

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/17 02:34:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1153392.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_SRR1153392 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1153392.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 17 02:34:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1153392.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	72,272,052
Mapped reads	71,714,379 / 99.23%
Unmapped reads	557,673 / 0.77%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	399,744 / 0.55%
Read min/max/mean length	30 / 100 / 100.23
Duplicated reads (estimated)	38,801,968 / 53.69%
Duplication rate	43.17%
Clipped reads	10,147,056 / 14.04%

2.2. ACGT Content

Number/percentage of A's	1,722,786,975 / 24.66%
Number/percentage of C's	1,768,938,625 / 25.32%
Number/percentage of T's	1,722,084,918 / 24.65%
Number/percentage of G's	1,771,388,392 / 25.36%
Number/percentage of N's	945,563 / 0.01%
GC Percentage	50.68%

2.3. Coverage

Mean	2.257

Standard Deviation	29.5719
--------------------	---------

2.4. Mapping Quality

Mean Mapping Quality	49.37
----------------------	-------

2.5. Mismatches and indels

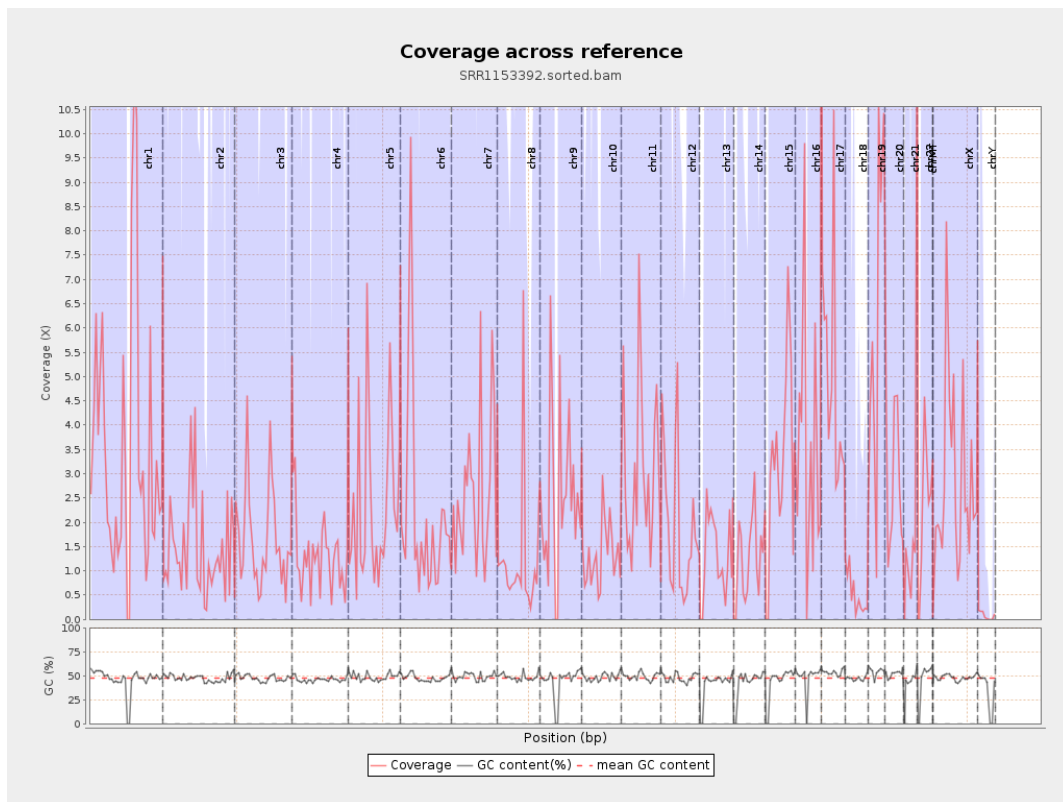
General error rate	0.3%
Mismatches	20,073,735
Insertions	507,454
Mapped reads with at least one insertion	0.7%
Deletions	328,379
Mapped reads with at least one deletion	0.45%
Homopolymer indels	45.09%

