

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 12:35:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818976.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_SRR1818976 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818976.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 12:35:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818976.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,526,013
Mapped reads	1,485,477 / 97.34%
Unmapped reads	40,536 / 2.66%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	23,256 / 1.52%
Read min/max/mean length	30 / 101 / 101.59
Duplicated reads (estimated)	568,851 / 37.28%
Duplication rate	32.72%
Clipped reads	1,506,314 / 98.71%

2.2. ACGT Content

Number/percentage of A's	39,396,586 / 28.71%
Number/percentage of C's	29,680,579 / 21.63%
Number/percentage of T's	38,855,705 / 28.32%
Number/percentage of G's	29,275,630 / 21.34%
Number/percentage of N's	6,753 / 0%
GC Percentage	42.97%

2.3. Coverage

Mean	0.0444

Standard Deviation	0.5384
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2.4. Mapping Quality

Mean Mapping Quality	49.26
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2.5. Mismatches and indels

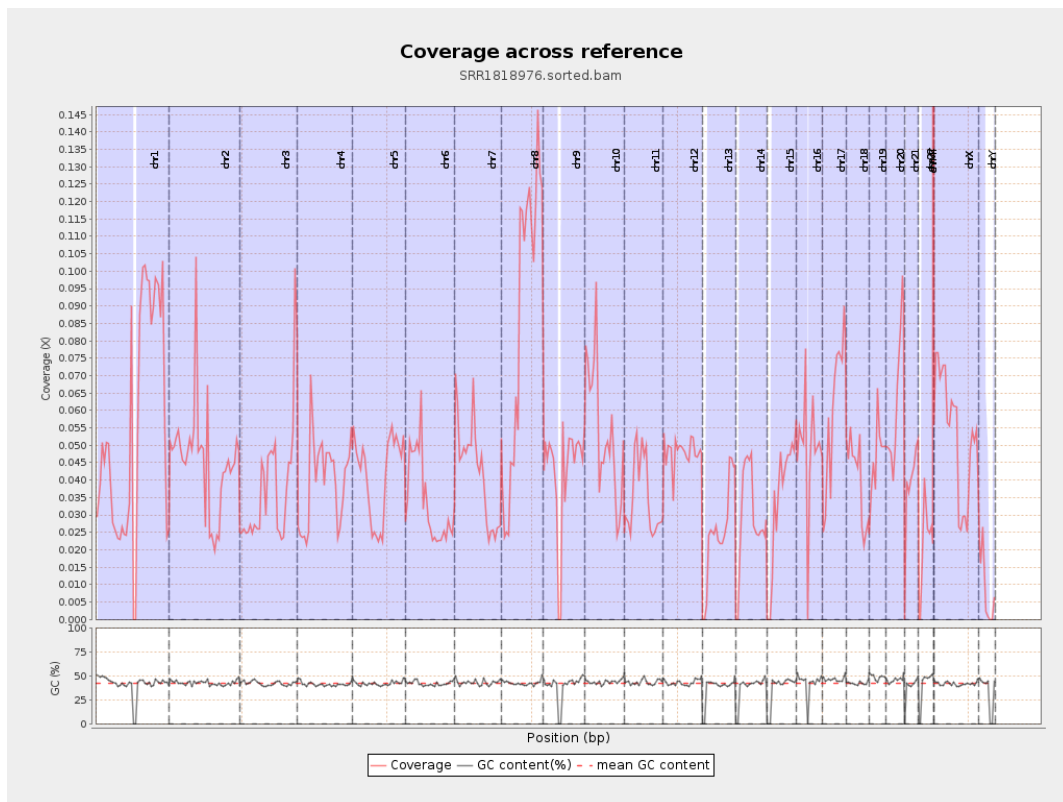
General error rate	0.66%
Mismatches	864,272
Insertions	18,930
Mapped reads with at least one insertion	1.24%
Deletions	44,317
Mapped reads with at least one deletion	2.92%
Homopolymer indels	41.52%

