16	90354753	6254819	0.0692	0.907
chr17	81195210	5611157	0.0691	0.5783
chr18	78077248	5547625	0.0711	0.8948
chr19	59128983	4211554	0.0712	1.0173
chr20	63025520	4562049	0.0724	0.5988
chr21	48129895	2815687	0.0585	0.5593
chr22	51304566	2471984	0.0482	0.4909
chrMT	16571	352165	21.2519	16.5919
chrX	155270560	6450727	0.0415	0.4944
chrY	59373566	1842255	0.031	1.4549

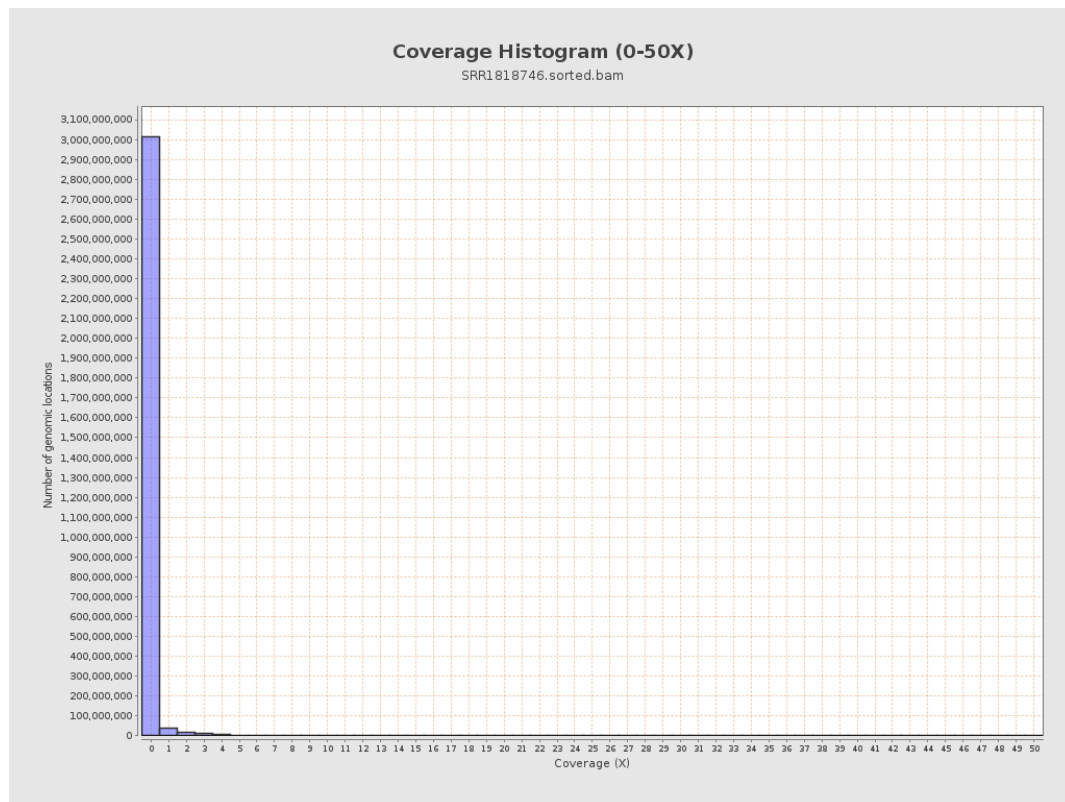
3. Results : Coverage across reference



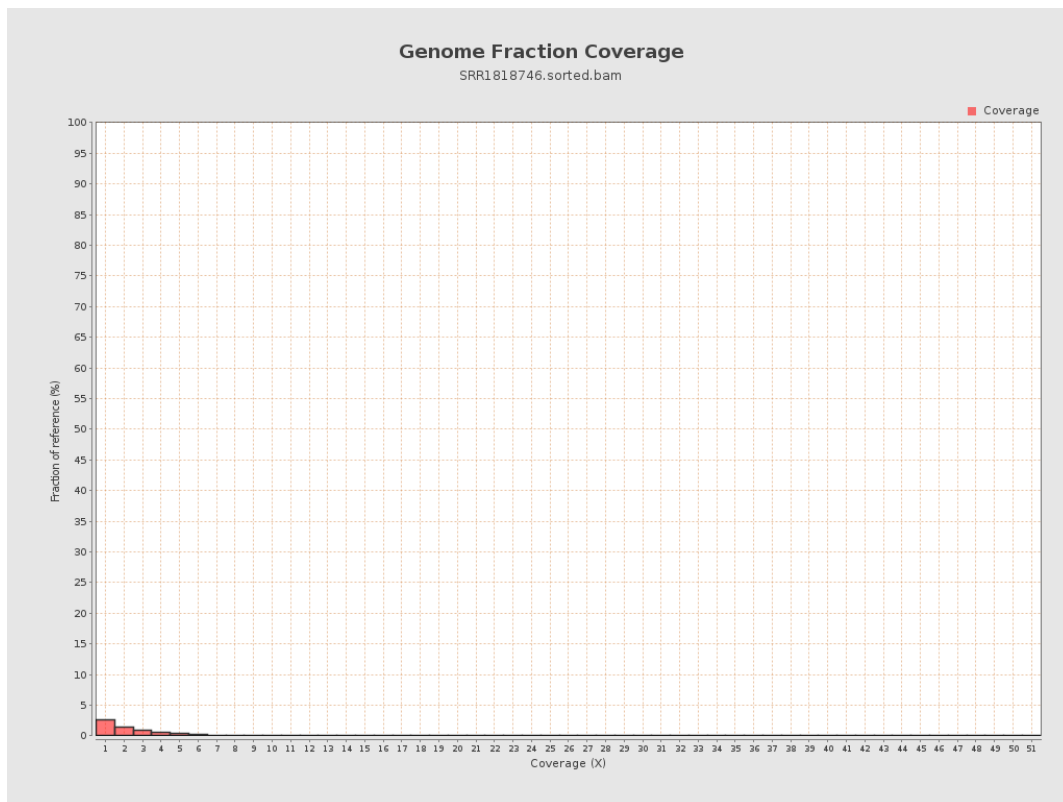
4. Results : Coverage Histogram



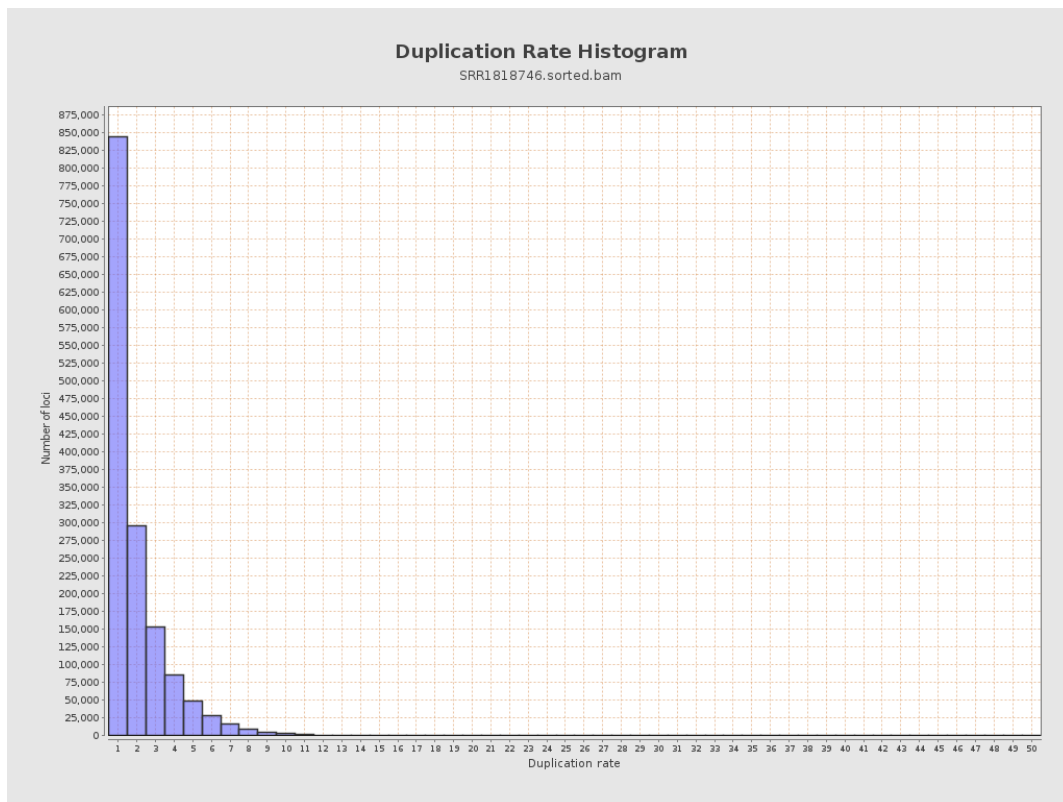