2.6. Chromosome stats

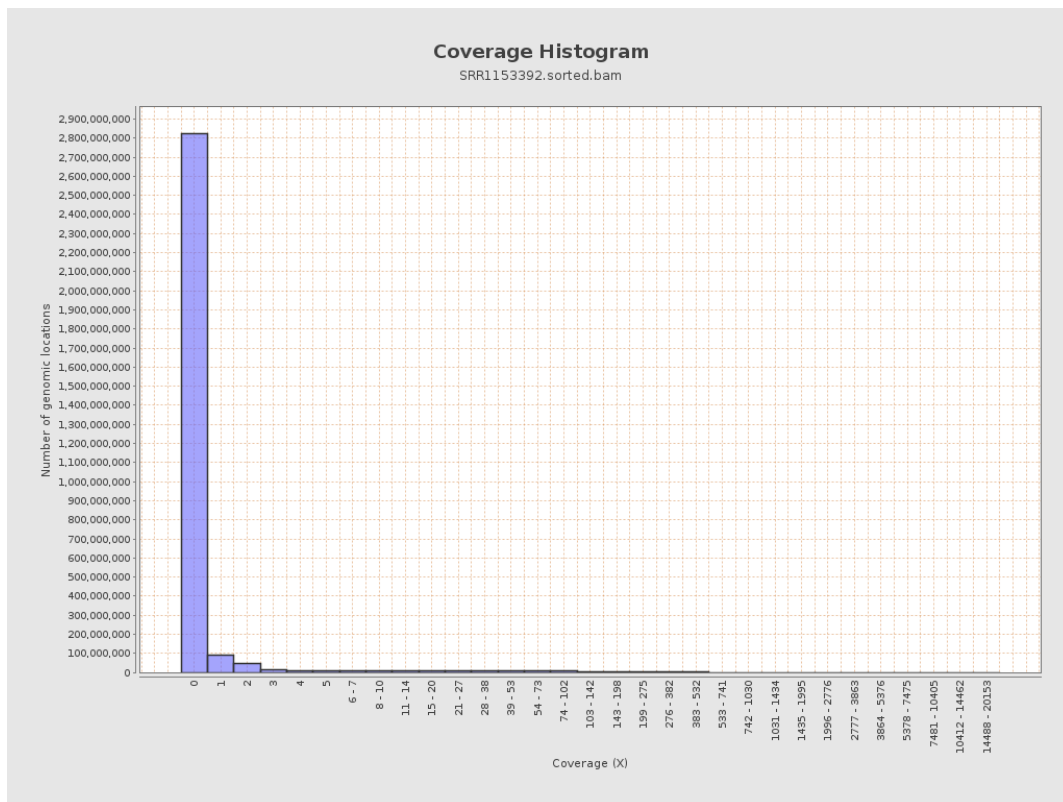
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	868857855	3.4859	33.8829
chr2	243199373	360415657	1.482	17.7637
chr3	198022430	334183413	1.6876	19.0418
chr4	191154276	249184387	1.3036	18.9209
chr5	180915260	437835039	2.4201	40.152
chr6	171115067	361699977	2.1138	25.1374
chr7	159138663	411397162	2.5851	33.3321

chr8	146364022	174715470	1.1937	22.9716
chr9	141213431	352323950	2.495	29.2045
chr10	135534747	179267897	1.3227	15.9772
chr11	135006516	416155939	3.0825	29.355
chr12	133851895	264048566	1.9727	22.6017
chr13	115169878	151612215	1.3164	19.8309
chr14	107349540	131302628	1.2231	16.2004
chr15	102531392	325861758	3.1782	33.468
chr16	90354753	307763643	3.4062	31.1183
chr17	81195210	406739832	5.0094	39.642
chr18	78077248	40377969	0.5172	8.573
chr19	59128983	366765988	6.2028	43.7319
chr20	63025520	176747337	2.8044	28.1859
chr21	48129895	110114986	2.2879	94.6435
chr22	51304566	116852110	2.2776	24.1496
chrMT	16571	704	0.0425	0.22
chrX	155270560	437888924	2.8202	33.2325
chrY	59373566	4806228	0.0809	5.6872