2.6. Chromosome stats

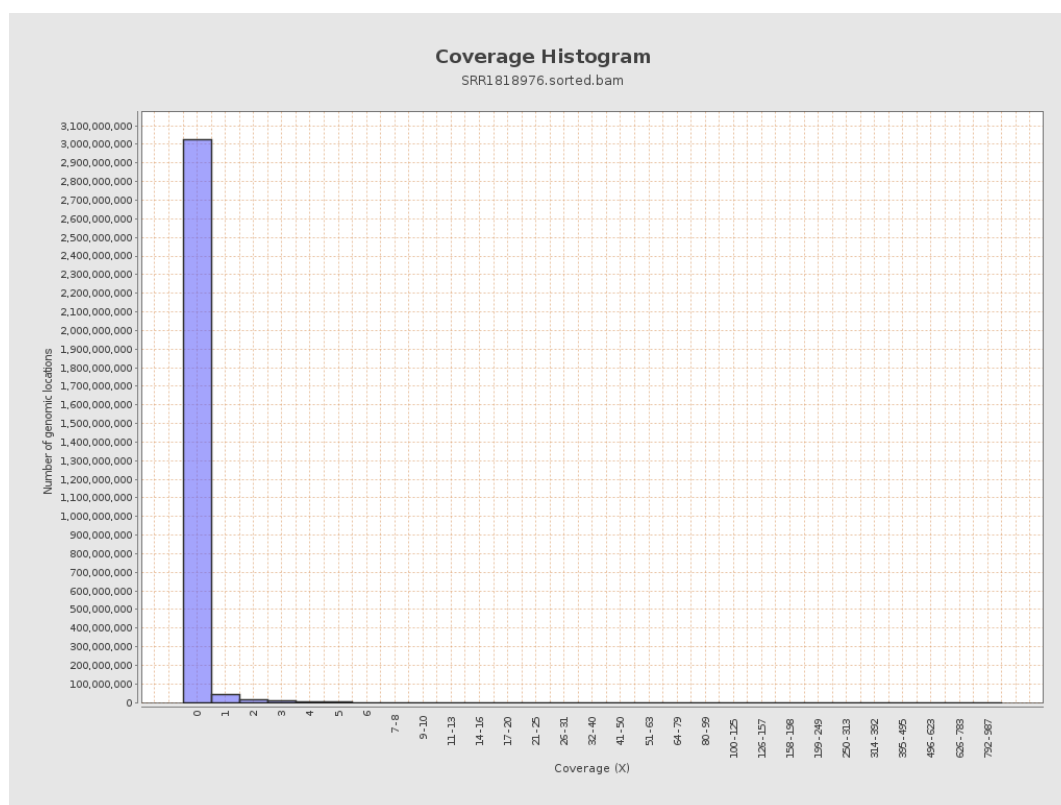
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	13796981	0.0554	0.9511
chr2	243199373	11067718	0.0455	0.734
chr3	198022430	7355179	0.0371	0.3165
chr4	191154276	7577612	0.0396	0.3824
chr5	180915260	7534677	0.0416	0.3456
chr6	171115067	5780697	0.0338	0.353
chr7	159138663	6705161	0.0421	0.6003

chr8	146364022	12571772	0.0859	0.5473
chr9	141213431	5954804	0.0422	0.4932
chr10	135534747	7250154	0.0535	0.6705
chr11	135006516	4735823	0.0351	0.3738
chr12	133851895	6436548	0.0481	0.3735
chr13	115169878	2884993	0.025	0.2617
chr14	107349540	3118842	0.0291	0.2967
chr15	102531392	3547611	0.0346	0.316
chr16	90354753	4404104	0.0487	0.6109
chr17	81195210	4932225	0.0607	0.473
chr18	78077248	3144342	0.0403	0.5747
chr19	59128983	2789719	0.0472	0.8315
chr20	63025520	3947522	0.0626	0.4455
chr21	48129895	1879235	0.039	0.3612
chr22	51304566	1093887	0.0213	0.2817
chrMT	16571	19867	1.1989	1.8593
chrX	155270560	8258999	0.0532	0.4312
chrY	59373566	509820	0.0086	0.5426

