

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 12:21:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818973.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_SRR1818973 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818973.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 12:21:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818973.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,635,520
Mapped reads	2,391,780 / 90.75%
Unmapped reads	243,740 / 9.25%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	33,889 / 1.29%
Read min/max/mean length	30 / 101 / 101.49
Duplicated reads (estimated)	1,179,732 / 44.76%
Duplication rate	42.29%
Clipped reads	2,404,871 / 91.25%

2.2. ACGT Content

Number/percentage of A's	65,965,393 / 29.78%
Number/percentage of C's	44,853,922 / 20.25%
Number/percentage of T's	63,448,296 / 28.64%
Number/percentage of G's	47,251,401 / 21.33%
Number/percentage of N's	10,768 / 0%
GC Percentage	41.58%

2.3. Coverage

Mean	0.0716

Standard Deviation	0.8045
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2.4. Mapping Quality

Mean Mapping Quality	49.13
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2.5. Mismatches and indels

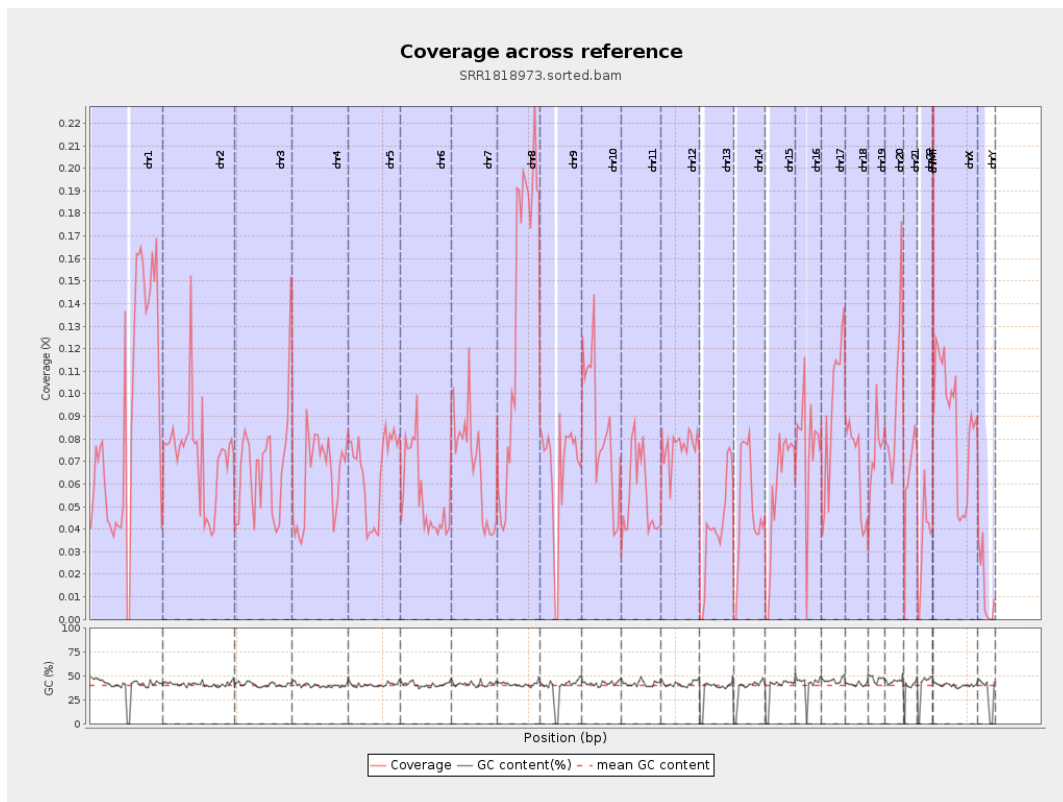
General error rate	0.64%
Mismatches	1,353,049
Insertions	33,113
Mapped reads with at least one insertion	1.35%
Deletions	69,353
Mapped reads with at least one deletion	2.84%
Homopolymer indels	42.51%

