

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/16 17:58:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1153380.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_SRR1153380 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1153380.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Dec 16 17:58:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1153380.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	41,837,836
Mapped reads	41,498,080 / 99.19%
Unmapped reads	339,756 / 0.81%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	335,540 / 0.8%
Read min/max/mean length	30 / 100 / 100.33
Duplicated reads (estimated)	20,086,970 / 48.01%
Duplication rate	31.74%
Clipped reads	5,705,545 / 13.64%

2.2. ACGT Content

Number/percentage of A's	1,054,424,832 / 26.2%
Number/percentage of C's	954,183,742 / 23.7%
Number/percentage of T's	1,074,818,829 / 26.7%
Number/percentage of G's	940,162,558 / 23.36%
Number/percentage of N's	1,691,278 / 0.04%
GC Percentage	47.06%

2.3. Coverage

Mean	1.3005

Standard Deviation	13.0341
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2.4. Mapping Quality

Mean Mapping Quality	49.76
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2.5. Mismatches and indels

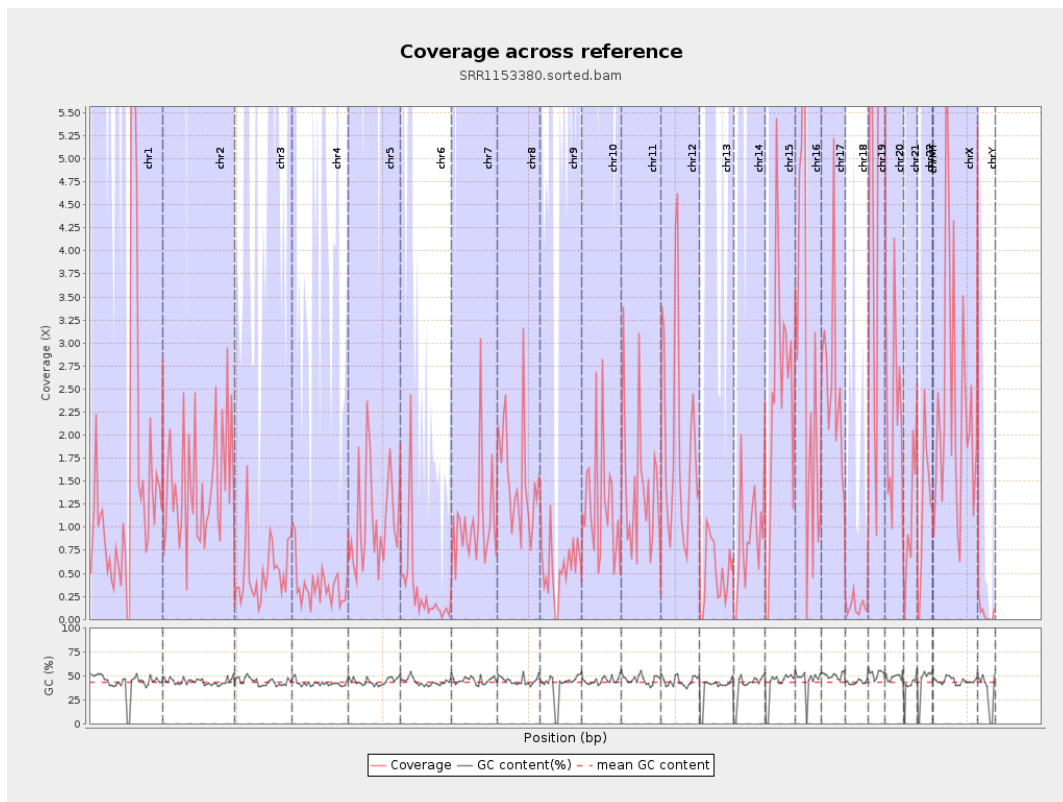
General error rate	0.3%
Mismatches	11,360,562
Insertions	435,242
Mapped reads with at least one insertion	1.04%
Deletions	342,996
Mapped reads with at least one deletion	0.82%
Homopolymer indels	49.85%