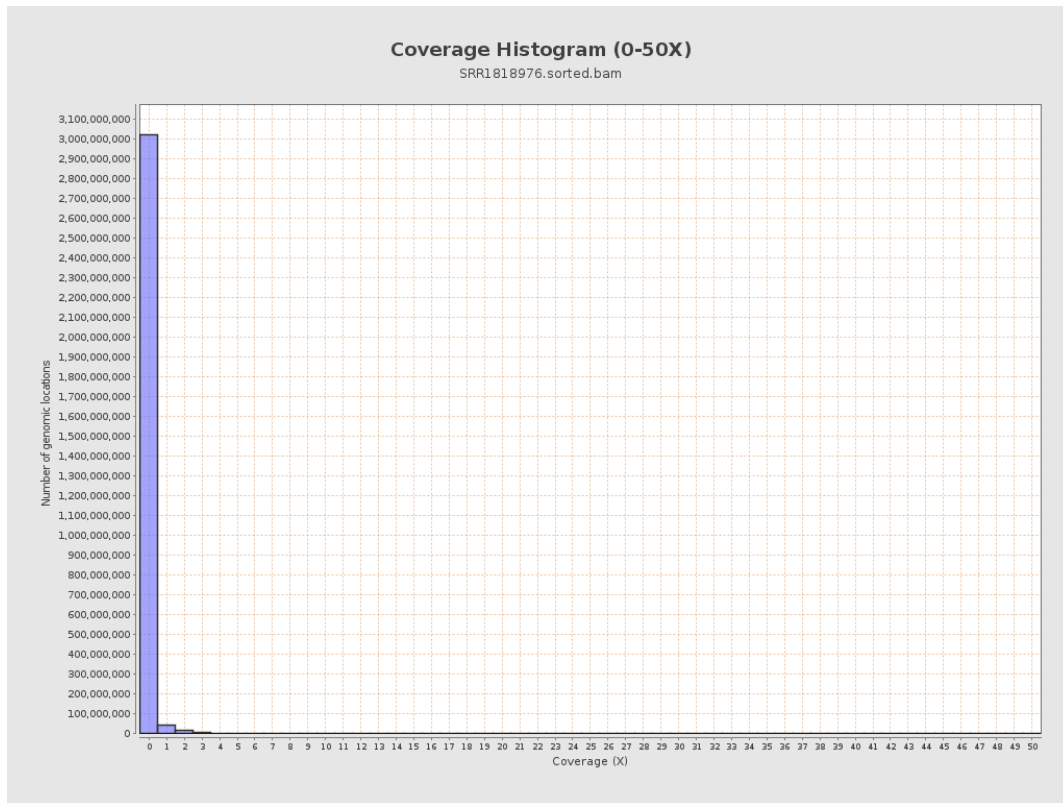
3. Results : Coverage across reference



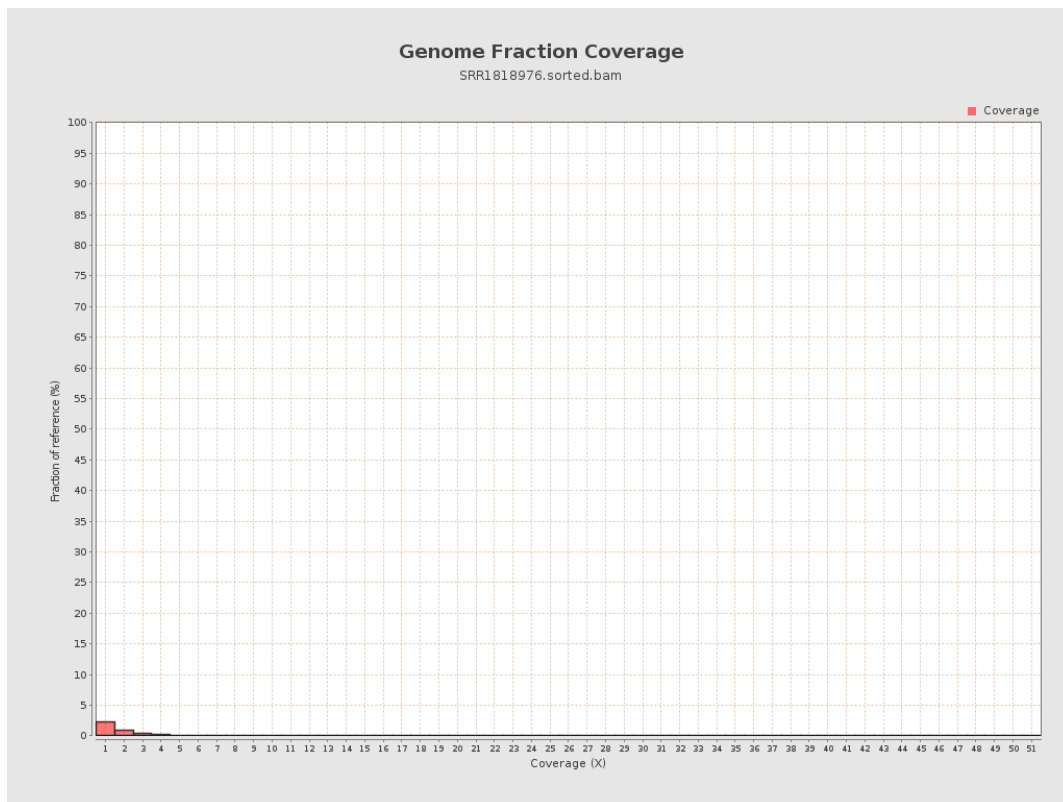