2.6. Chromosome stats

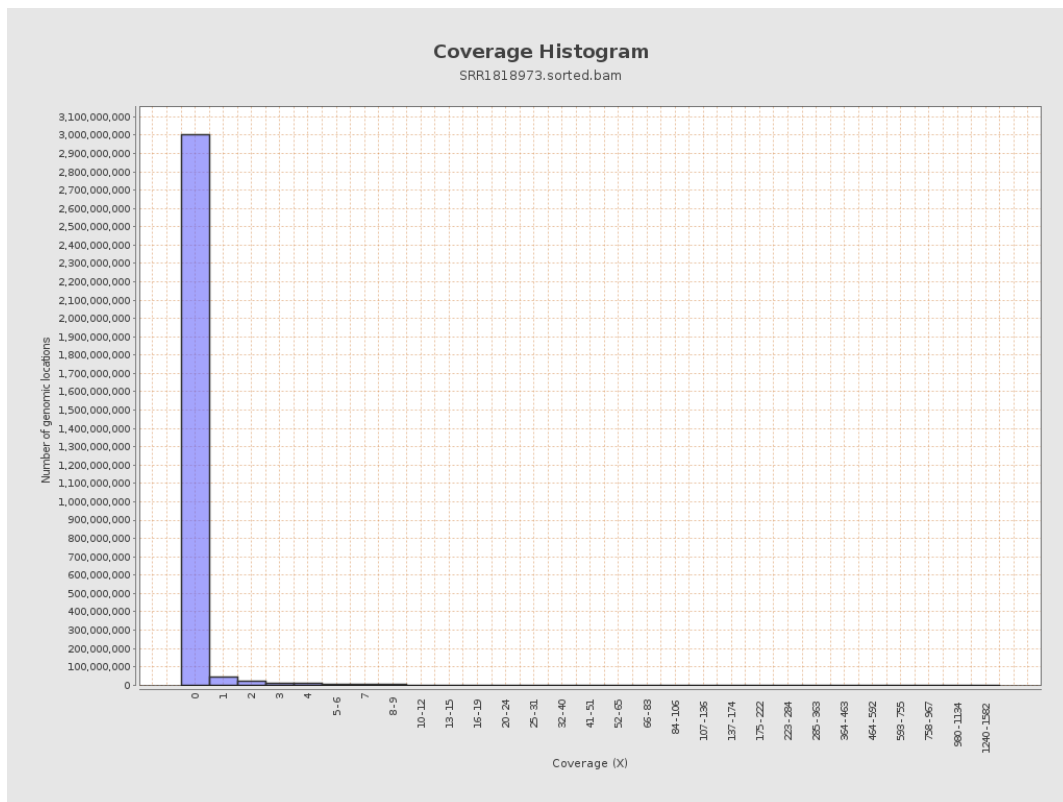
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	22005778	0.0883	1.404
chr2	243199373	17649027	0.0726	1.0536
chr3	198022430	13453400	0.0679	0.5053
chr4	191154276	12139600	0.0635	0.5486
chr5	180915260	11935656	0.066	0.5123
chr6	171115067	9394397	0.0549	0.5501
chr7	159138663	10910607	0.0686	0.9754

chr8	146364022	20284026	0.1386	0.8296
chr9	141213431	9441783	0.0669	0.7859
chr10	135534747	11277701	0.0832	0.9365
chr11	135006516	7422648	0.055	0.5418
chr12	133851895	10305989	0.077	0.5646
chr13	115169878	4742032	0.0412	0.3911
chr14	107349540	5282960	0.0492	0.4541
chr15	102531392	5766782	0.0562	0.4624
chr16	90354753	6883321	0.0762	0.8663
chr17	81195210	7498109	0.0923	0.6611
chr18	78077248	5278560	0.0676	0.9193
chr19	59128983	4412658	0.0746	1.3655
chr20	63025520	6224020	0.0988	0.6464
chr21	48129895	3095748	0.0643	0.531
chr22	51304566	1733098	0.0338	0.3807
chrMT	16571	37340	2.2533	2.8933
chrX	155270560	13702383	0.0882	0.6757
chrY	59373566	777638	0.0131	0.7478

