Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/16 14:46:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1153372.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_SRR1153372 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1153372.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Dec 16 14:46:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1153372.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	63,640,482
Mapped reads	62,882,077 / 98.81%
Unmapped reads	758,405 / 1.19%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	349,196 / 0.55%
Read min/max/mean length	30 / 100 / 100.22
Duplicated reads (estimated)	26,654,721 / 41.88%
Duplication rate	34.83%
Clipped reads	2,555,707 / 4.02%

2.2. ACGT Content

Number/percentage of A's	1,621,743,225 / 25.92%
Number/percentage of C's	1,502,167,497 / 24.01%
Number/percentage of T's	1,633,003,940 / 26.1%
Number/percentage of G's	1,499,852,250 / 23.97%
Number/percentage of N's	289,340 / 0%
GC Percentage	47.98%

2.3. Coverage

Mean	2.0215

Standard Deviation	20.5531

2.4. Mapping Quality

Mean Mapping Quality	48.86

2.5. Mismatches and indels

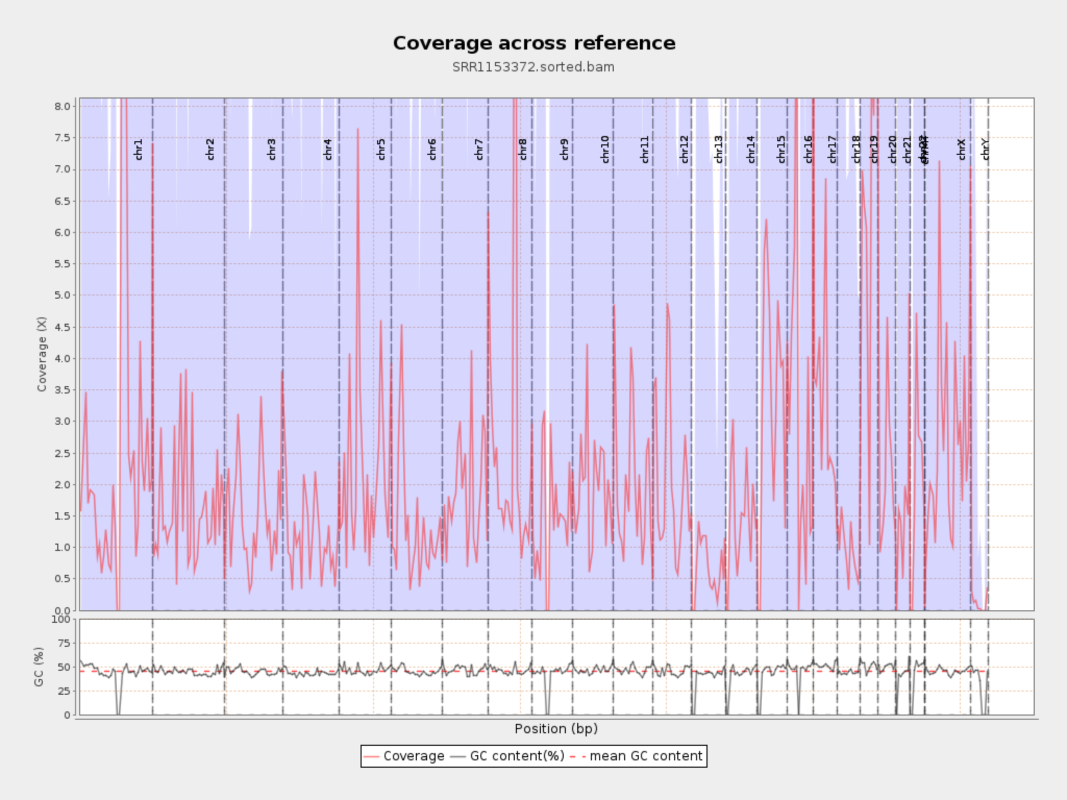
General error rate	0.31%
Mismatches	18,745,715
Insertions	547,502
Mapped reads with at least one insertion	0.86%
Deletions	378,696
Mapped reads with at least one deletion	0.59%
Homopolymer indels	48.15%