4. Results : Coverage Histogram



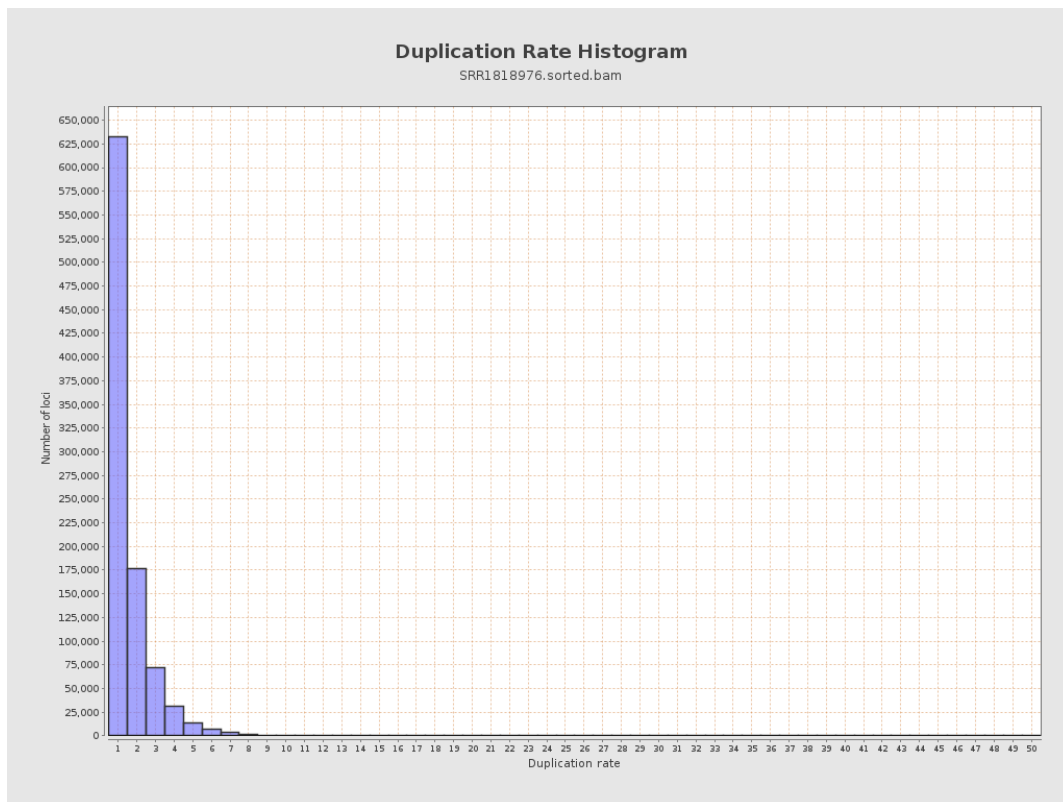
5. Results : Coverage Histogram (0-50X)