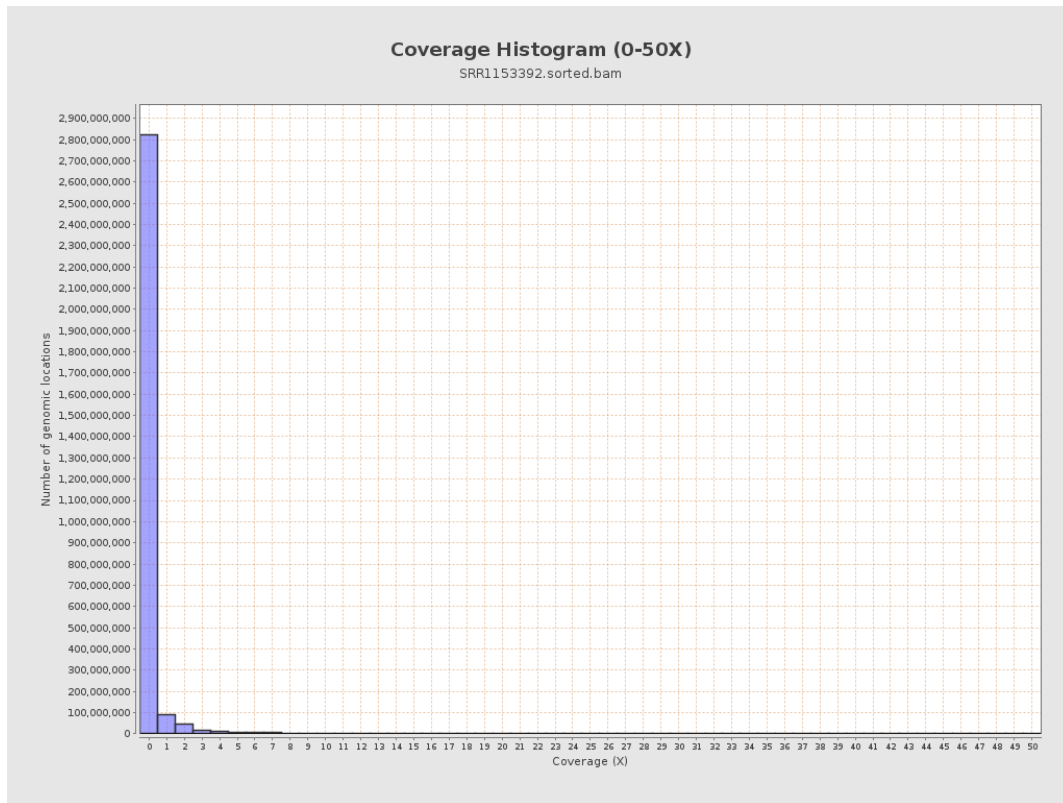
3. Results : Coverage across reference



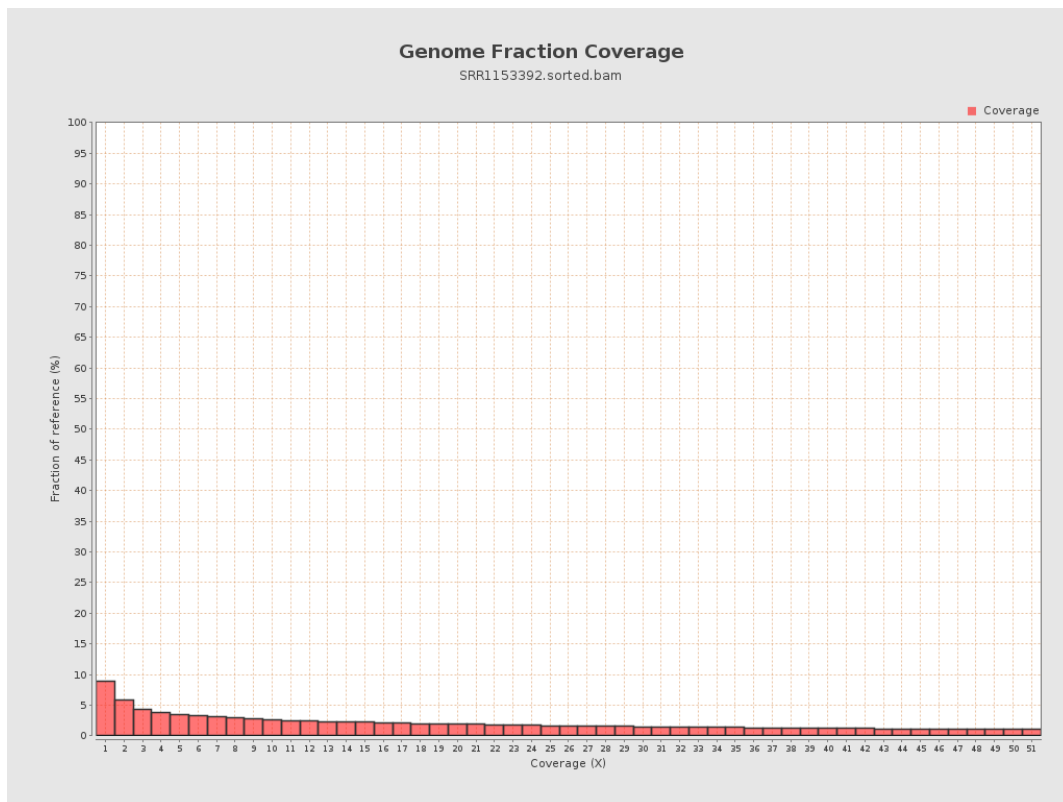