2.6. Chromosome stats

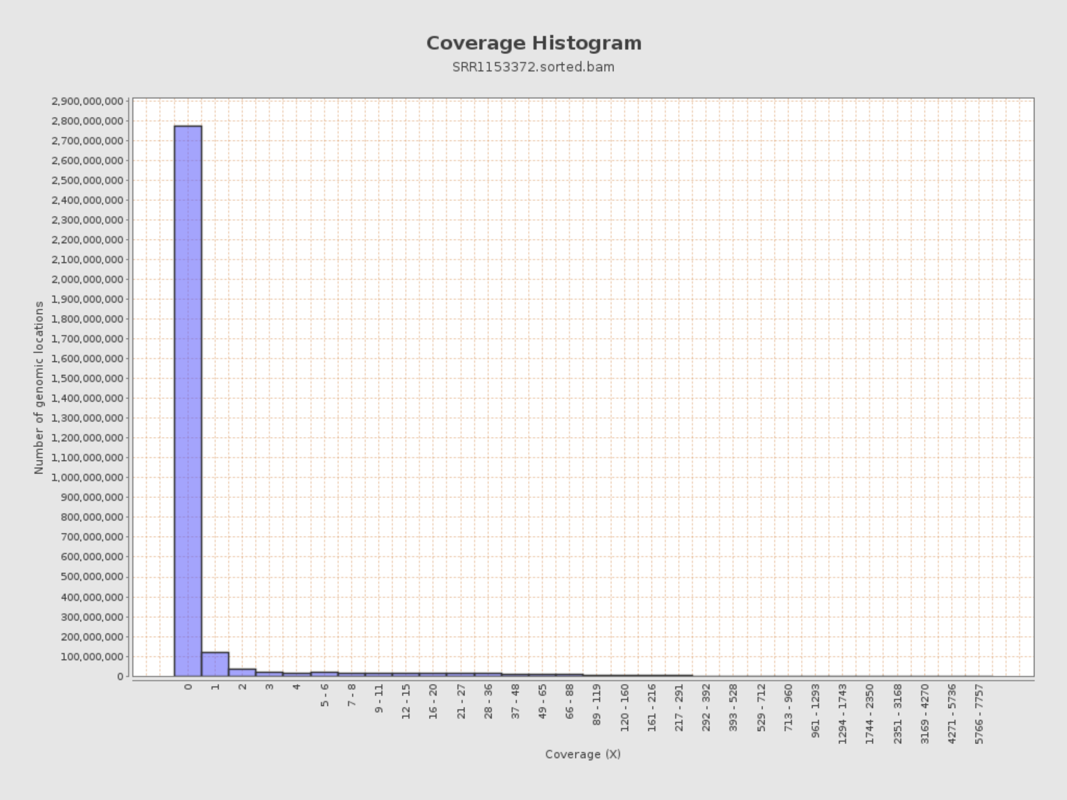
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	643730117	2.5827	21.975
chr2	243199373	400195499	1.6455	13.8442
chr3	198022430	302317868	1.5267	12.6635
chr4	191154276	233270684	1.2203	12.9214
chr5	180915260	416491938	2.3021	32.7841
chr6	171115067	223301648	1.305	11.324
chr7	159138663	297557310	1.8698	19.0693

chr8	146364022	367876035	2.5134	41.9326
chr9	141213431	205241231	1.4534	13.6848
chr10	135534747	267994741	1.9773	16.0376
chr11	135006516	275553692	2.041	15.1579
chr12	133851895	280128471	2.0928	15.9906
chr13	115169878	76269843	0.6622	7.0754
chr14	107349540	151507232	1.4113	12.1257
chr15	102531392	333022688	3.248	24.9331
chr16	90354753	288020126	3.1877	24.6482
chr17	81195210	264260836	3.2546	20.8554
chr18	78077248	72374874	0.927	8.9196
chr19	59128983	405123099	6.8515	36.5548
chr20	63025520	147397434	2.3387	16.8885
chr21	48129895	79041153	1.6422	26.9032
chr22	51304566	106068034	2.0674	16.4017
chrMT	16571	835	0.0504	0.2874
chrX	155270560	414106140	2.667	23.6638
chrY	59373566	7051331	0.1188	5.3875