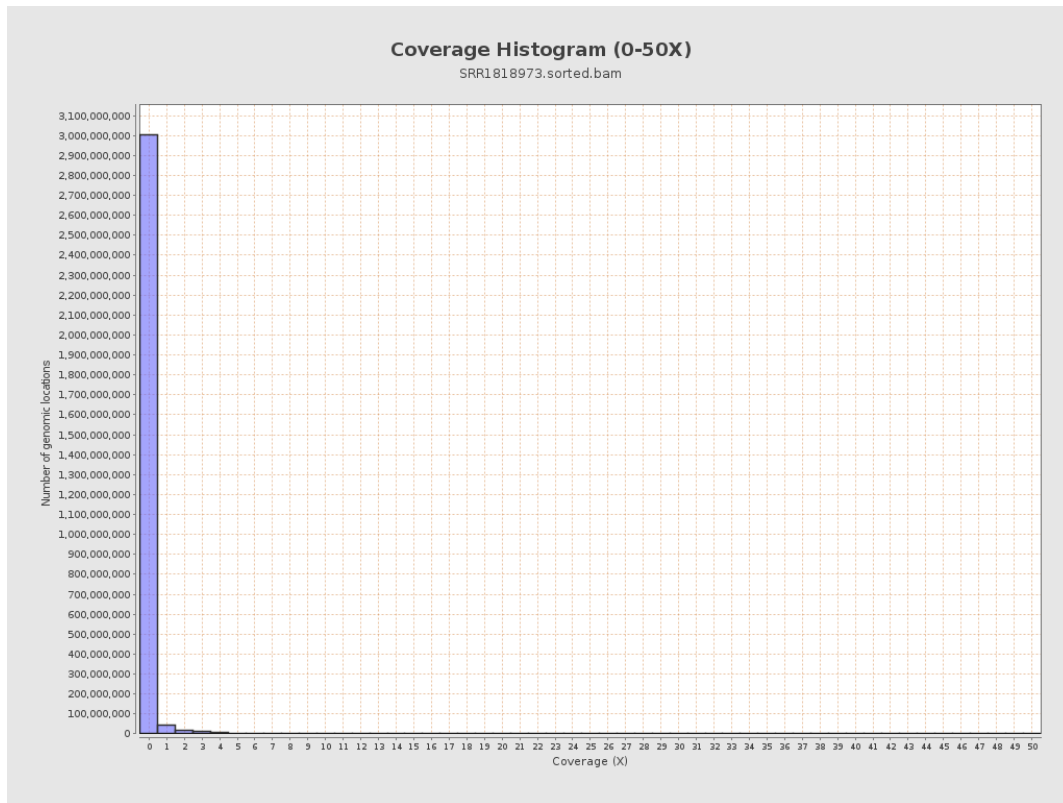
3. Results : Coverage across reference



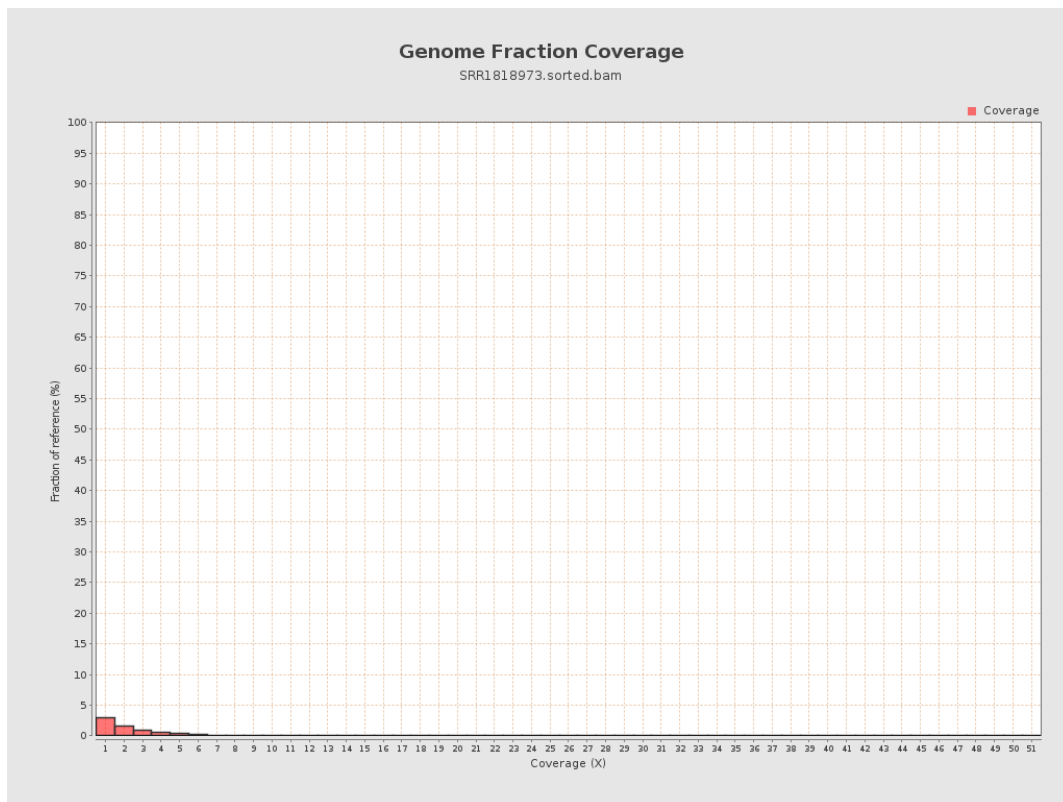