5. Results : Coverage Histogram (0-50X)



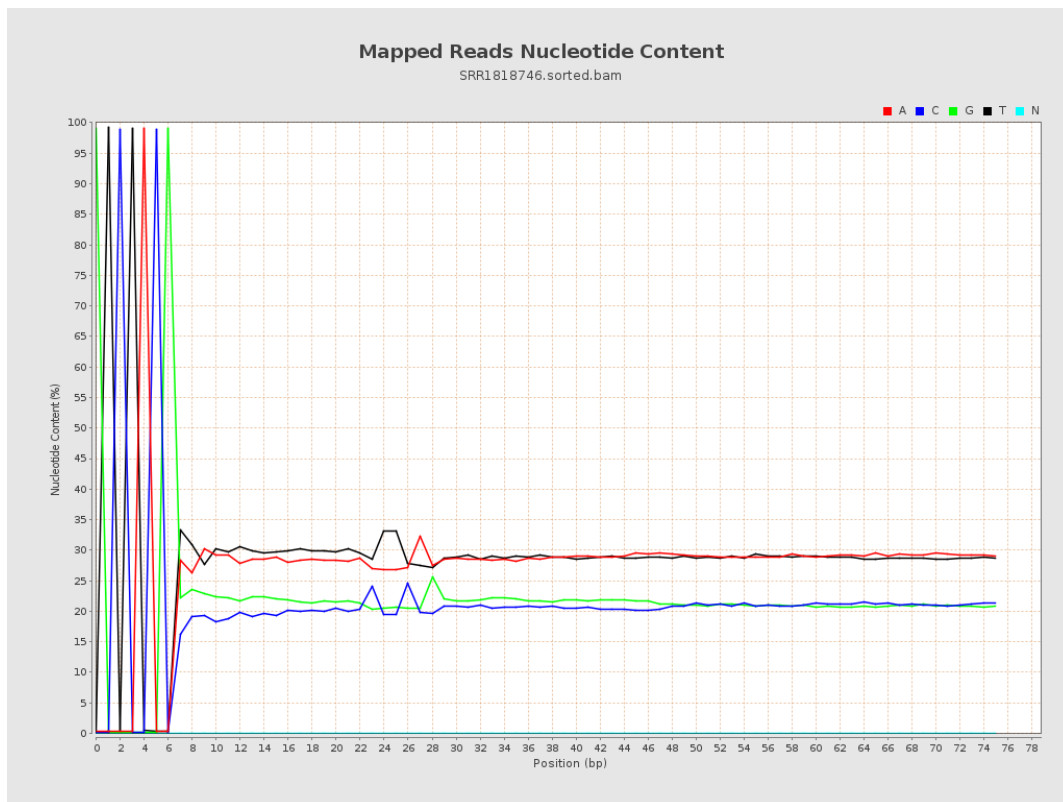
6. Results : Genome Fraction Coverage



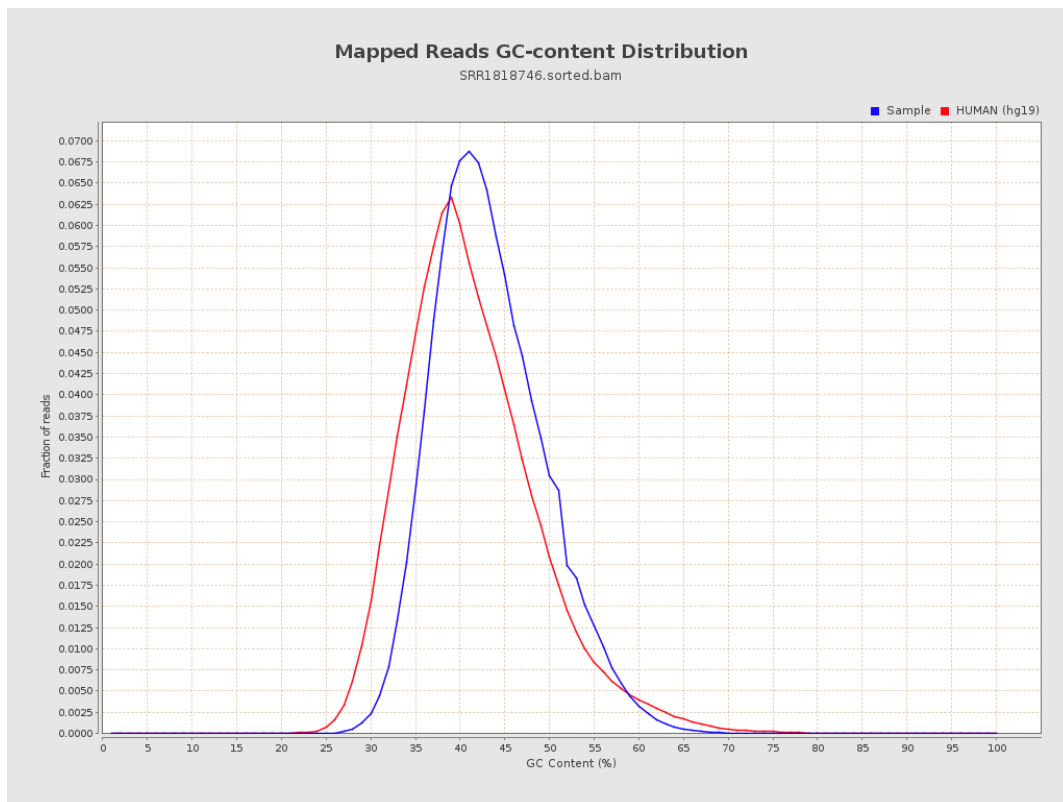
7. Results : Duplication Rate Histogram