4. Results : Coverage Histogram



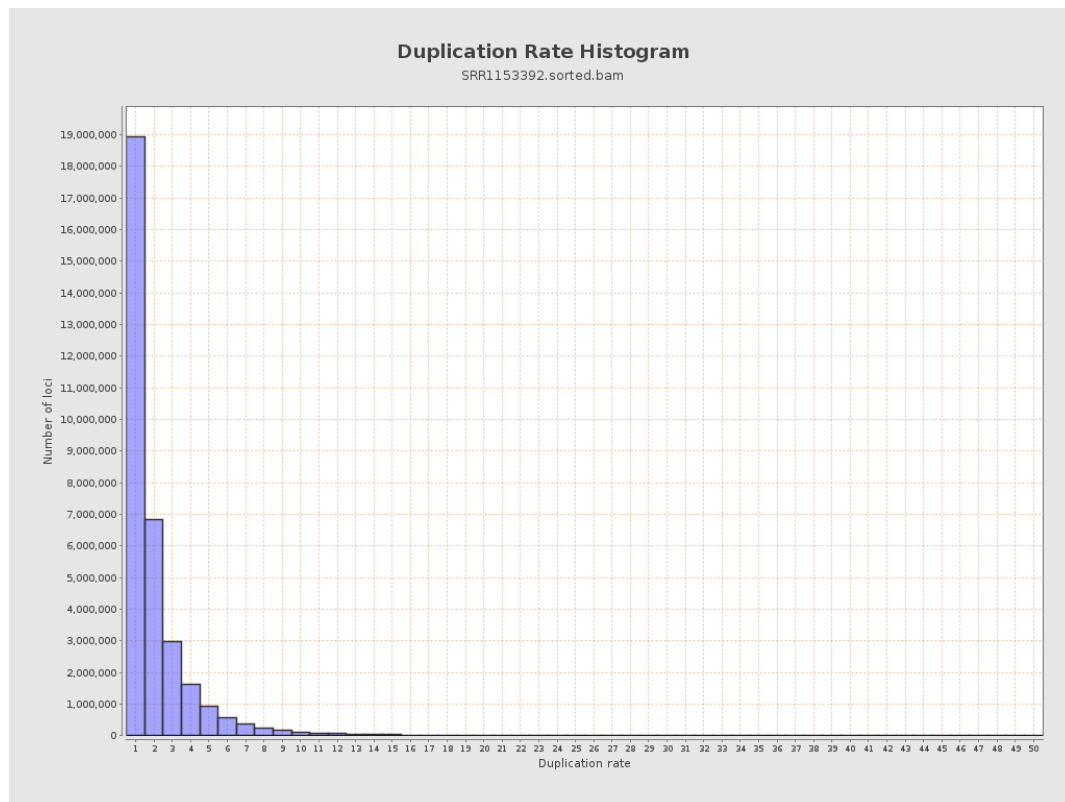
5. Results : Coverage Histogram (0-50X)