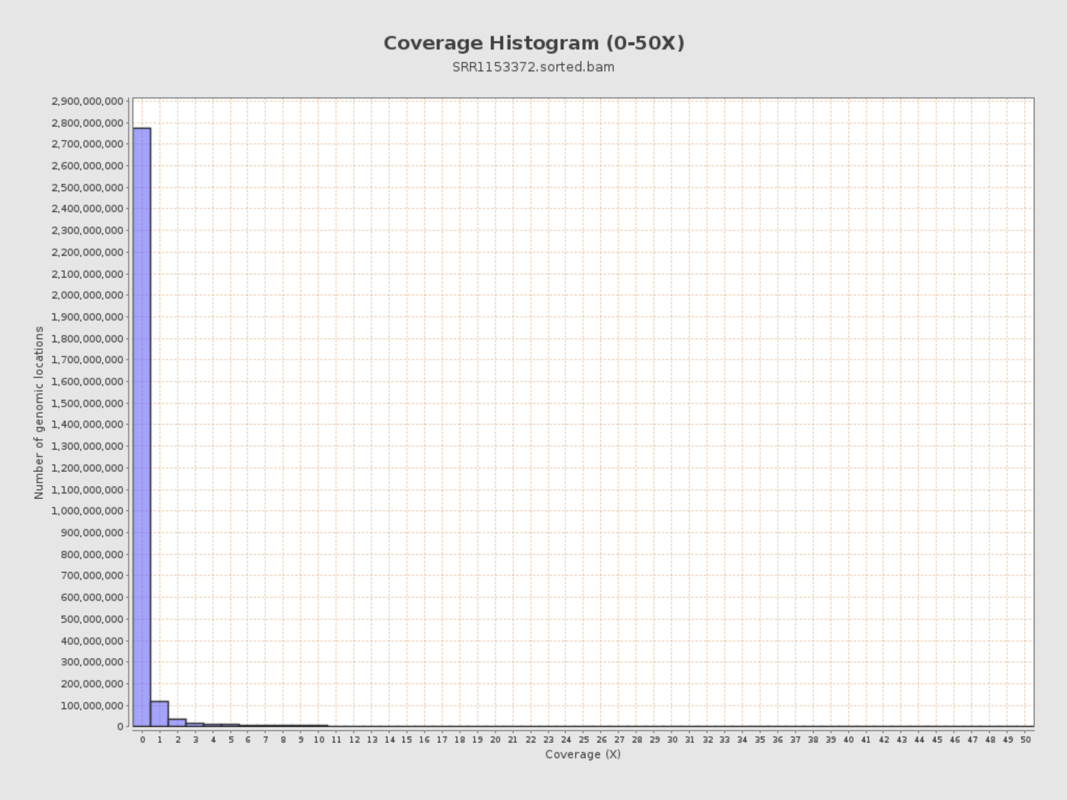
3. Results : Coverage across reference



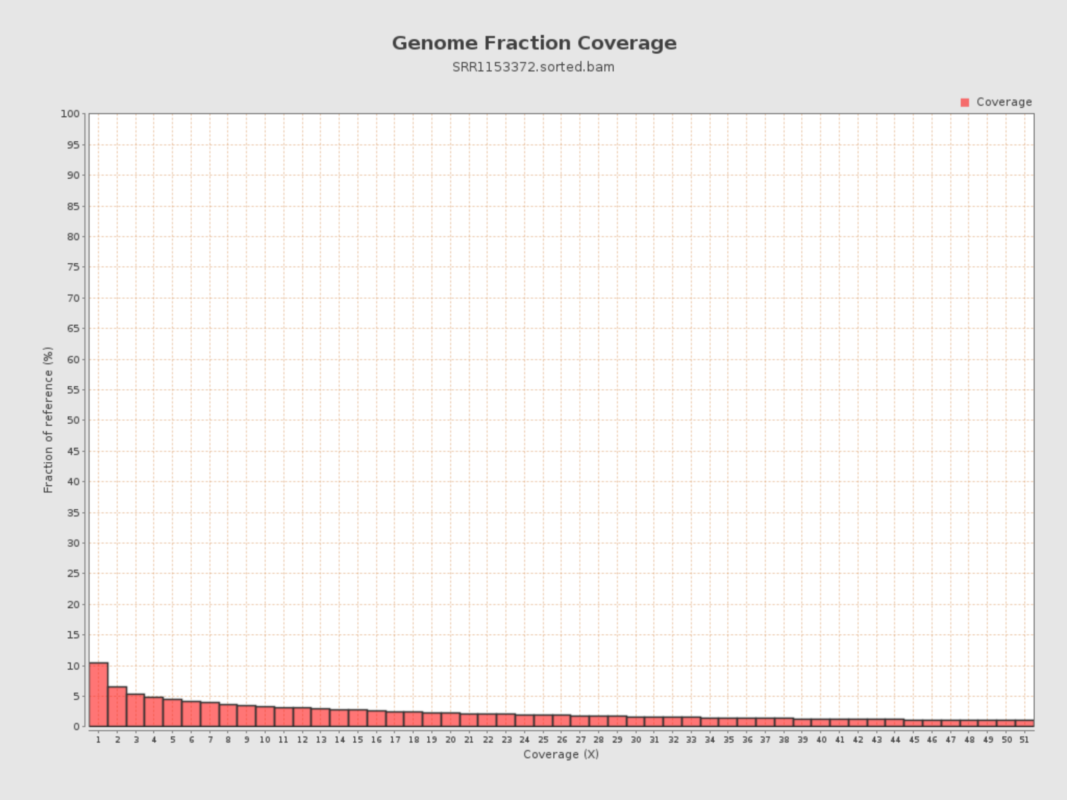
