

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/16 17:13:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1153376.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_SRR1153376 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1153376.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Dec 16 17:13:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1153376.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	36,448,700
Mapped reads	36,179,560 / 99.26%
Unmapped reads	269,140 / 0.74%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	278,792 / 0.76%
Read min/max/mean length	30 / 100 / 100.31
Duplicated reads (estimated)	15,934,903 / 43.72%
Duplication rate	29.69%
Clipped reads	4,914,502 / 13.48%

2.2. ACGT Content

Number/percentage of A's	929,823,328 / 26.52%
Number/percentage of C's	818,818,331 / 23.35%
Number/percentage of T's	949,094,756 / 27.07%
Number/percentage of G's	807,050,592 / 23.02%
Number/percentage of N's	1,411,897 / 0.04%
GC Percentage	46.37%

2.3. Coverage

Mean	1.1328

Standard Deviation	10.8396
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2.4. Mapping Quality

Mean Mapping Quality	50.26
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2.5. Mismatches and indels

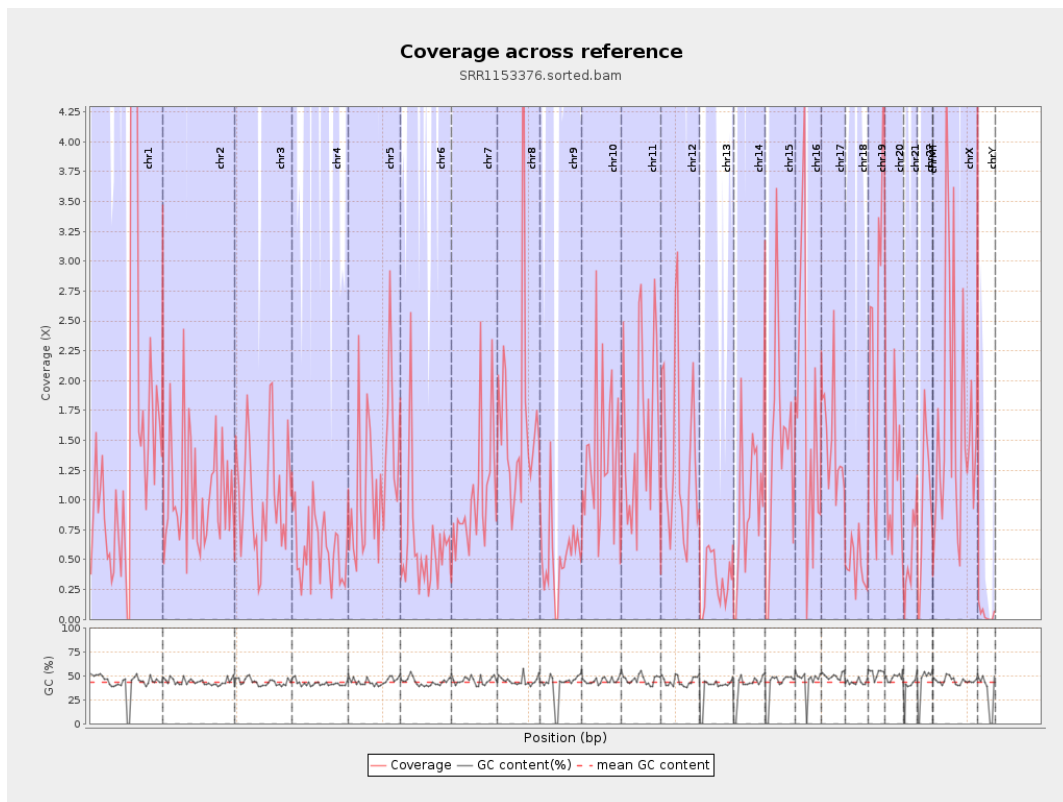
General error rate	0.28%
Mismatches	9,411,948
Insertions	373,636
Mapped reads with at least one insertion	1.02%
Deletions	296,376
Mapped reads with at least one deletion	0.81%
Homopolymer indels	49.85%