4. Results : Coverage Histogram



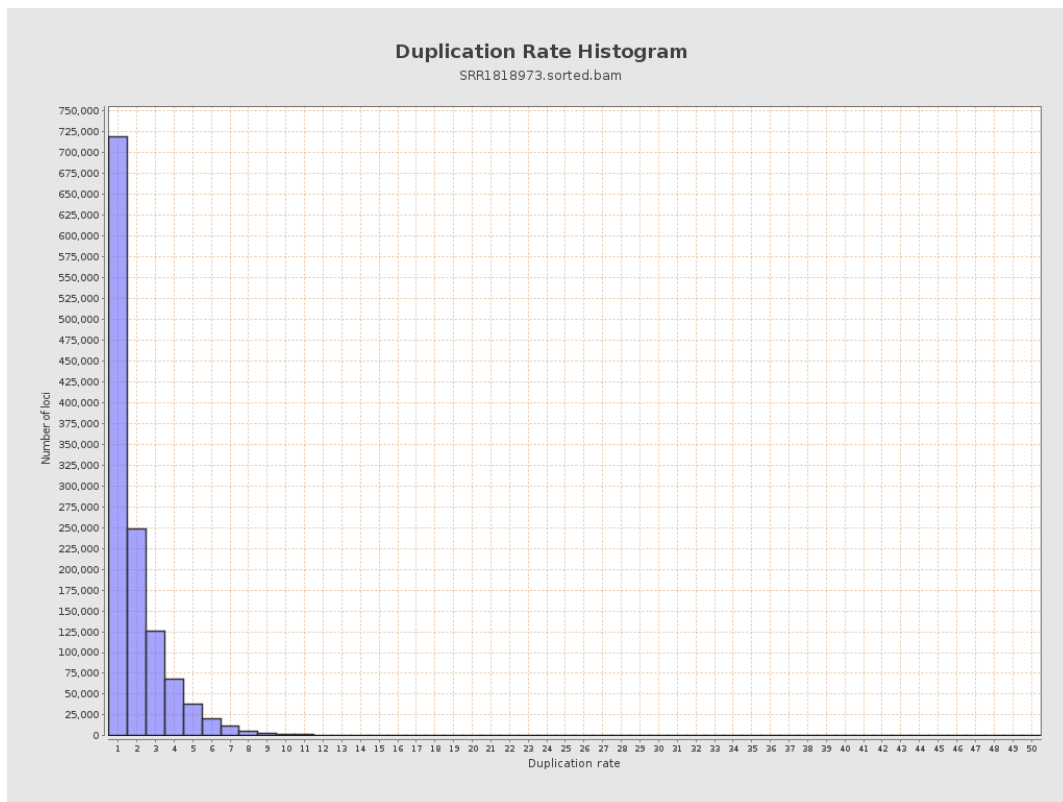
5. Results : Coverage Histogram (0-50X)