4. Results : Coverage Histogram



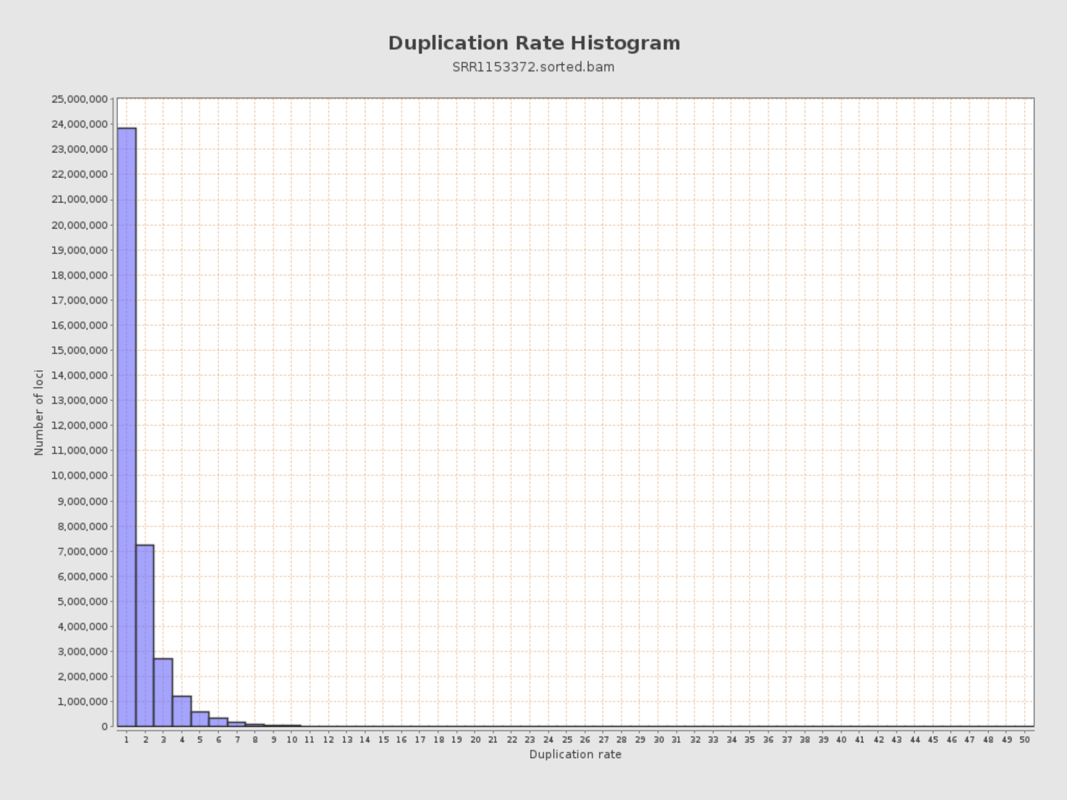
5. Results : Coverage Histogram (0-50X)