2.6. Chromosome stats

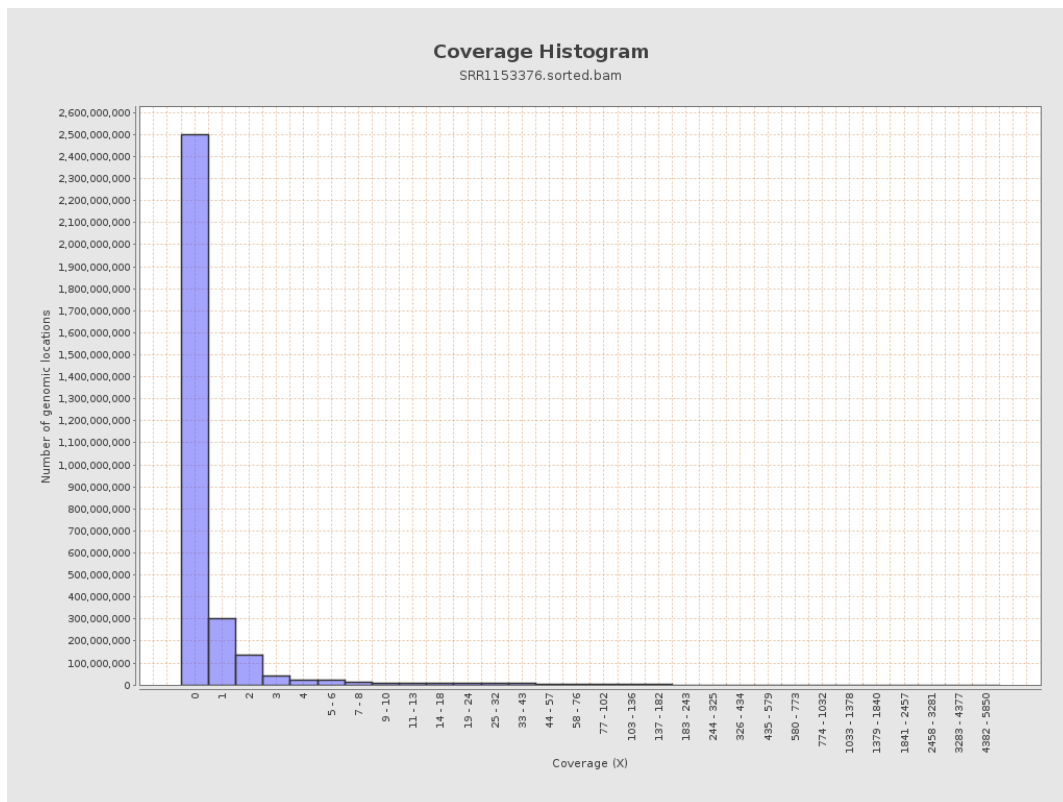
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	386647000	1.5512	15.4659
chr2	243199373	253373566	1.0418	8.4887
chr3	198022430	205574311	1.0381	8.1171
chr4	191154276	113272686	0.5926	5.3065
chr5	180915260	219802314	1.2149	10.7063
chr6	171115067	101854527	0.5952	5.9466
chr7	159138663	161148171	1.0126	9.0814

chr8	146364022	248980465	1.7011	21.6569
chr9	141213431	73157534	0.5181	5.0468
chr10	135534747	185749125	1.3705	10.4732
chr11	135006516	214174704	1.5864	11.5662
chr12	133851895	187397718	1.4	9.8632
chr13	115169878	37311342	0.324	3.3051
chr14	107349540	103800419	0.9669	7.9451
chr15	102531392	141212215	1.3773	10.6276
chr16	90354753	152290464	1.6855	12.987
chr17	81195210	122155078	1.5045	9.5471
chr18	78077248	35010853	0.4484	4.2339
chr19	59128983	147297372	2.4911	17.3095
chr20	63025520	72104364	1.1441	8.6766
chr21	48129895	26987763	0.5607	5.1069
chr22	51304566	50614690	0.9866	10.1394
chrMT	16571	5884	0.3551	0.8149
chrX	155270560	264424280	1.703	15.346
chrY	59373566	2479006	0.0418	1.4937