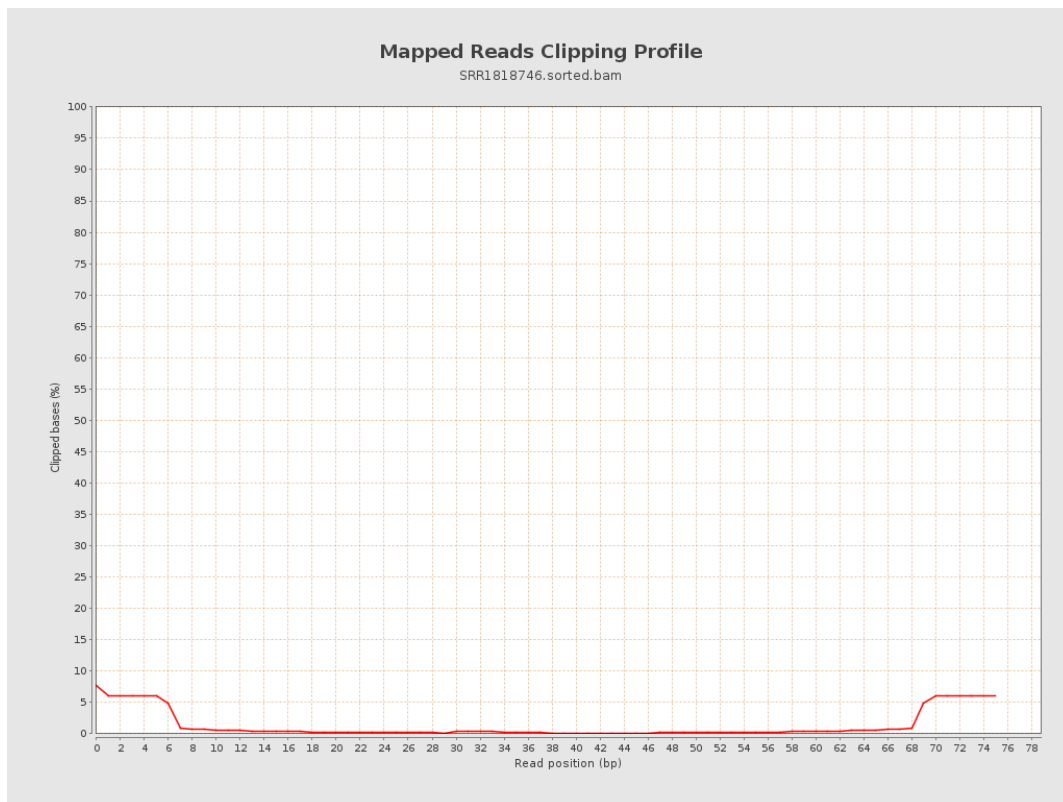
8. Results : Mapped Reads Nucleotide Content



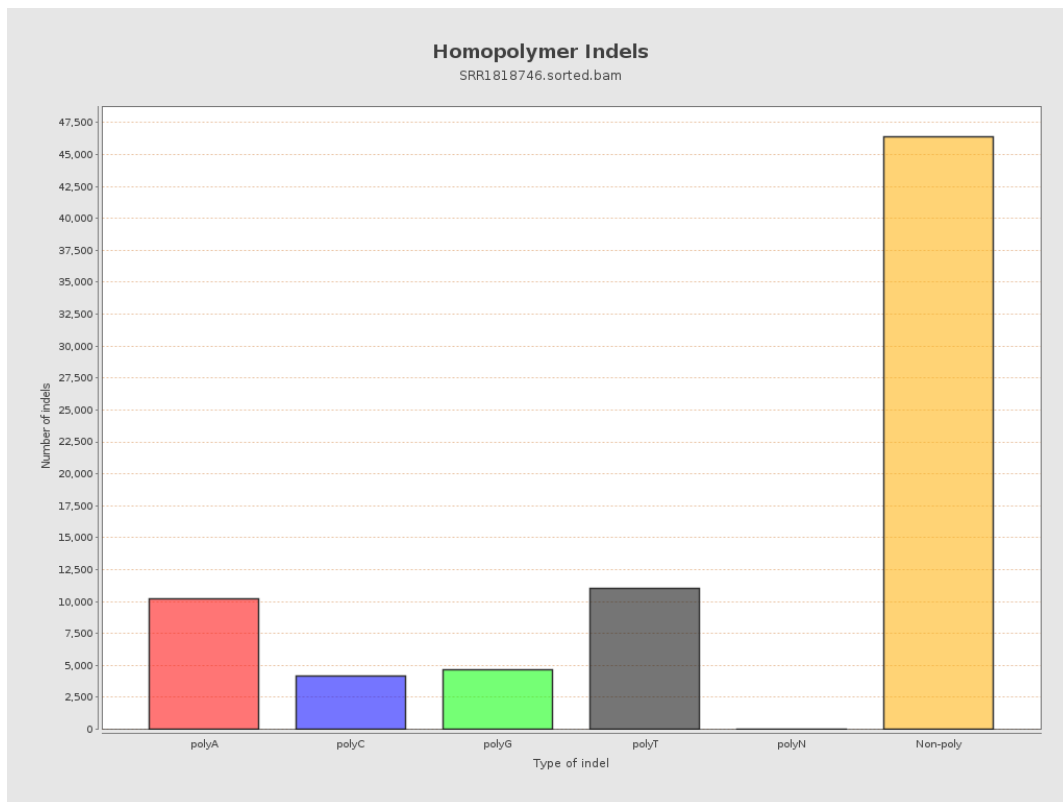
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

