

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 03:15:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1548973.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_SRR1548973 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1548973.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 03:15:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1548973.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,781,316
Mapped reads	3,870,953 / 44.08%
Unmapped reads	4,910,363 / 55.92%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	107,177 / 1.22%
Duplication rate	1.95%
Clipped reads	348,842 / 3.97%

2.2. ACGT Content

Number/percentage of A's	46,671,191 / 30.51%
Number/percentage of C's	29,493,399 / 19.28%
Number/percentage of T's	46,969,562 / 30.71%
Number/percentage of G's	29,819,540 / 19.49%
Number/percentage of N's	8,152 / 0.01%
GC Percentage	38.78%

2.3. Coverage

Mean	0.0494
Standard Deviation	0.373

2.4. Mapping Quality

Mean Mapping Quality	43.86
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2.5. Mismatches and indels

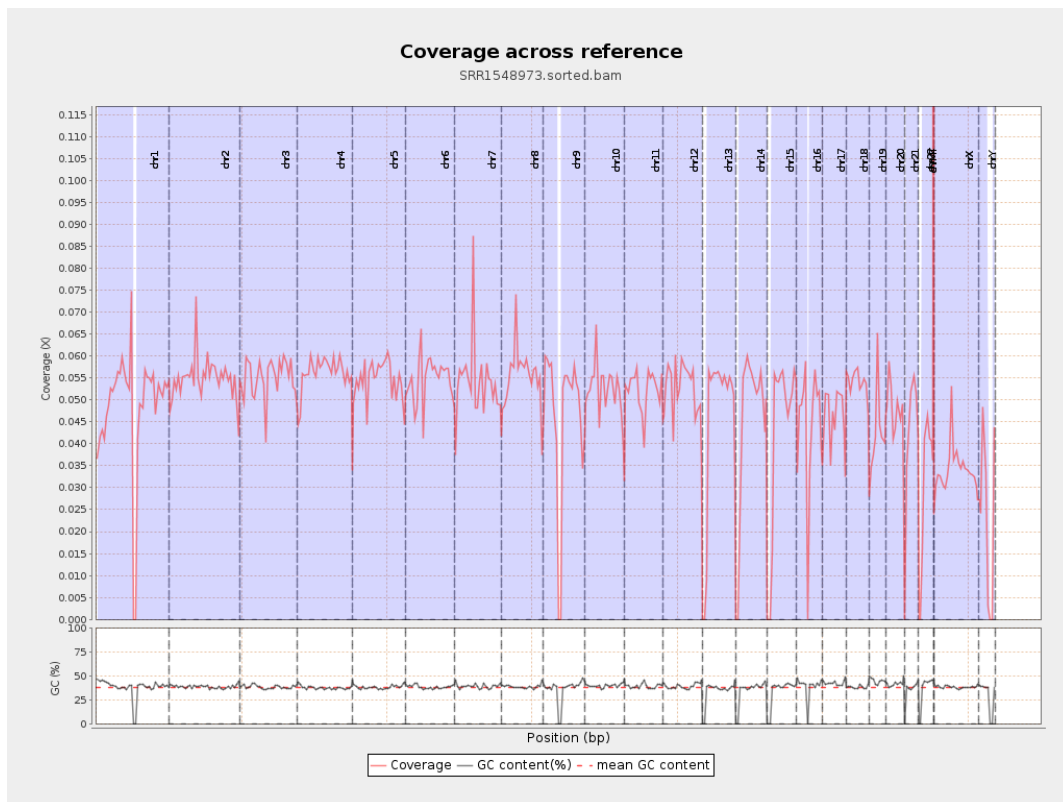
General error rate	0.31%
Mismatches	474,363
Insertions	6,131
Mapped reads with at least one insertion	0.16%
Deletions	16,268
Mapped reads with at least one deletion	0.42%
Homopolymer indels	45.03%