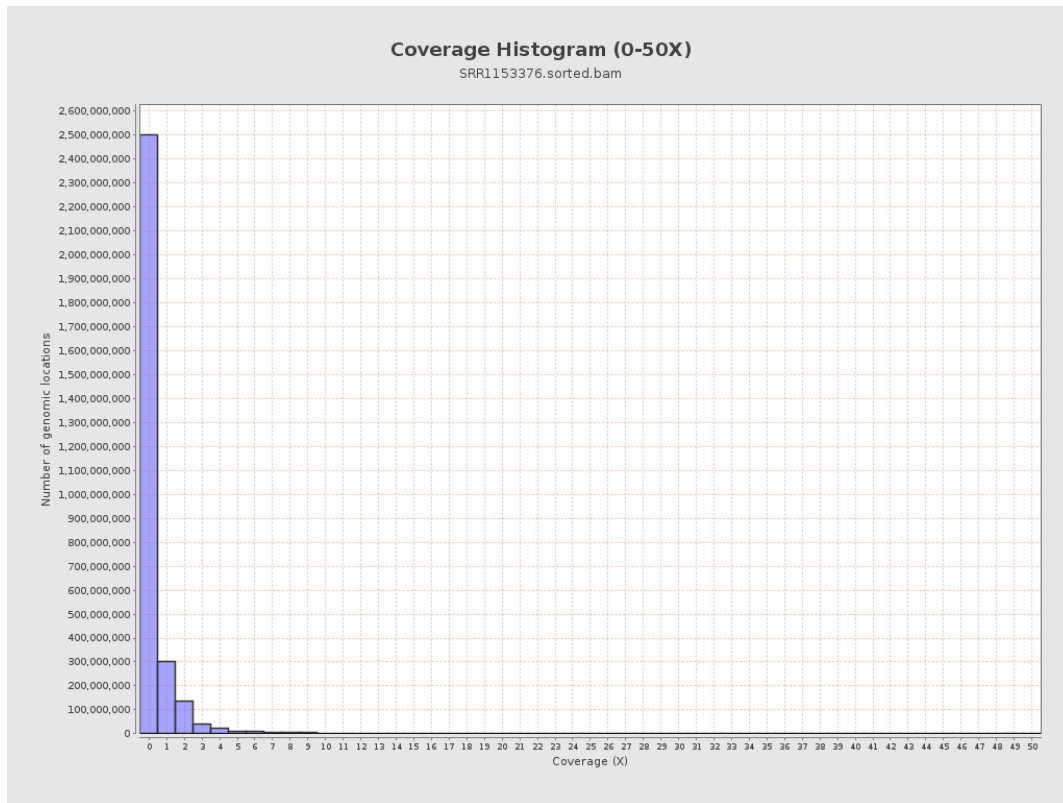
3. Results : Coverage across reference



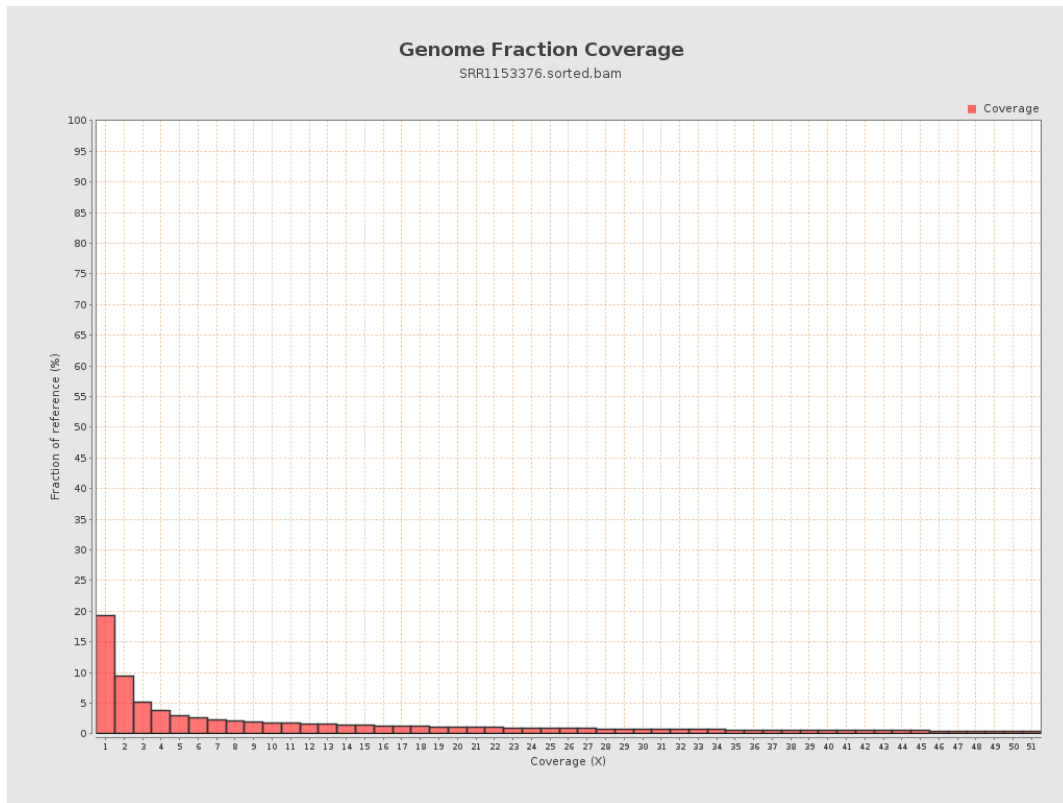