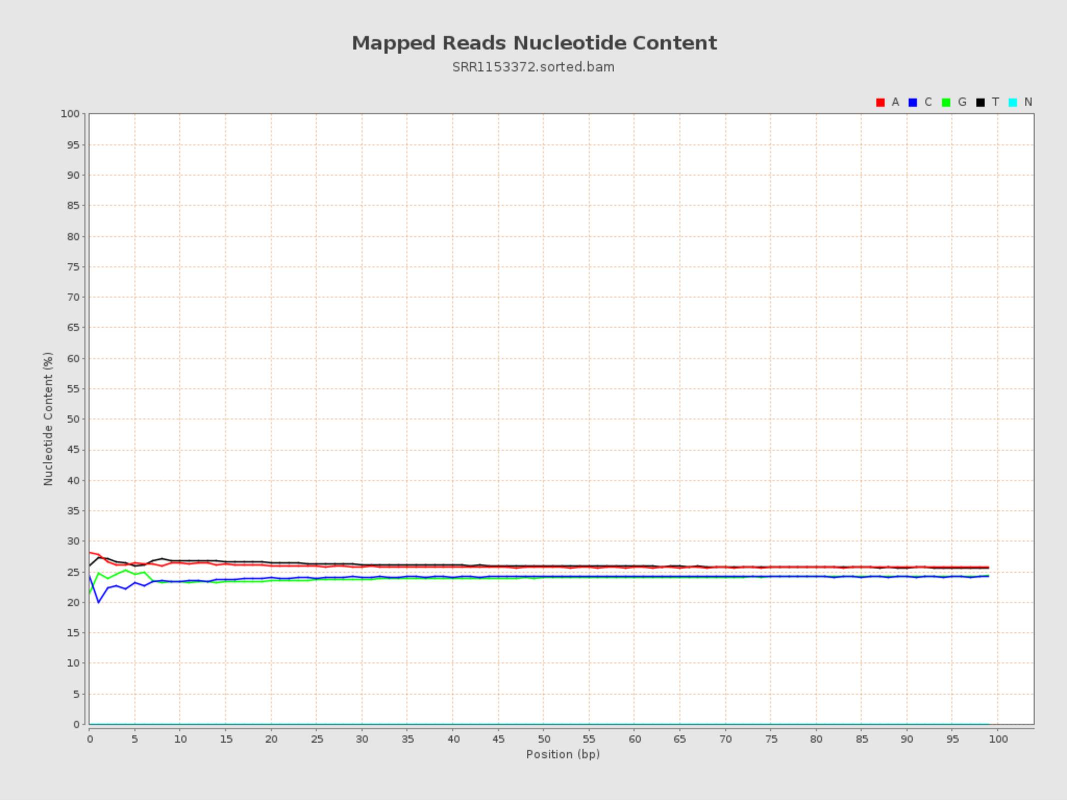
6. Results : Genome Fraction Coverage



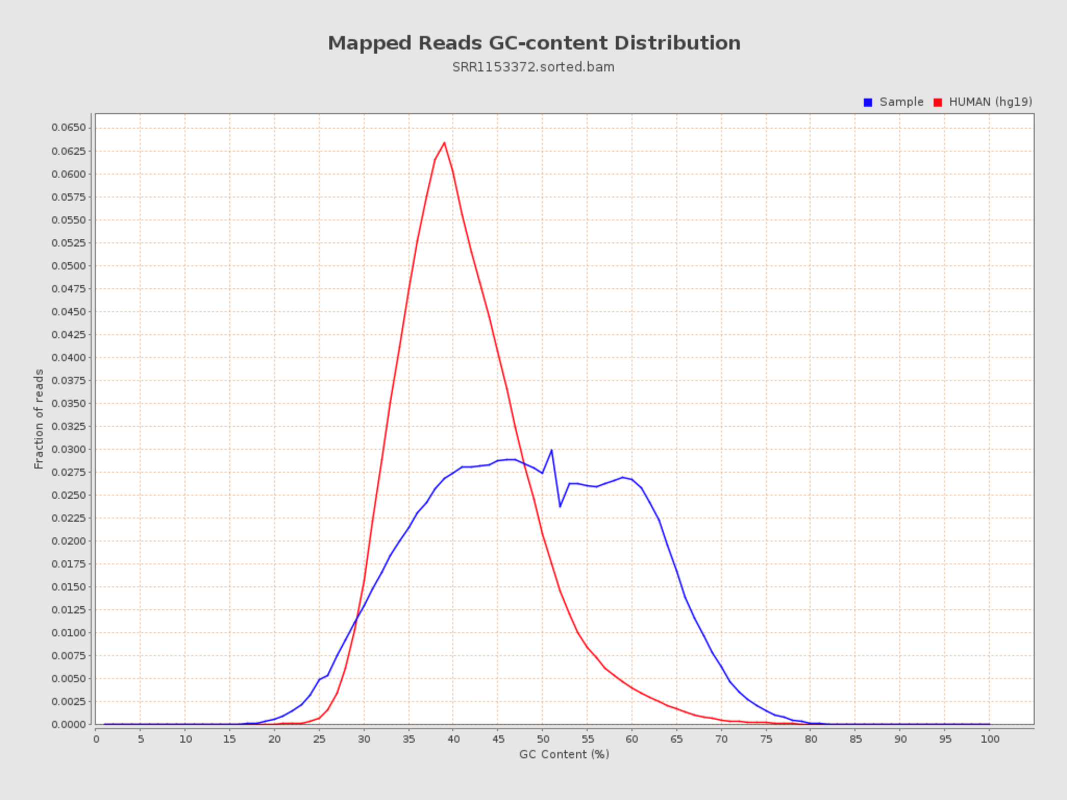