2.6. Chromosome stats

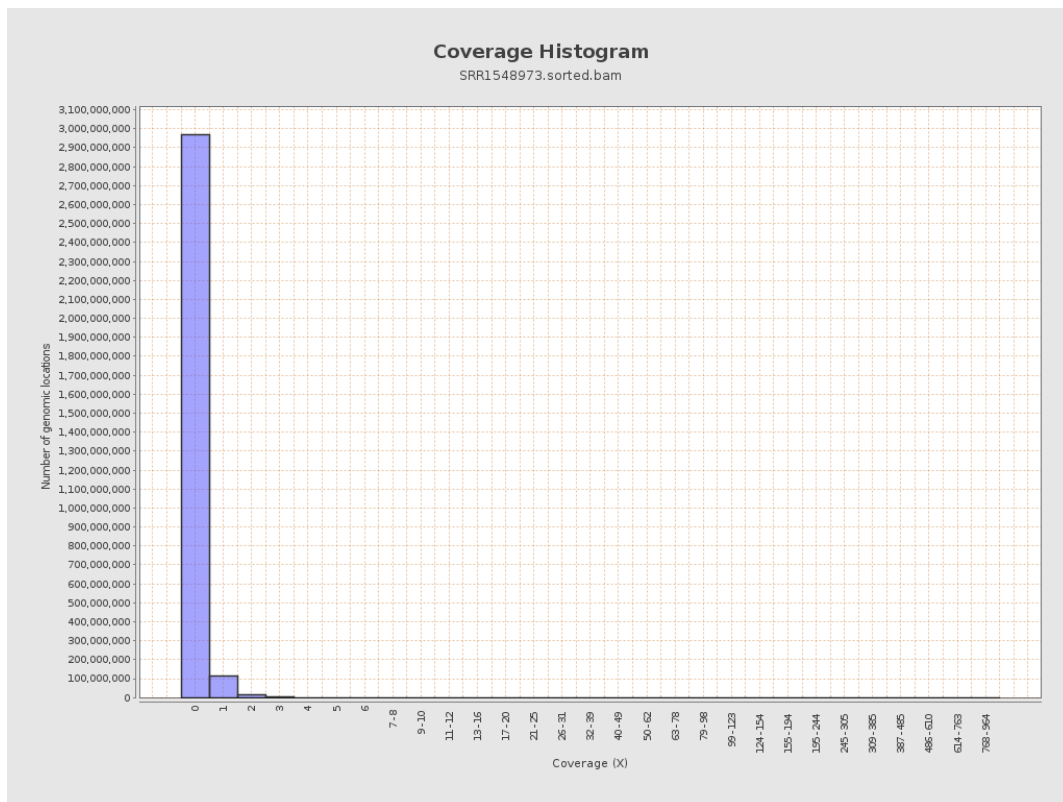
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	12100716	0.0485	0.6391
chr2	243199373	13349301	0.0549	0.3493
chr3	198022430	10919751	0.0551	0.2713
chr4	191154276	10741465	0.0562	0.2787
chr5	180915260	9880923	0.0546	0.2734
chr6	171115067	9362834	0.0547	0.3041
chr7	159138663	8661190	0.0544	0.5336
chr8	146364022	8101911	0.0554	0.5

chr9	141213431	6582623	0.0466	0.3258
chr10	135534747	7127157	0.0526	0.3231
chr11	135006516	7028976	0.0521	0.358
chr12	133851895	7050502	0.0527	0.2737
chr13	115169878	5220713	0.0453	0.2441
chr14	107349540	4835401	0.045	0.285
chr15	102531392	4384338	0.0428	0.2365
chr16	90354753	3980398	0.0441	0.2555
chr17	81195210	3722212	0.0458	0.2615
chr18	78077248	4218884	0.054	0.5631
chr19	59128983	2539751	0.043	0.597
chr20	63025520	3007143	0.0477	0.2591
chr21	48129895	2037801	0.0423	0.2575
chr22	51304566	1508891	0.0294	0.2117
chrMT	16571	6386	0.3854	0.7042
chrX	155270560	5290276	0.0341	0.2504
chrY	59373566	1322618	0.0223	0.2556