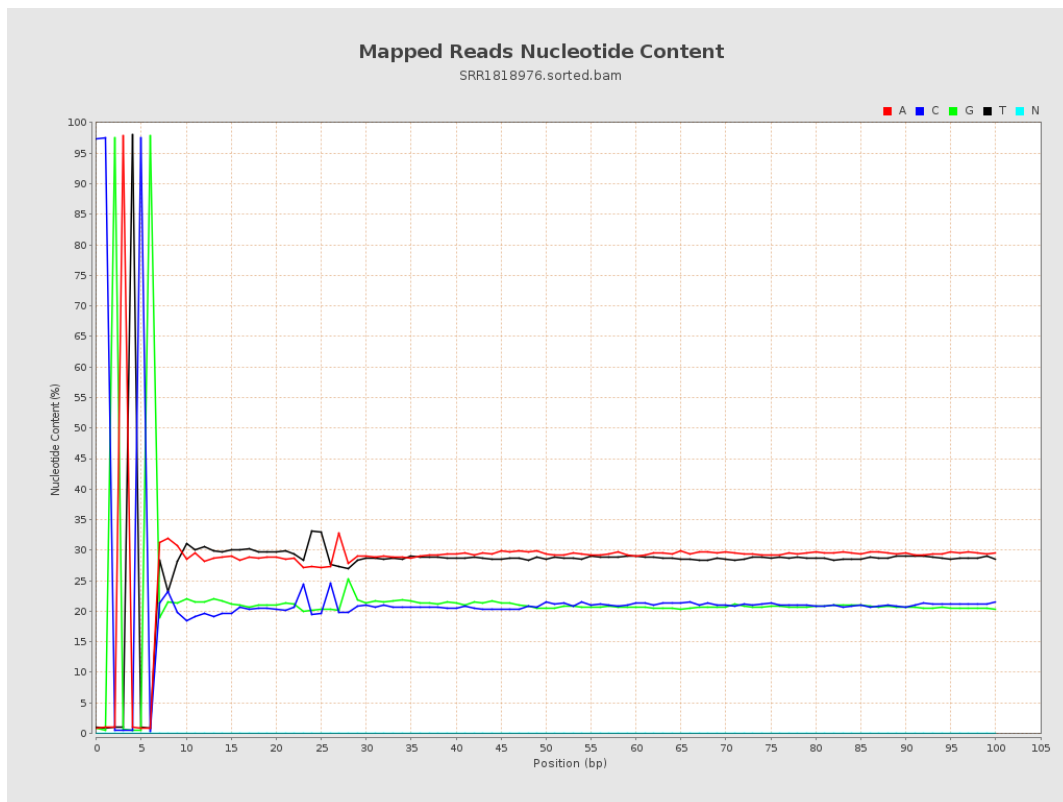
6. Results : Genome Fraction Coverage



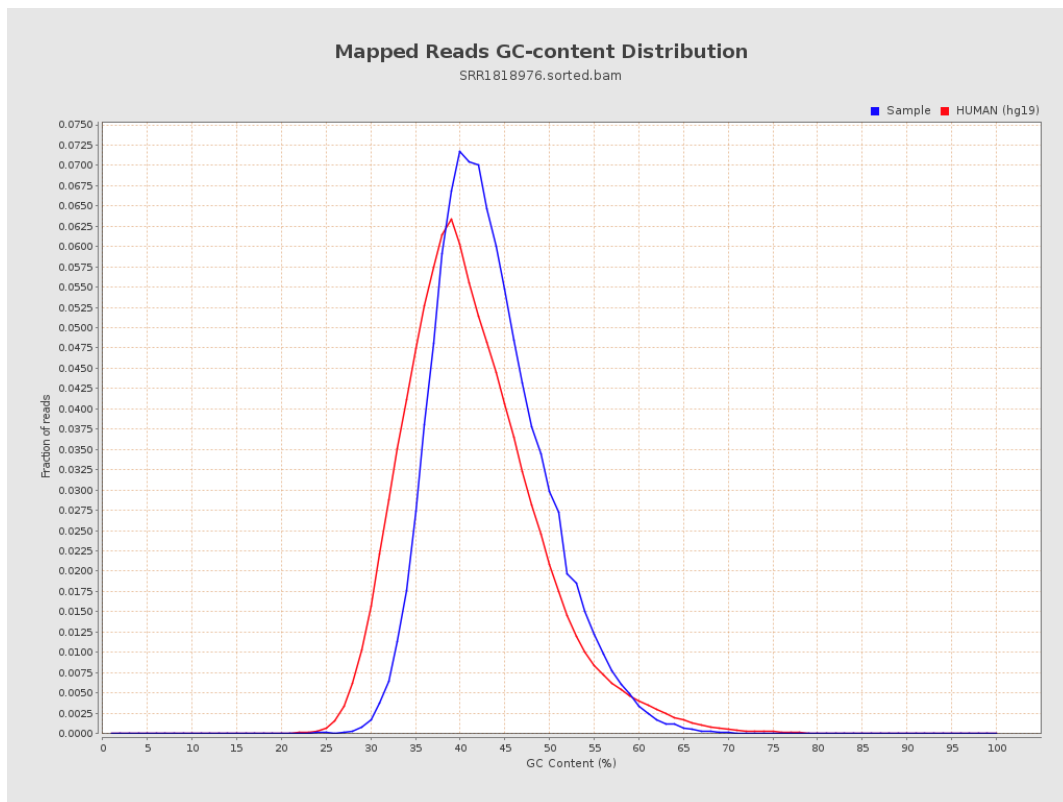