4. Results : Coverage Histogram



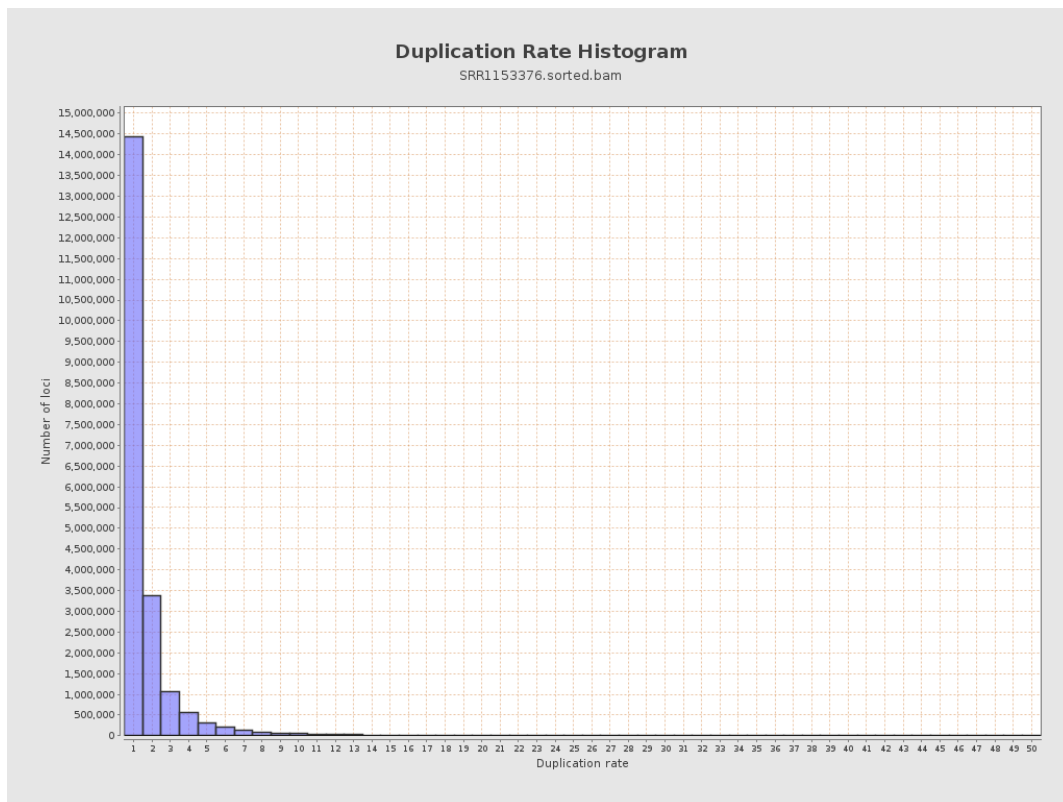
5. Results : Coverage Histogram (0-50X)