7. Results : Duplication Rate Histogram



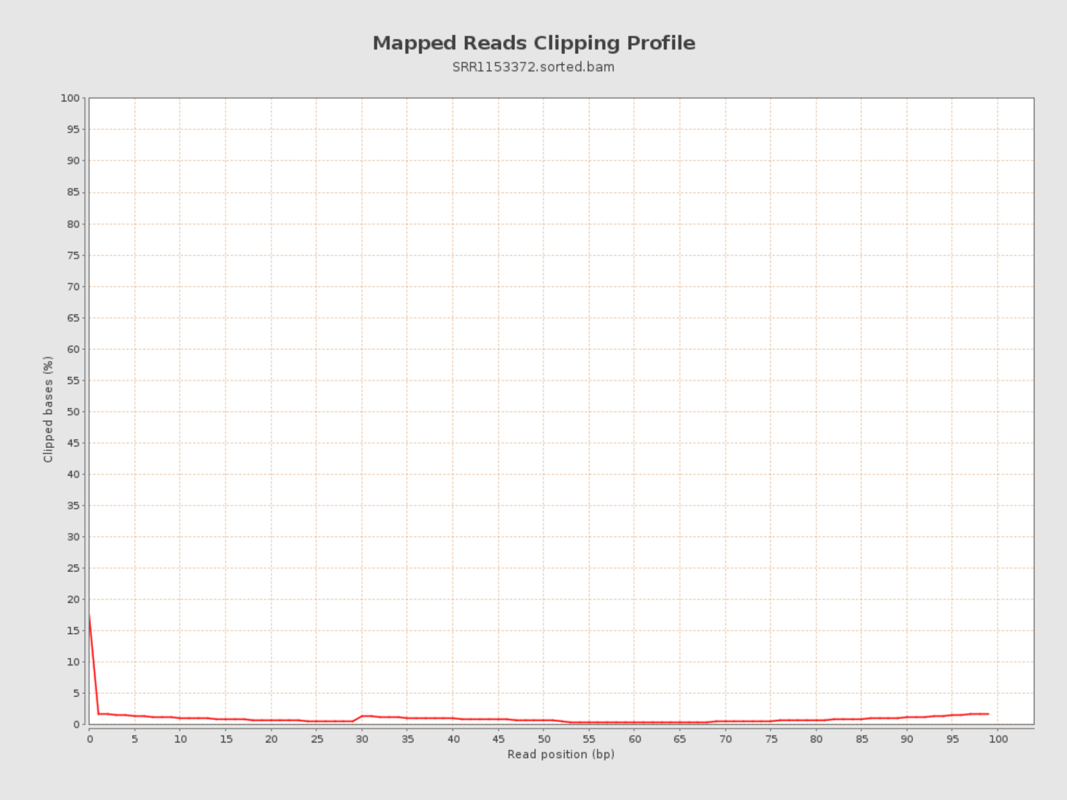
8. Results : Mapped Reads