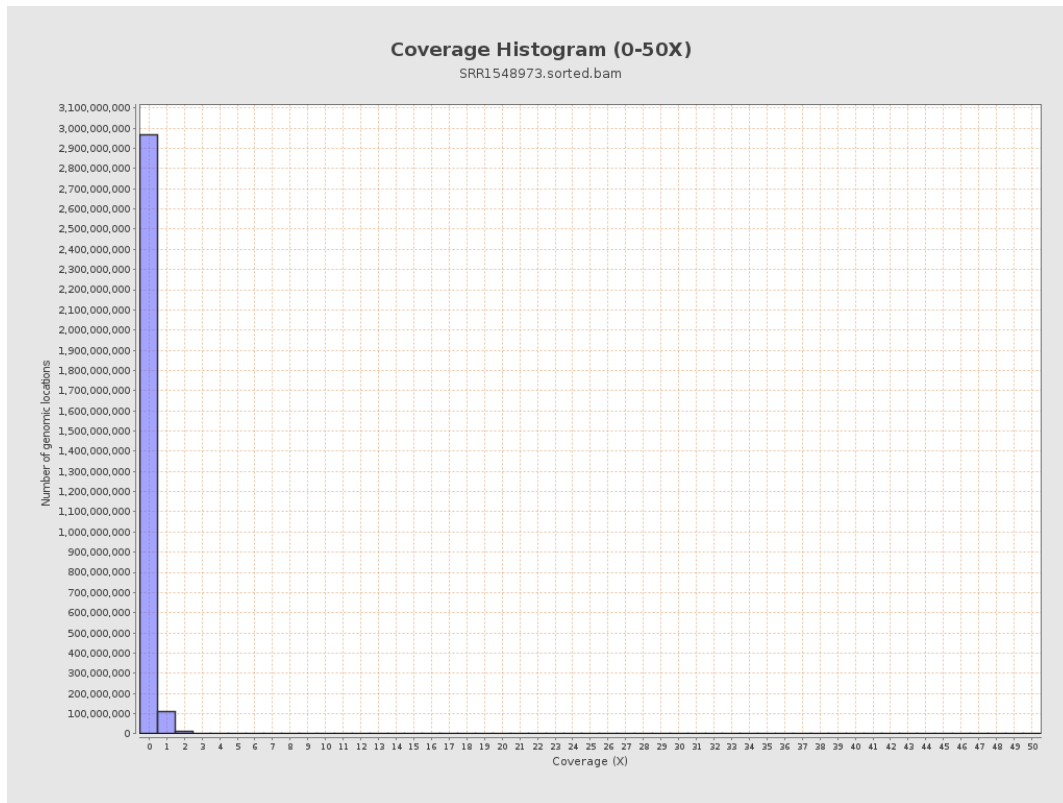
3. Results : Coverage across reference



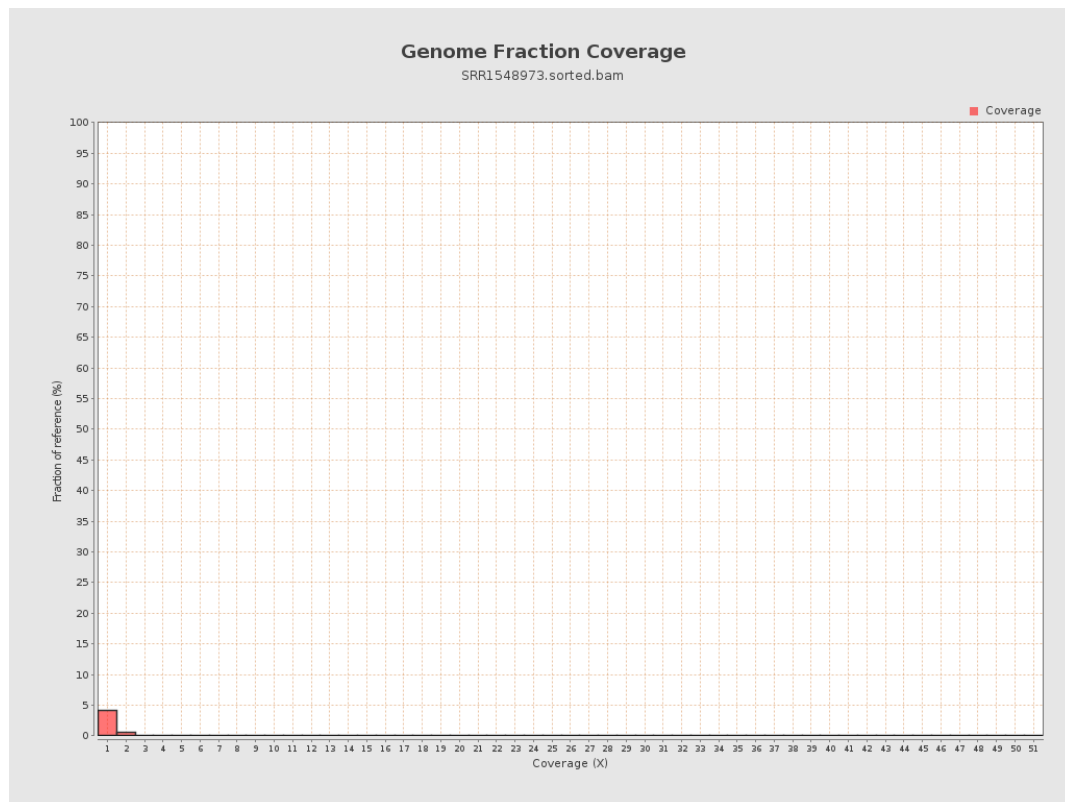
4. Results : Coverage Histogram



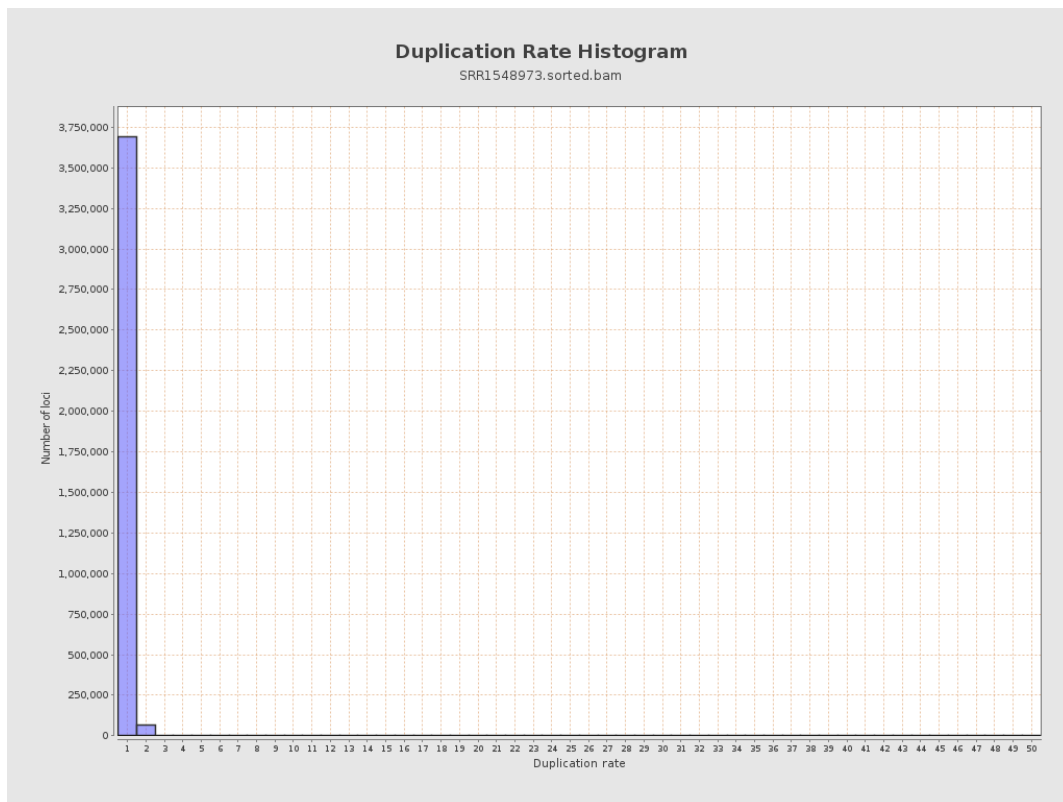
5. Results : Coverage Histogram (0-50X)