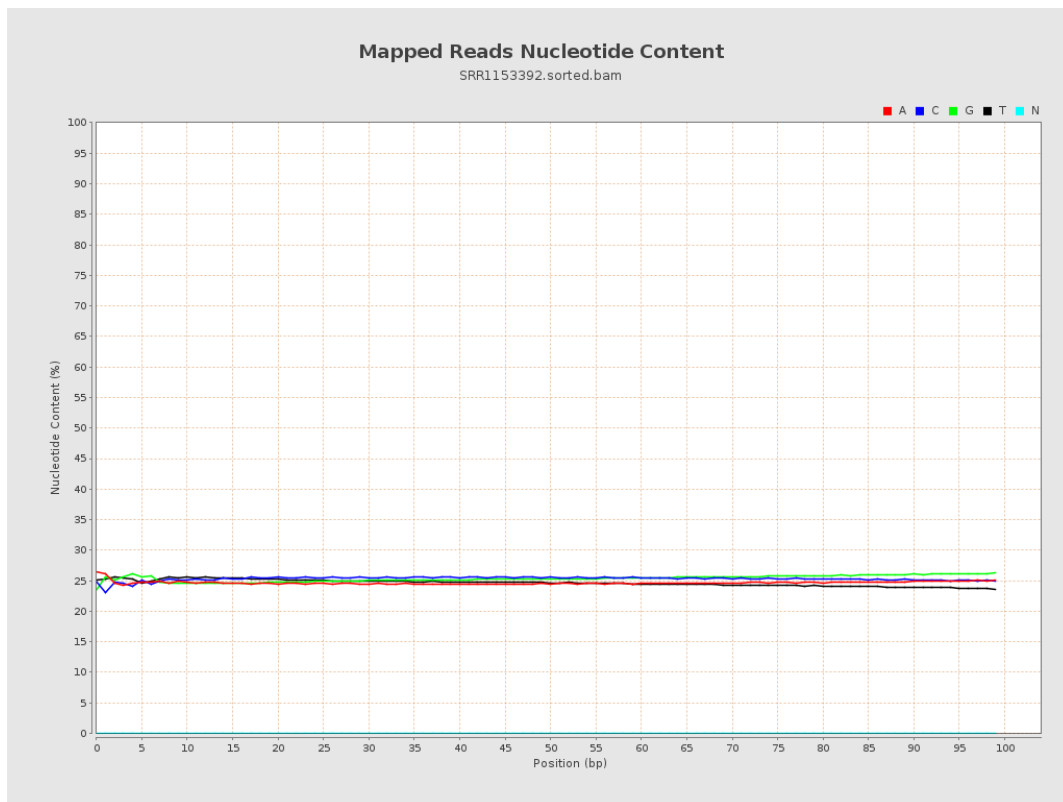
6. Results : Genome Fraction Coverage



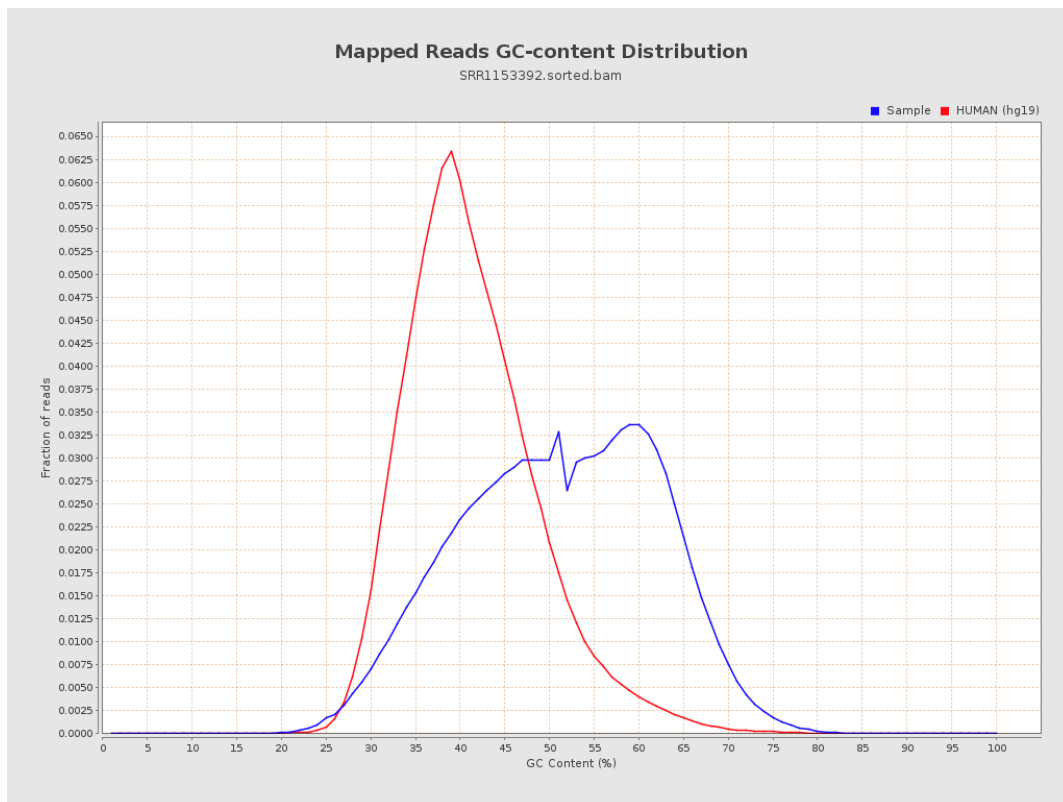