7. Results : Duplication Rate Histogram



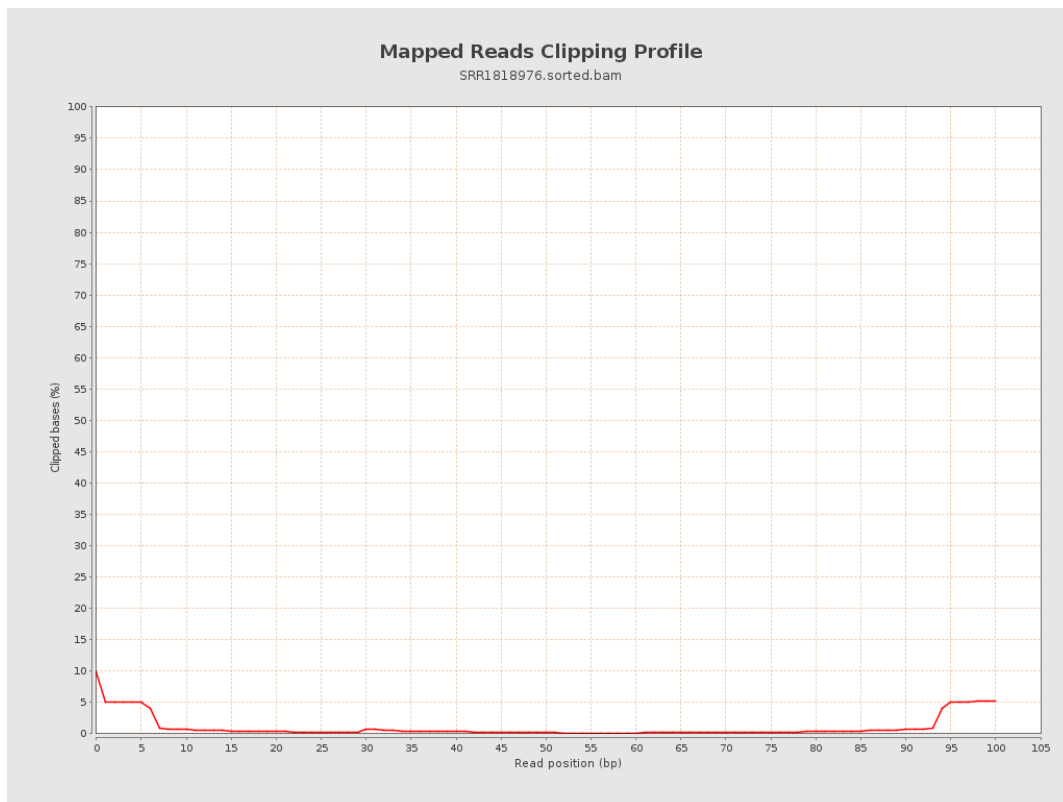
8. Results : Mapped Reads Nucleotide Content