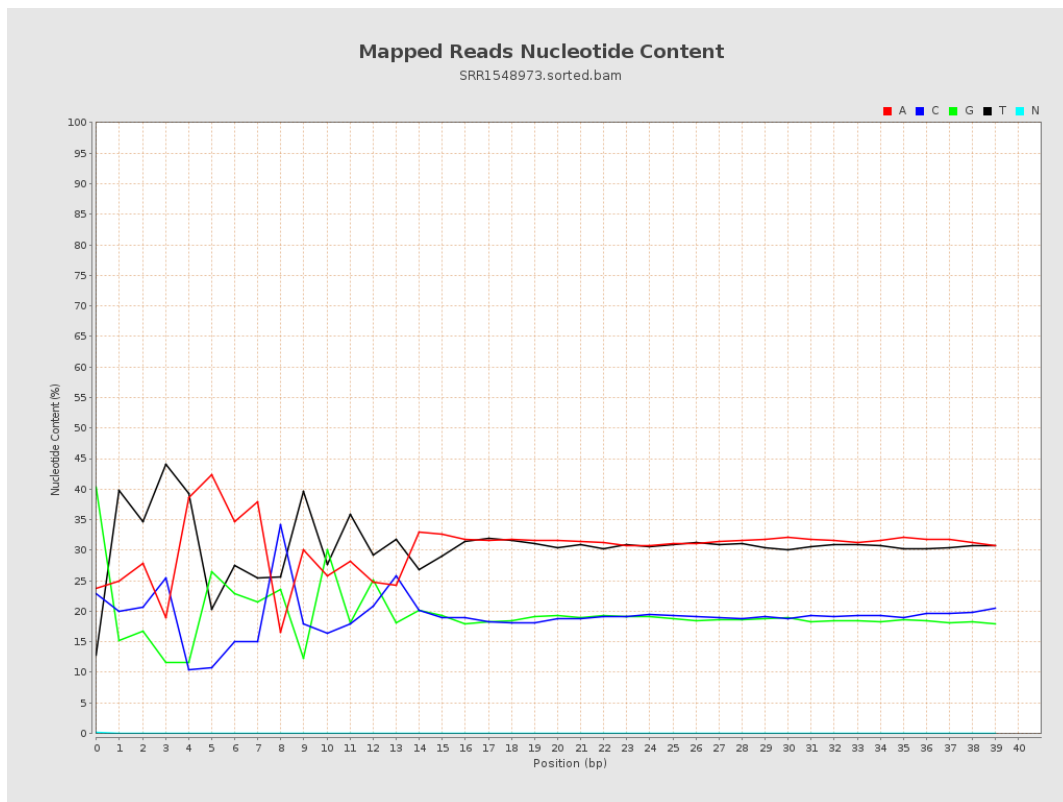
6. Results : Genome Fraction Coverage



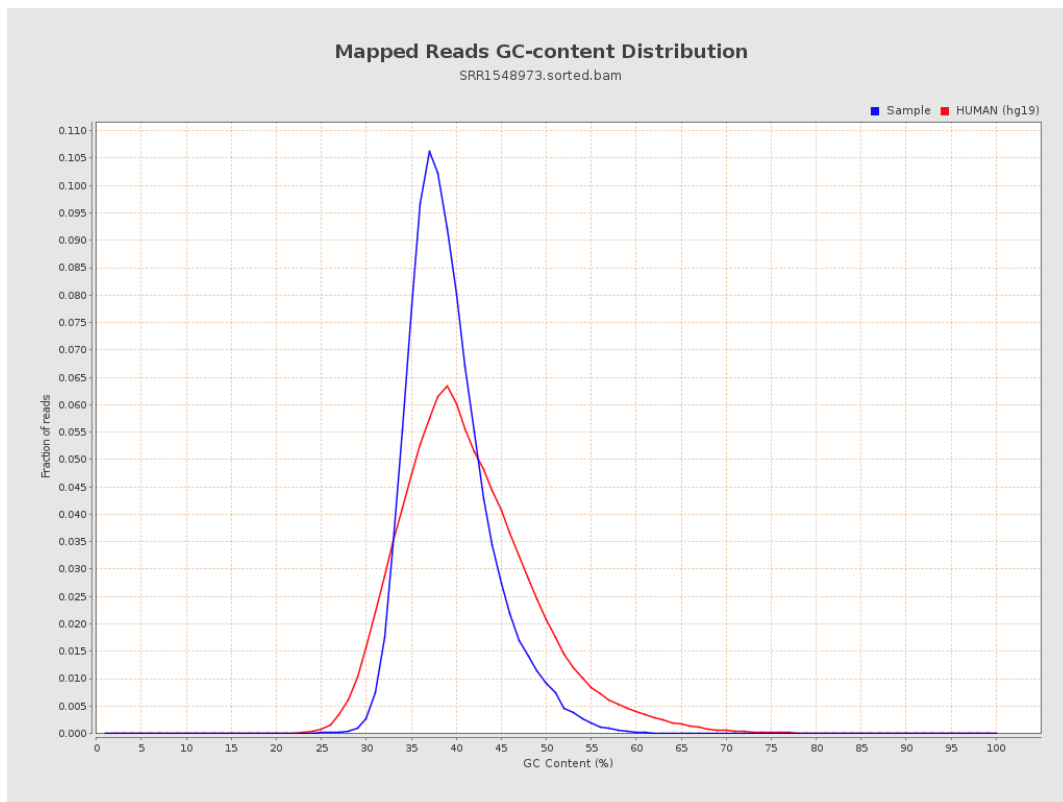
7. Results : Duplication Rate Histogram



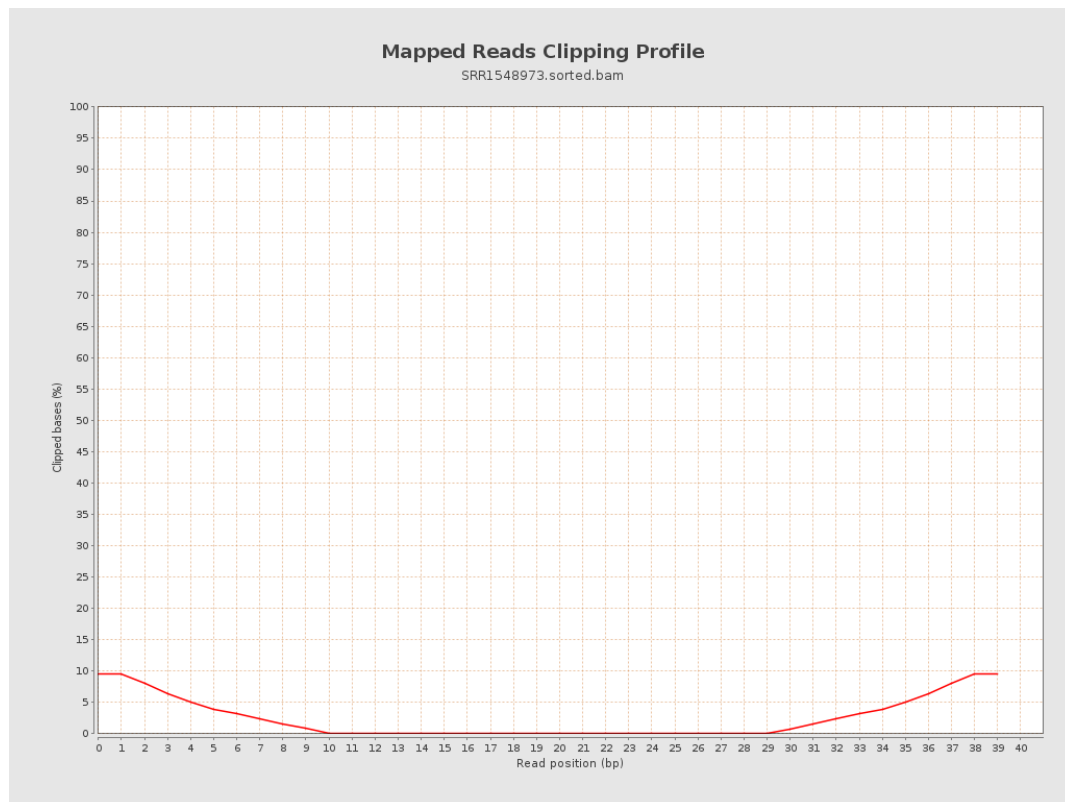
8. Results : Mapped Reads Nucleotide Content