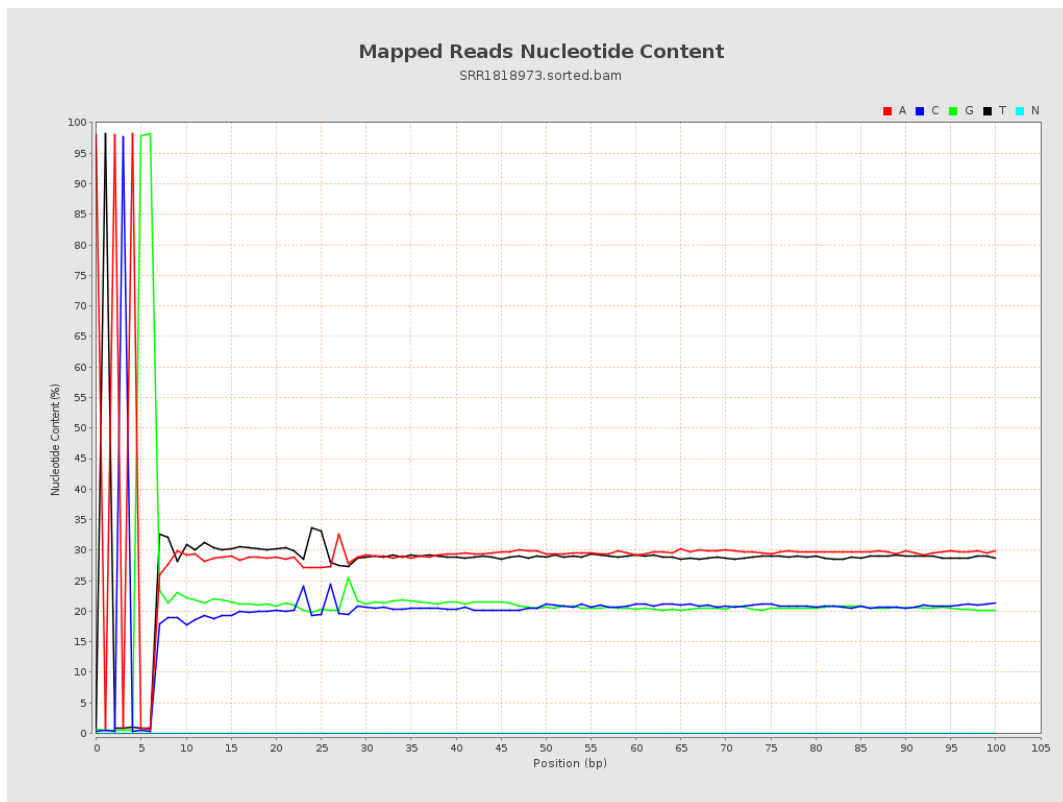
6. Results : Genome Fraction Coverage



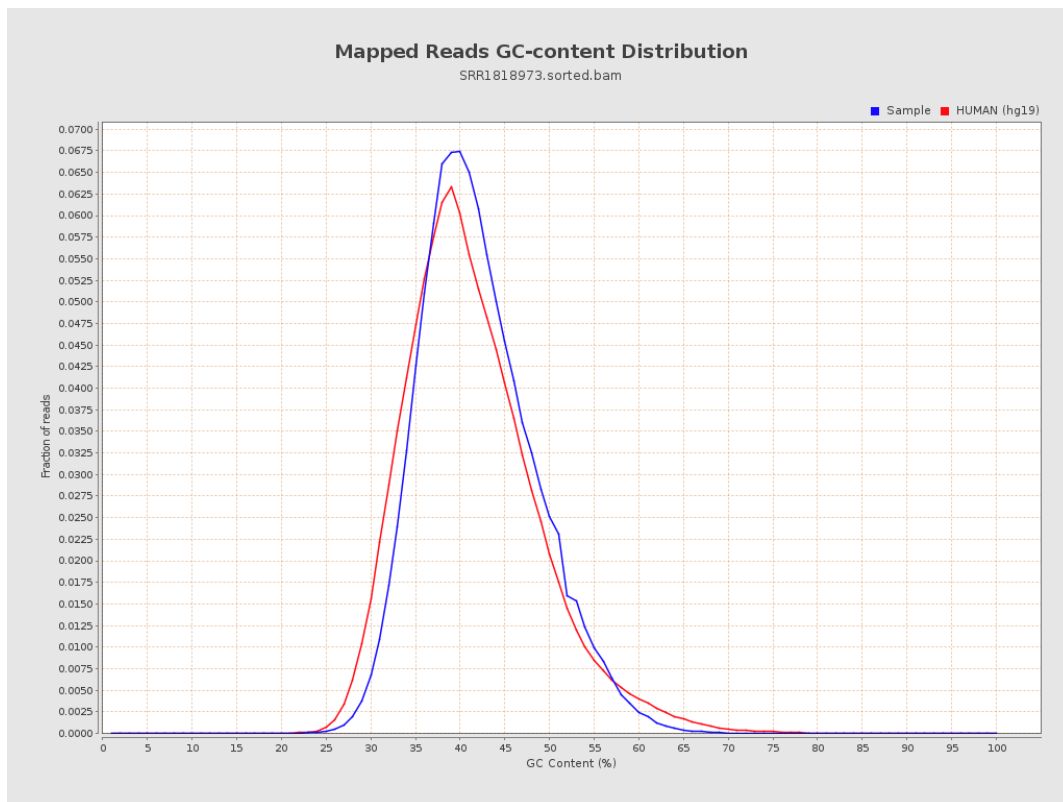