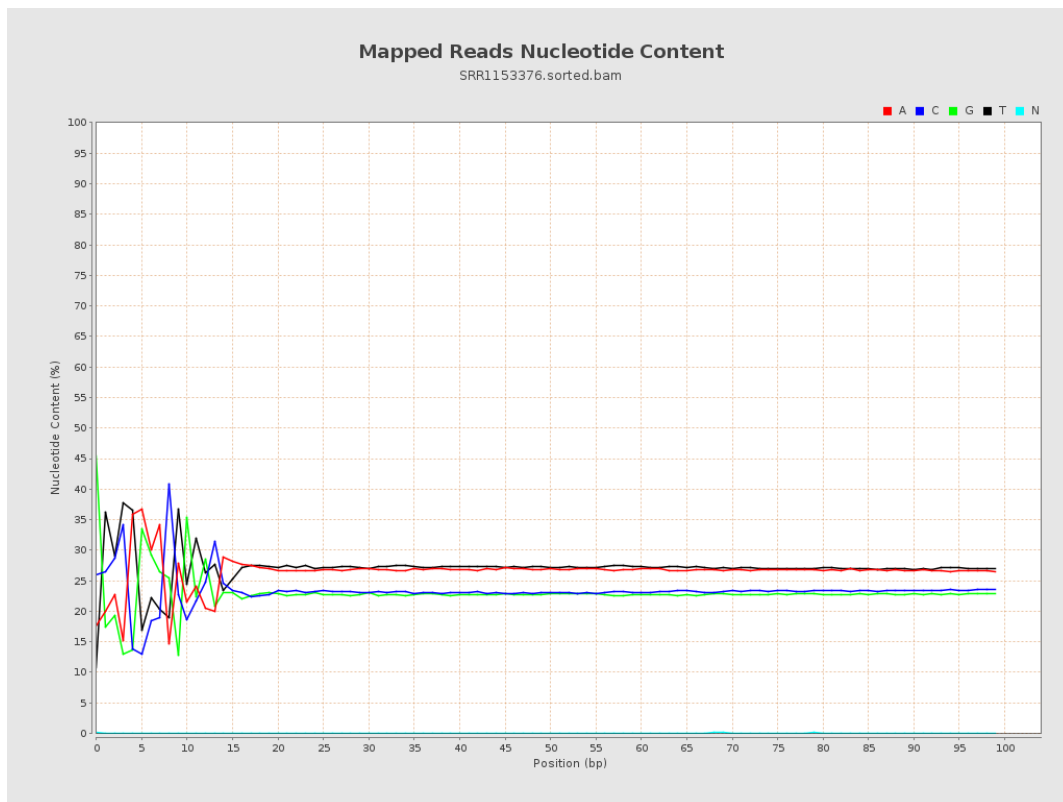
6. Results : Genome Fraction Coverage



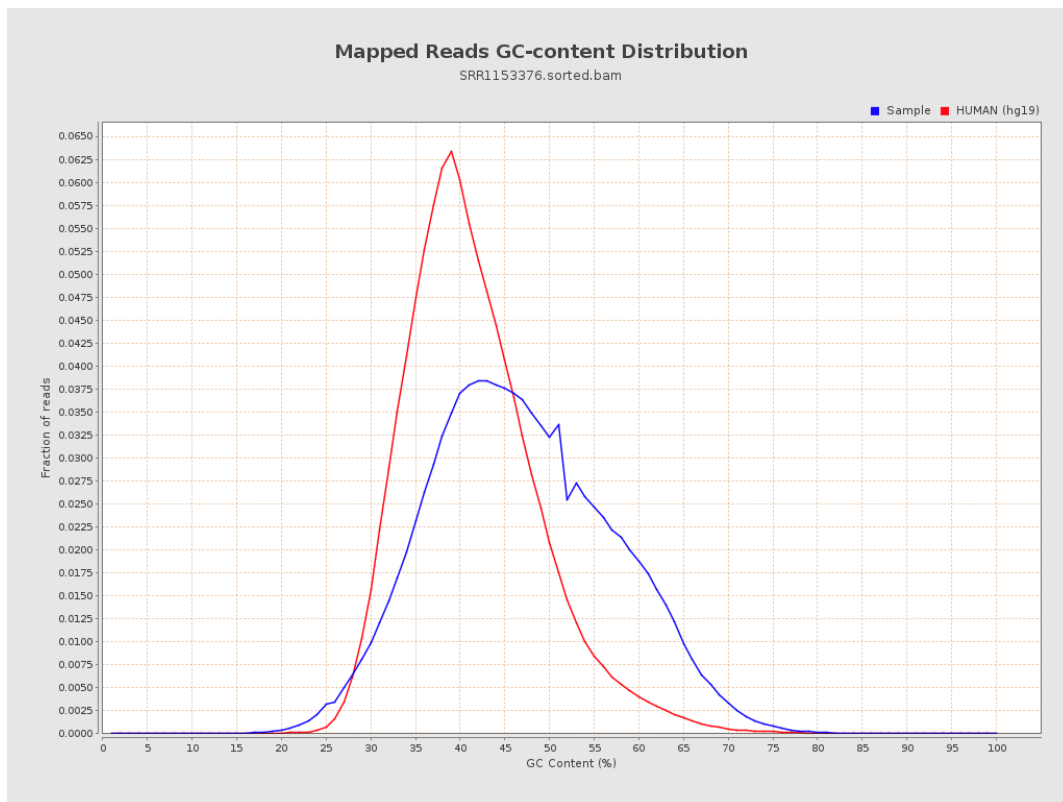