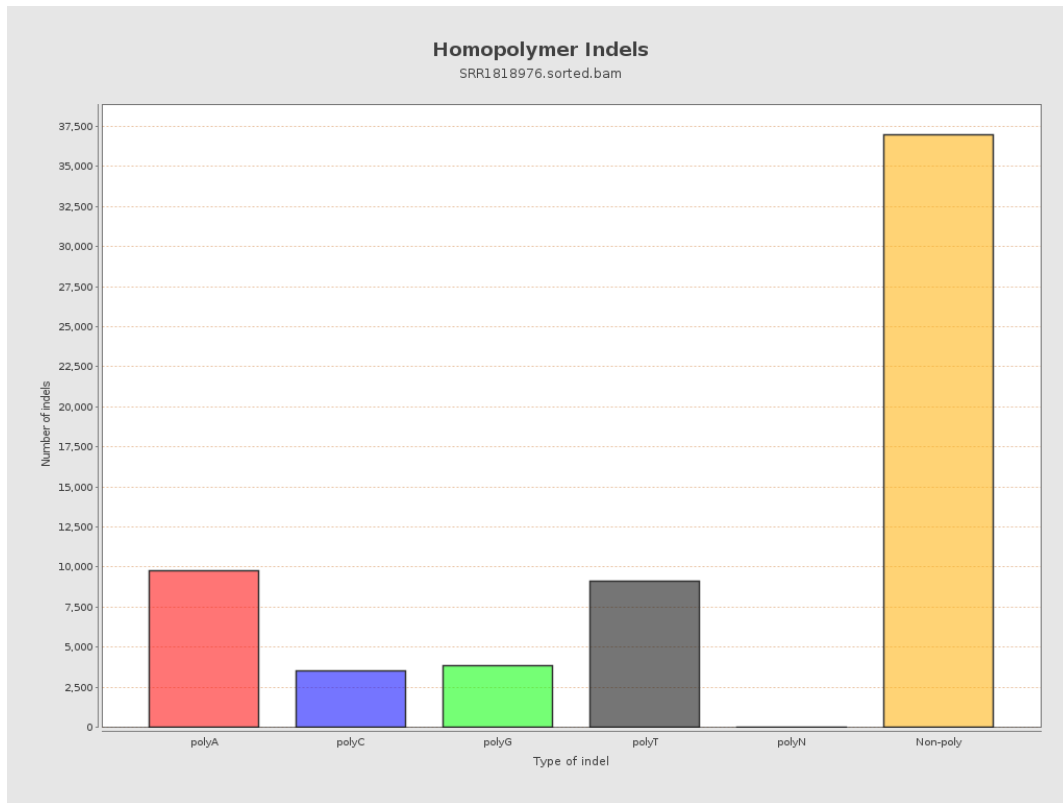
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