7. Results : Duplication Rate Histogram



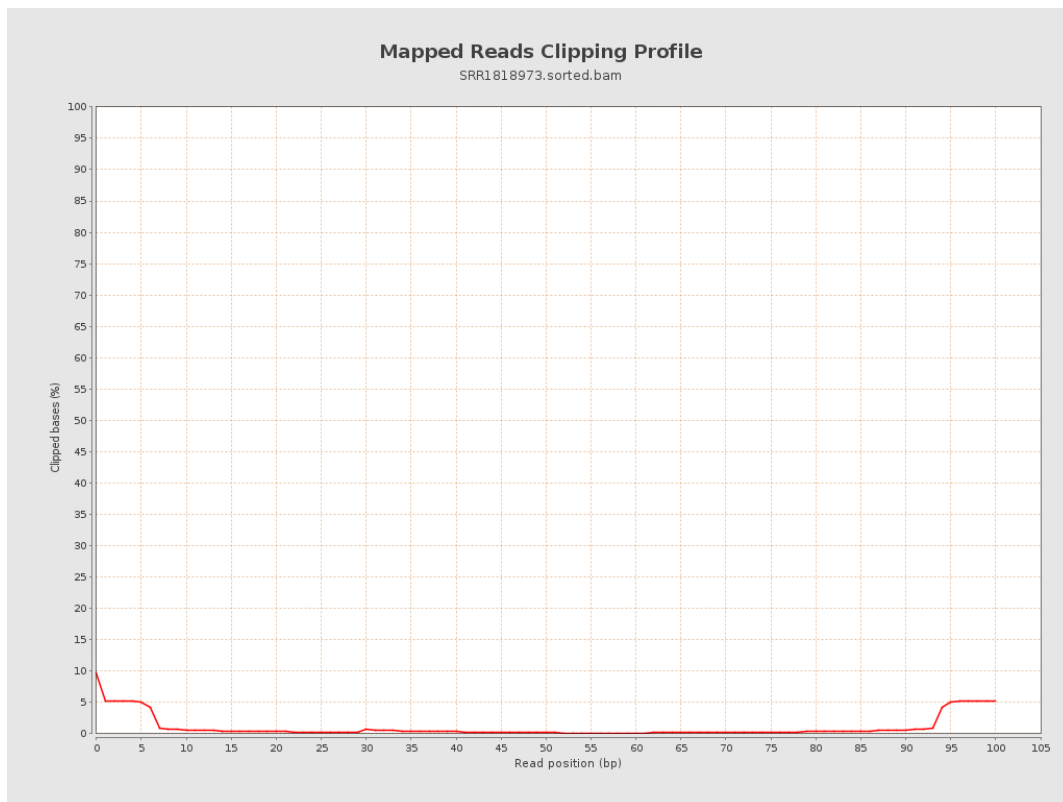
8. Results : Mapped Reads Nucleotide Content