7. Results : Duplication Rate Histogram



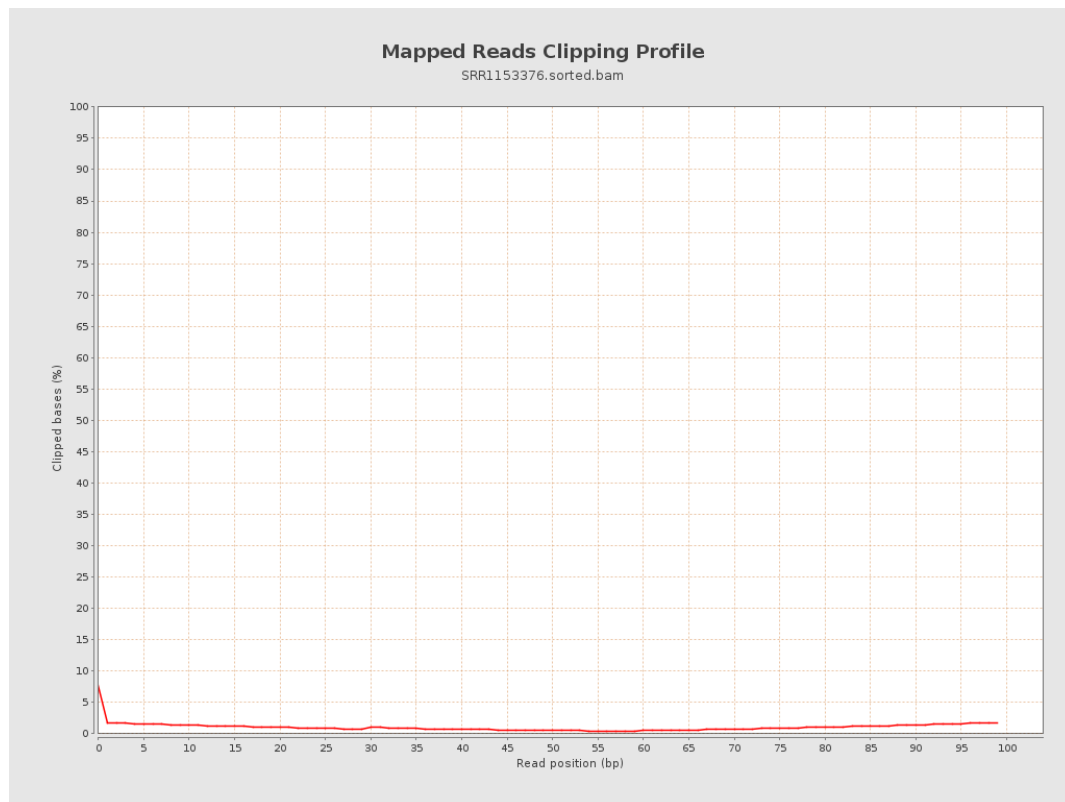
8. Results : Mapped Reads Nucleotide Content