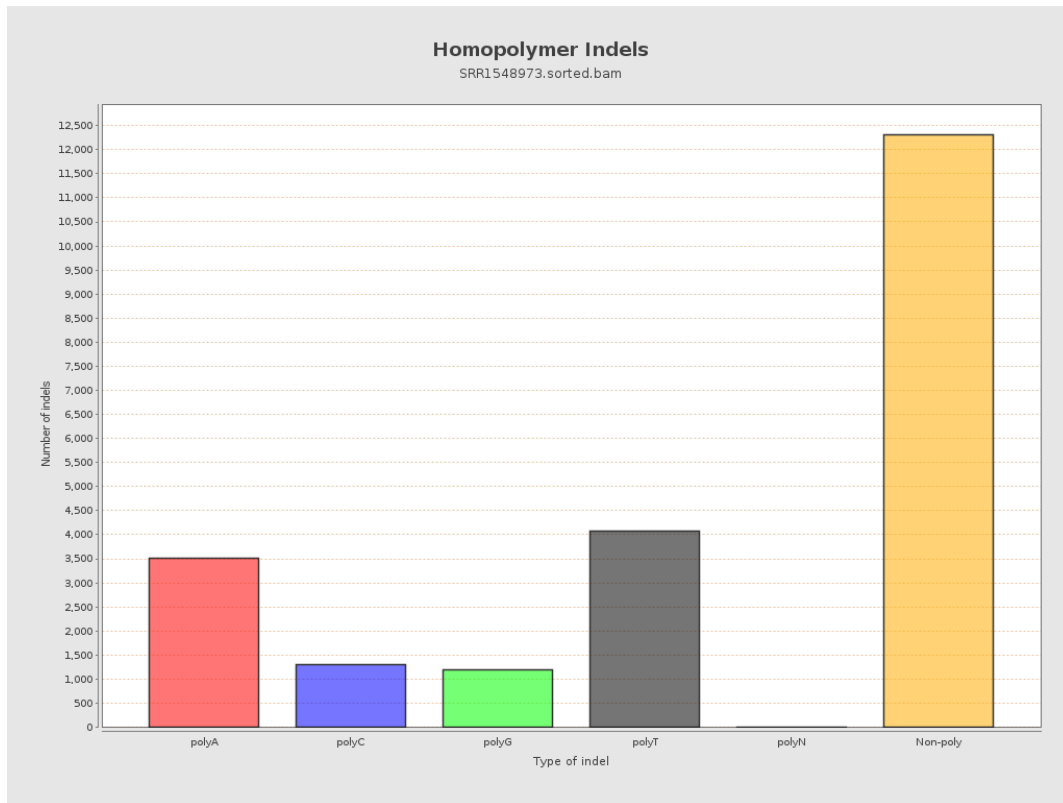
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