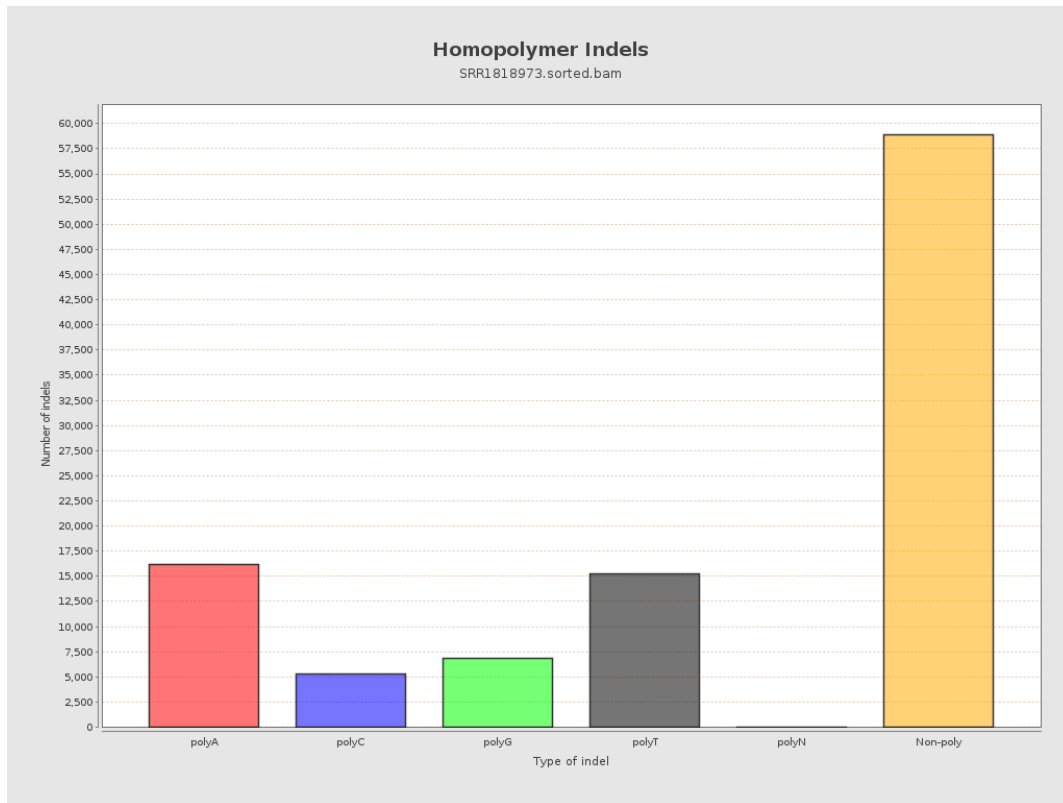
9. Results : Mapped Reads GC-content Distribution



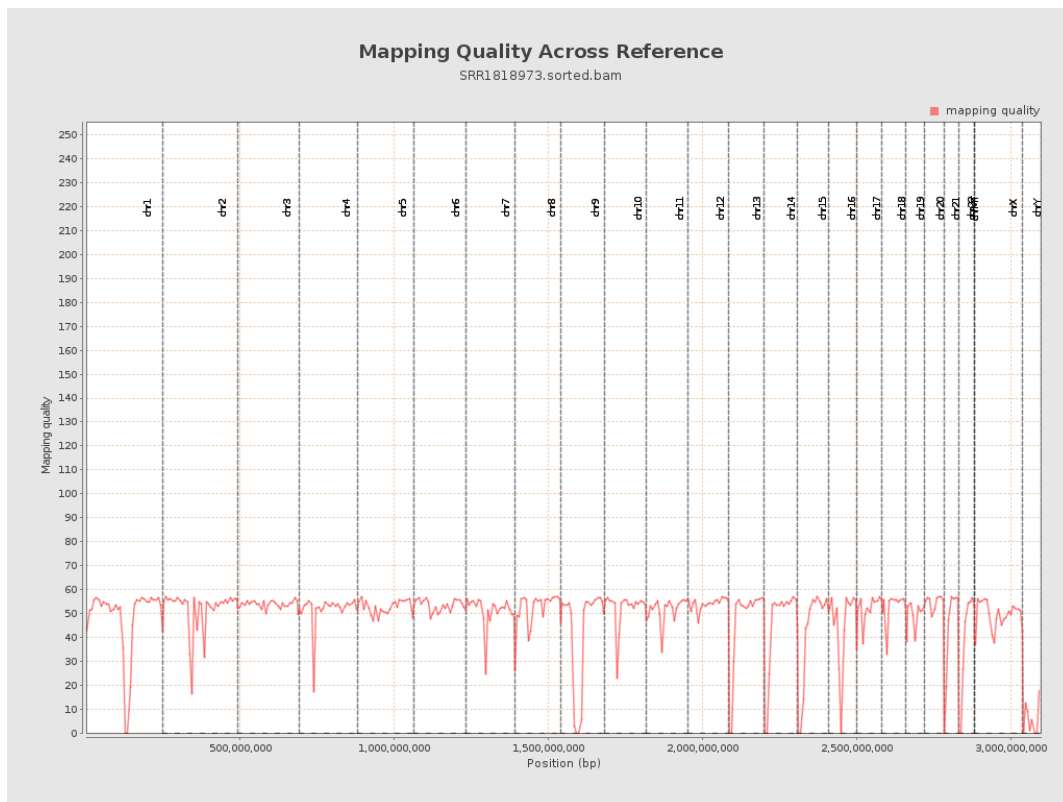
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