7. Results : Duplication Rate Histogram



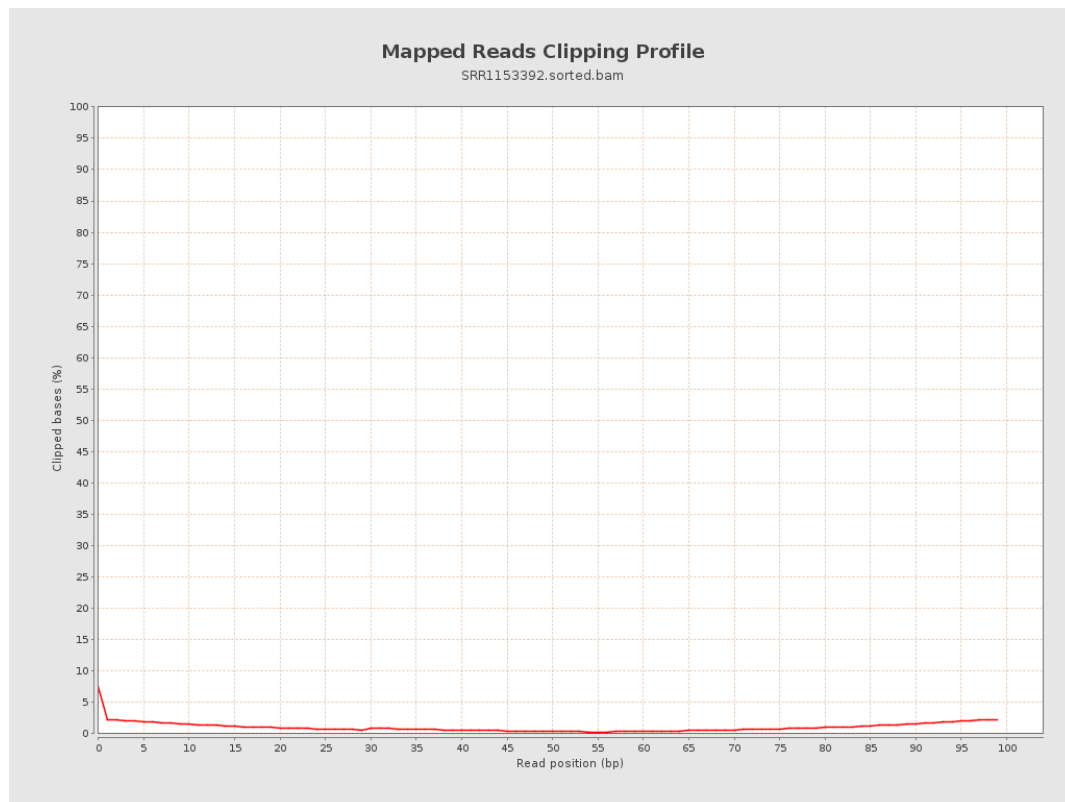
8. Results : Mapped Reads Nucleotide Content



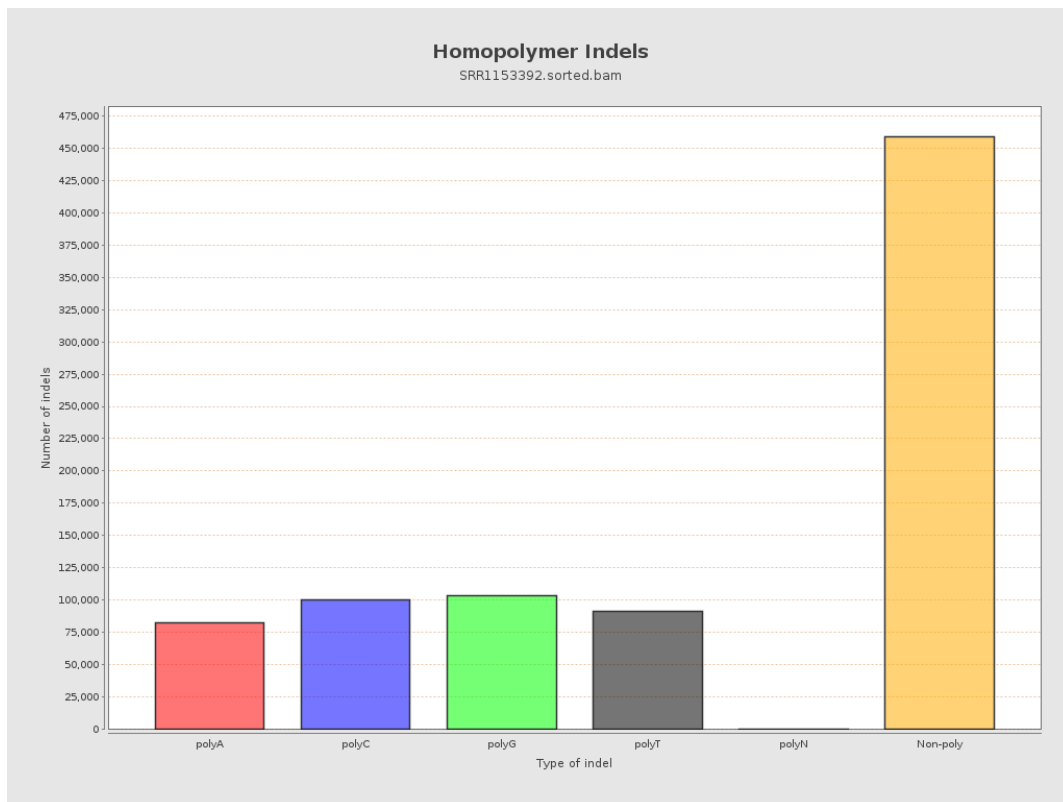
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