Nucleotide Content



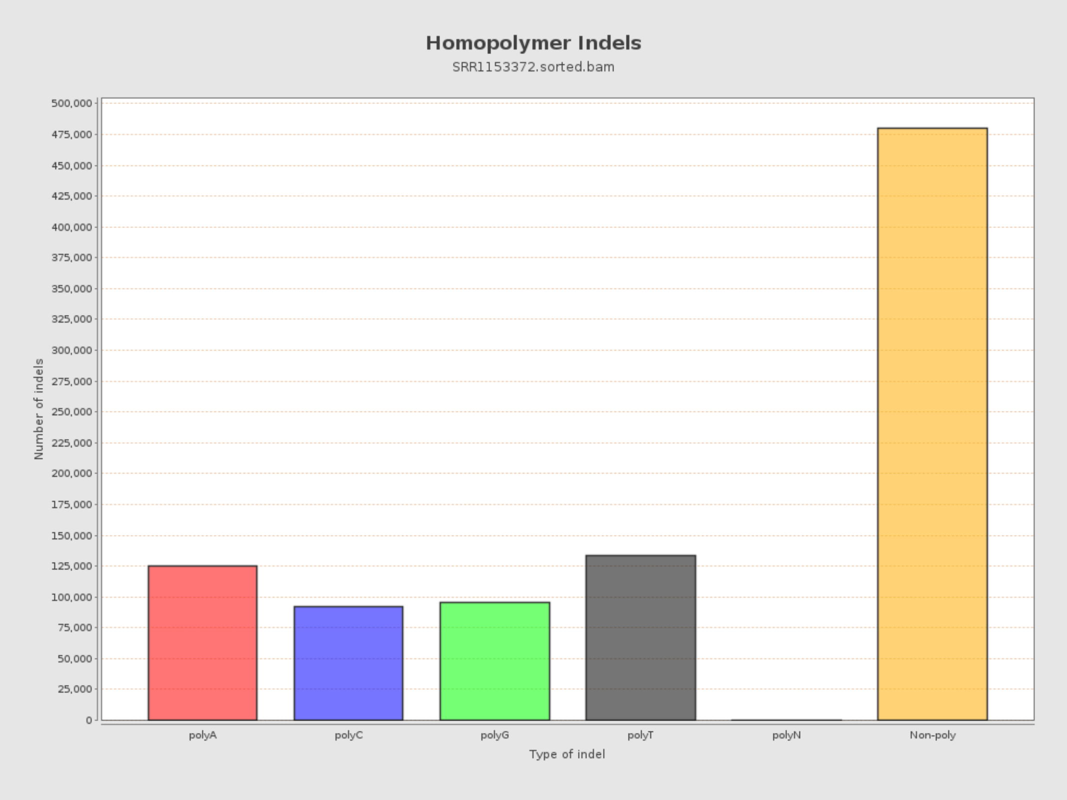
9. Results : Mapped Reads GC-content Distribution