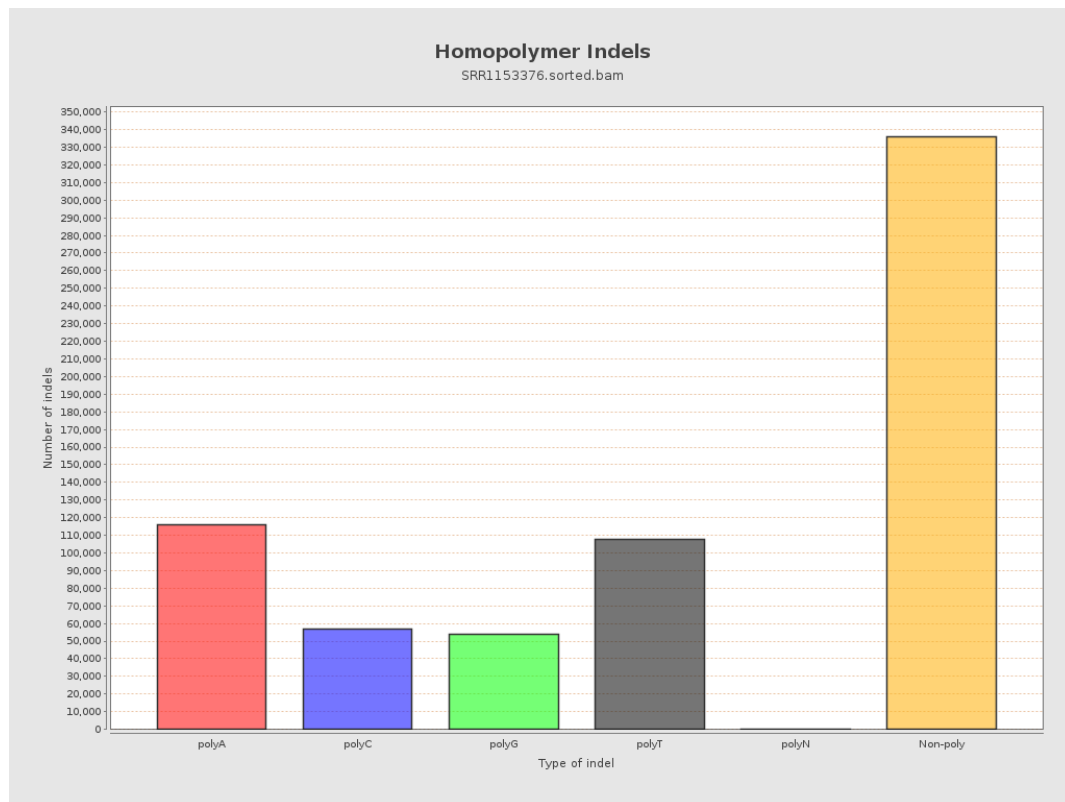
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