2.6. Chromosome stats

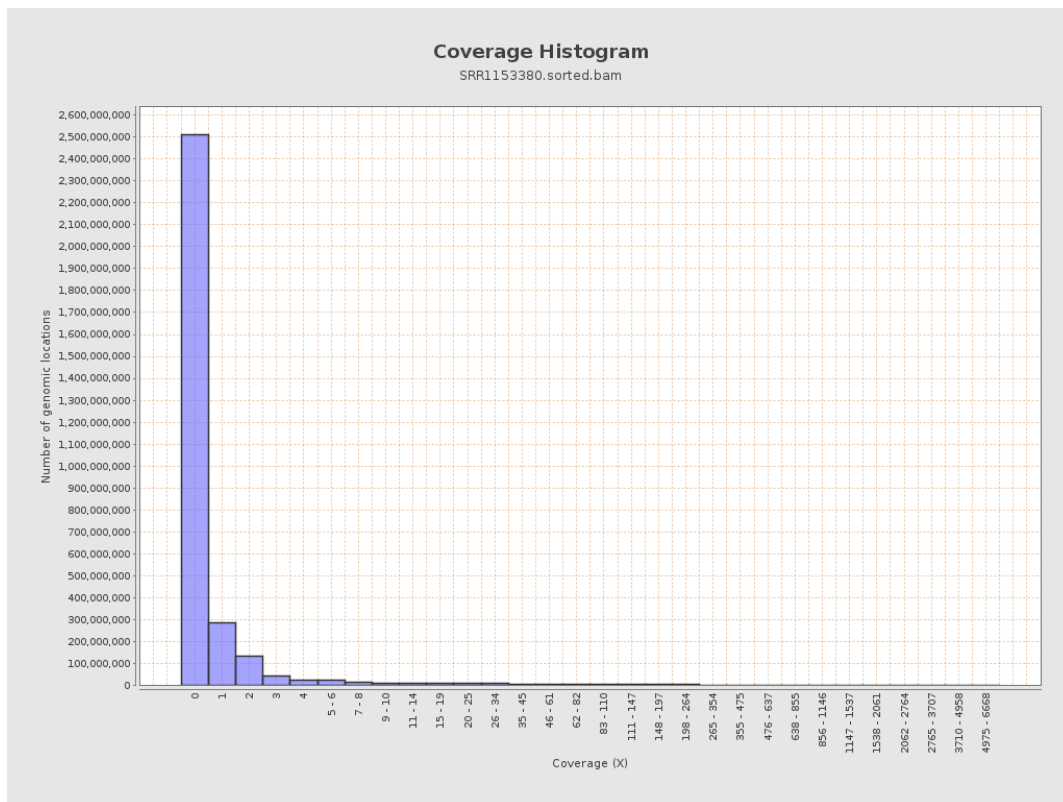
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	362813507	1.4556	15.607
chr2	243199373	355141294	1.4603	11.5436
chr3	198022430	102562819	0.5179	5.0626
chr4	191154276	70478453	0.3687	4.3864
chr5	180915260	198047955	1.0947	9.8652
chr6	171115067	52256148	0.3054	5.4009
chr7	159138663	165573394	1.0404	8.8923

chr8	146364022	222022318	1.5169	13.8492
chr9	141213431	77538948	0.5491	4.9558
chr10	135534747	168473179	1.243	9.9774
chr11	135006516	191189212	1.4161	11.0016
chr12	133851895	262494012	1.9611	14.3374
chr13	115169878	58605764	0.5089	5.4357
chr14	107349540	91826062	0.8554	7.3506
chr15	102531392	239566881	2.3365	19.4417
chr16	90354753	249358422	2.7598	21.3464
chr17	81195210	213039547	2.6238	17.4168
chr18	78077248	11290480	0.1446	2.3308
chr19	59128983	307907293	5.2074	37.3747
chr20	63025520	137951484	2.1888	17.0644
chr21	48129895	56054717	1.1647	11.3731
chr22	51304566	62735160	1.2228	10.2305
chrMT	16571	14963	0.903	1.9286
chrX	155270560	365142161	2.3517	21.2887
chrY	59373566	3924975	0.0661	2.546

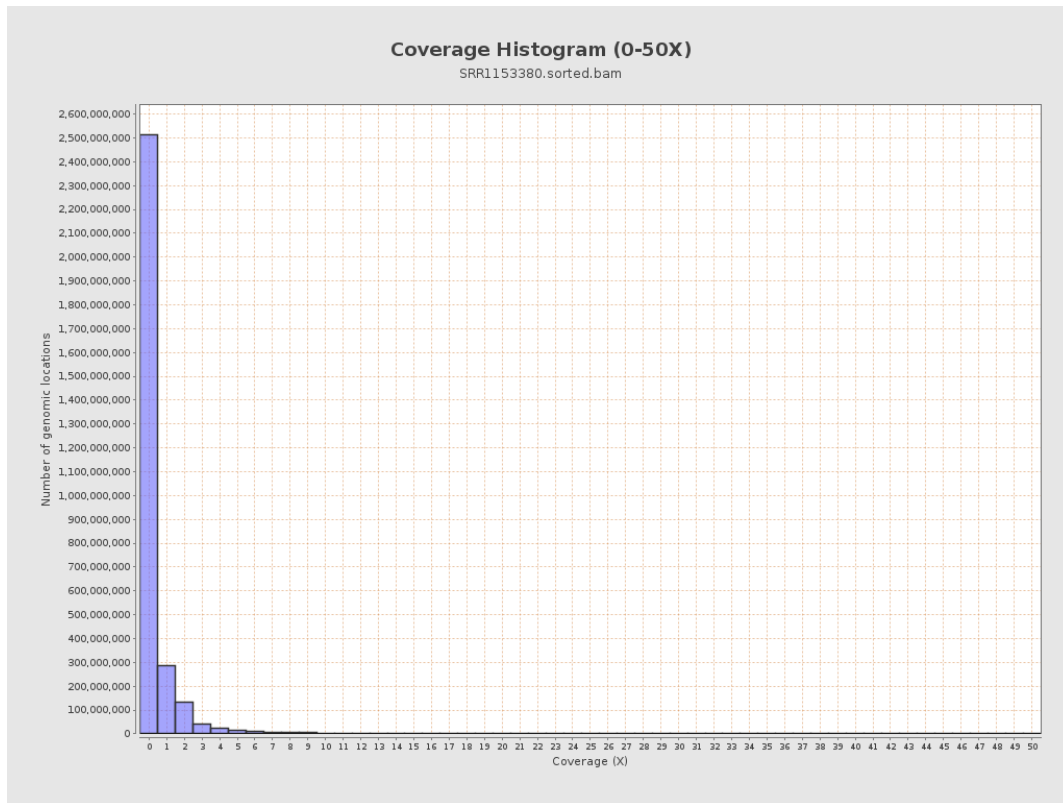
3. Results : Coverage across reference



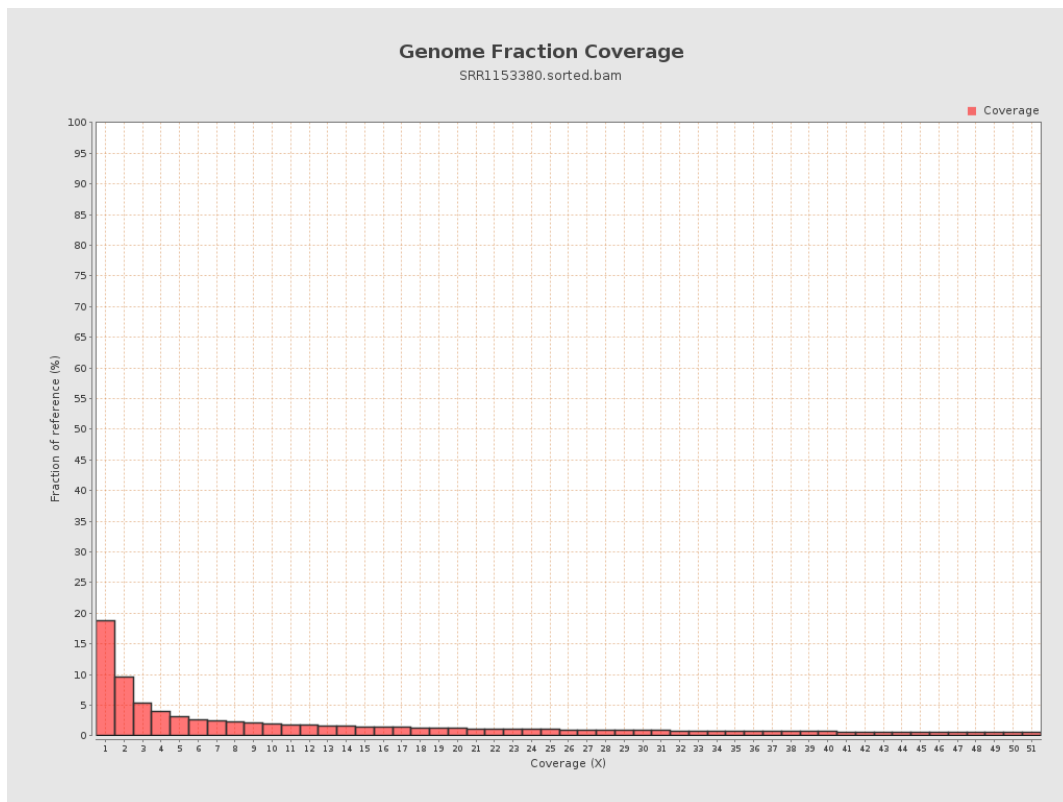
4. Results : Coverage Histogram



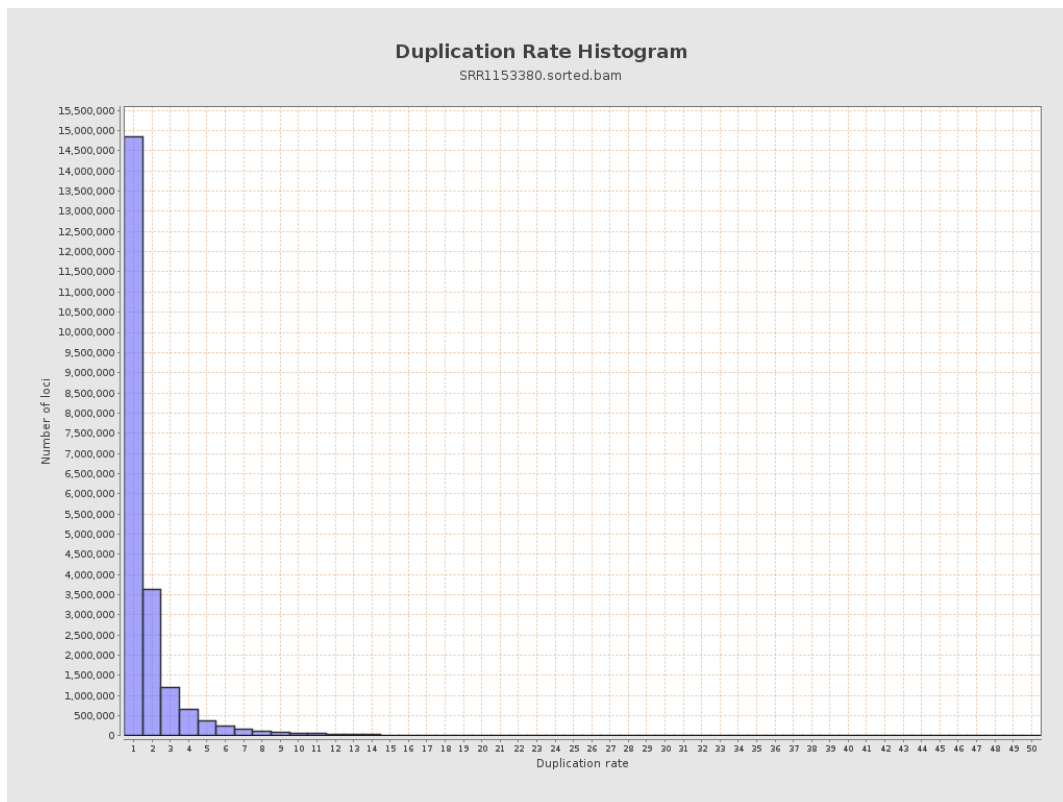
5. Results : Coverage Histogram (0-50X)



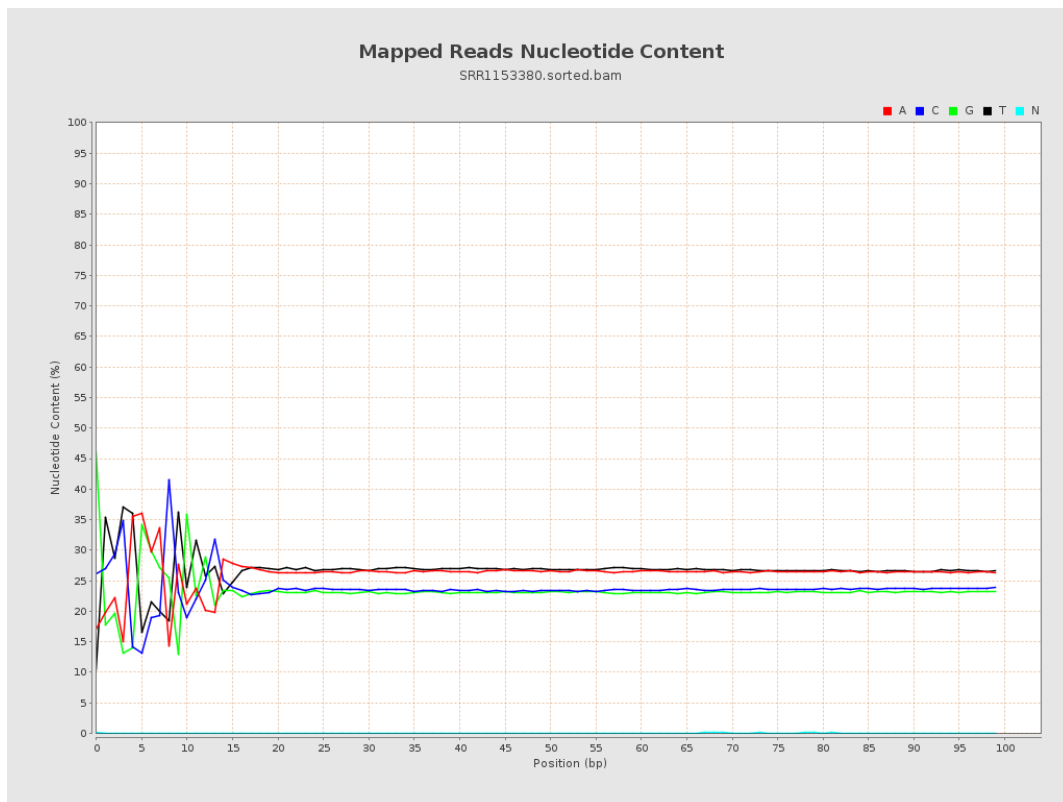
6. Results : Genome Fraction Coverage



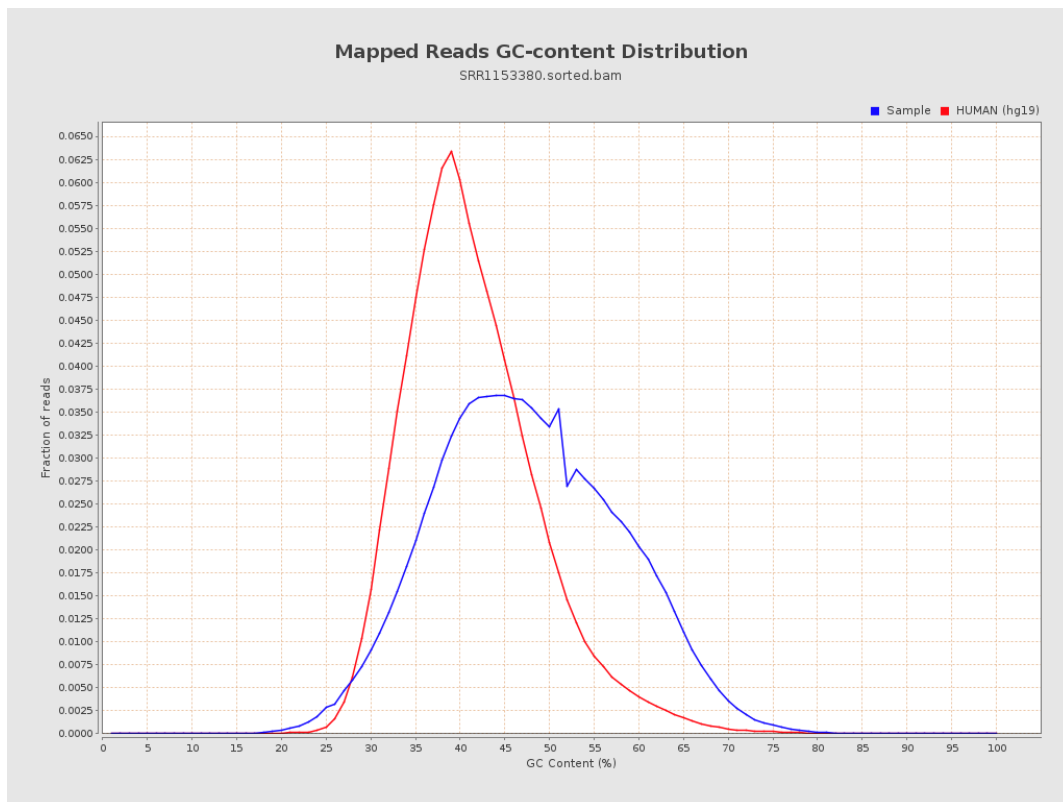
7. Results : Duplication Rate Histogram



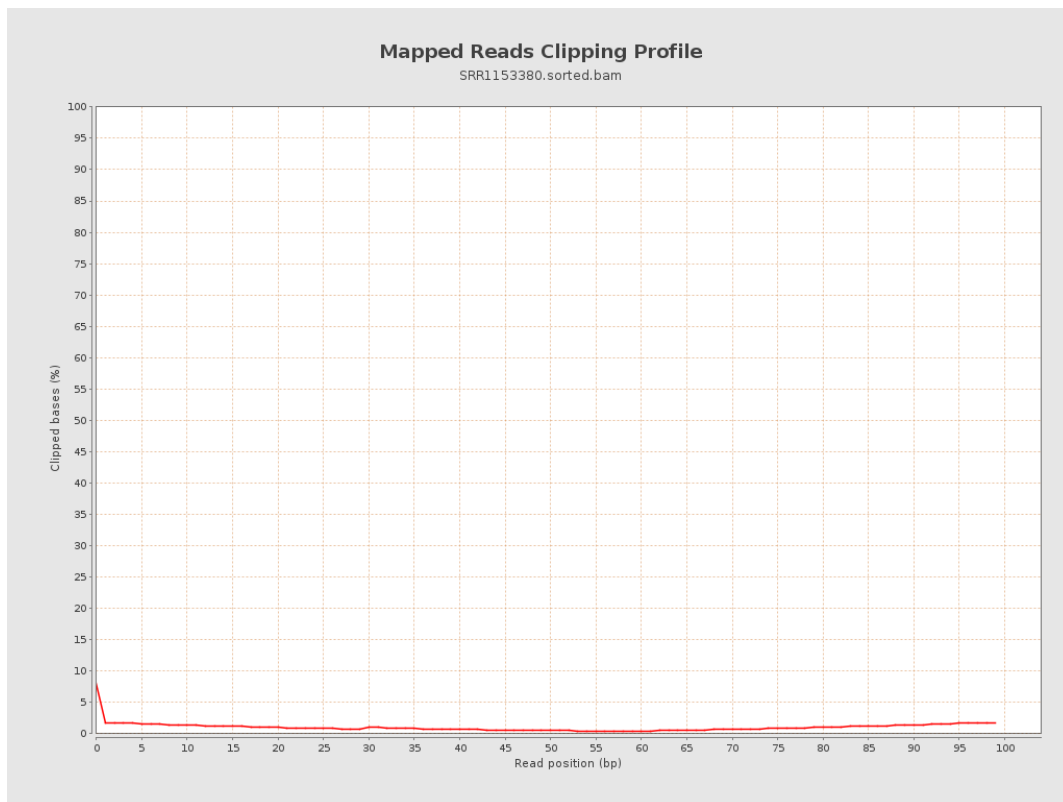
8. Results : Mapped Reads Nucleotide Content



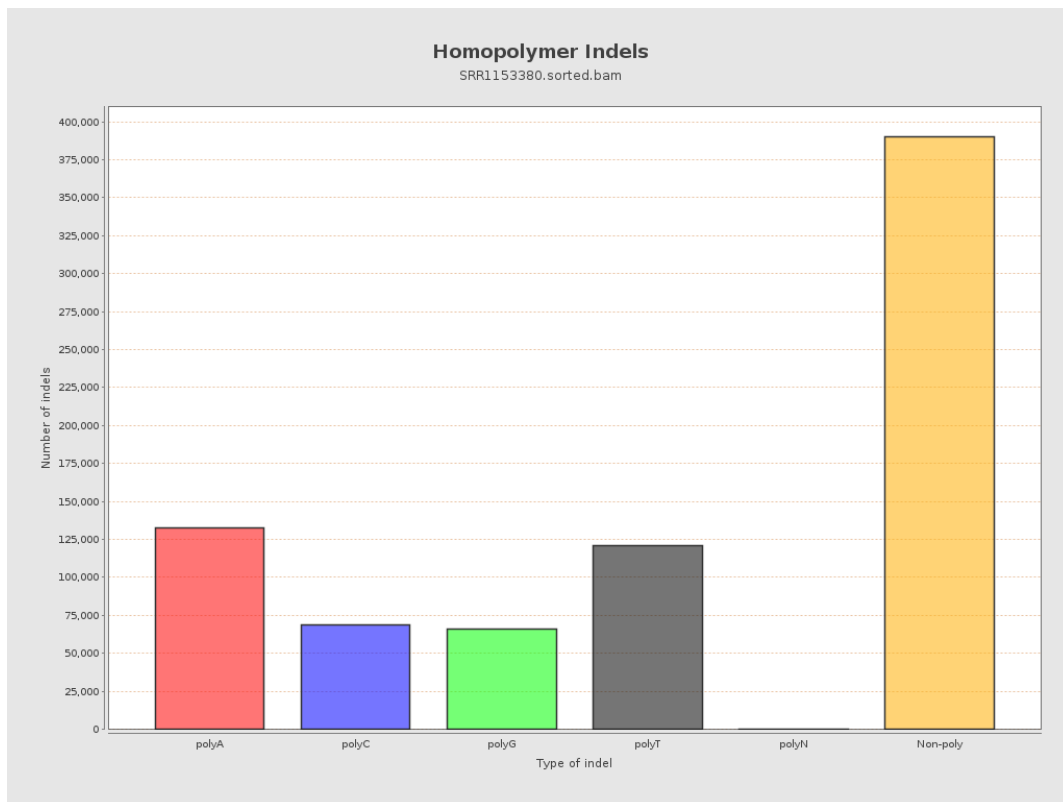
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