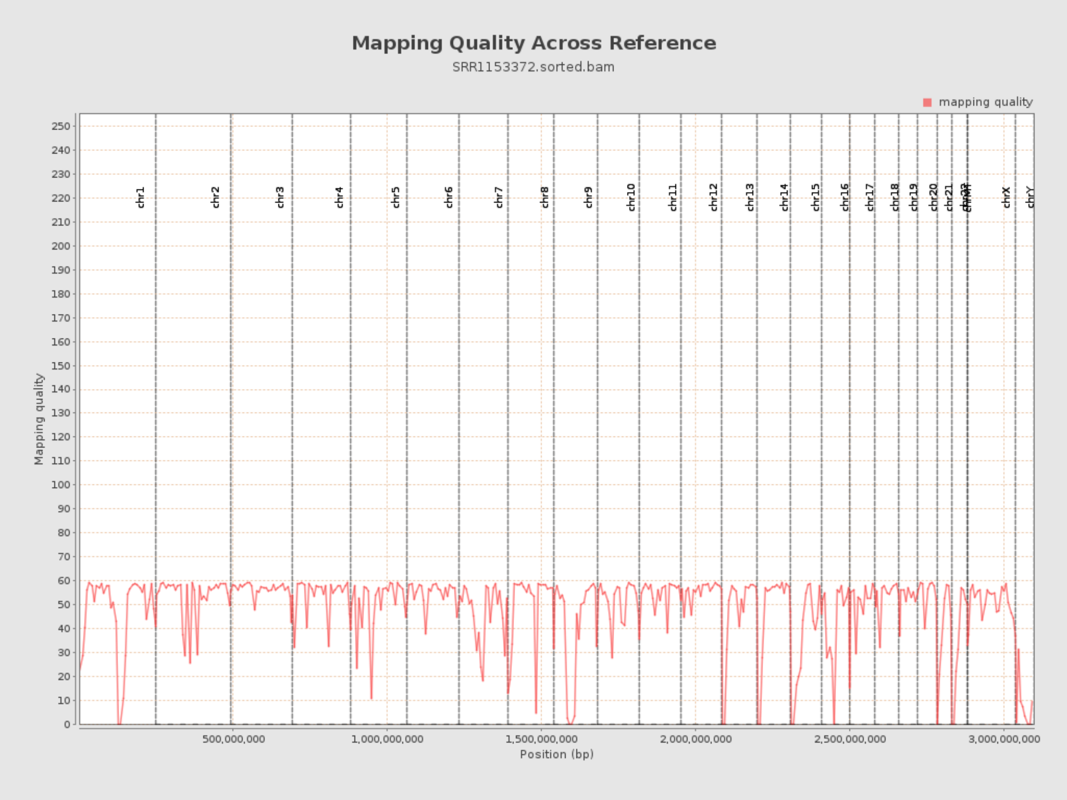
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram