Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 18:38:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8751197.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_SRR8751197 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8751197.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 18:38:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8751197.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,783,185
Mapped reads	7,686,490 / 98.76%
Unmapped reads	96,695 / 1.24%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	254,660 / 3.27%
Read min/max/mean length	30 / 151 / 152.72
Duplicated reads (estimated)	1,163,963 / 14.95%
Duplication rate	13.94%
Clipped reads	1,804,781 / 23.19%

2.2. ACGT Content

Number/percentage of A's	321,633,930 / 28.78%
Number/percentage of C's	237,185,313 / 21.22%
Number/percentage of T's	323,437,284 / 28.94%
Number/percentage of G's	235,317,426 / 21.06%
Number/percentage of N's	10,239 / 0%
GC Percentage	42.28%

2.3. Coverage

Mean	0.3611

Standard Deviation	2.1134

2.4. Mapping Quality

Mean Mapping Quality	52.53

2.5. Mismatches and indels

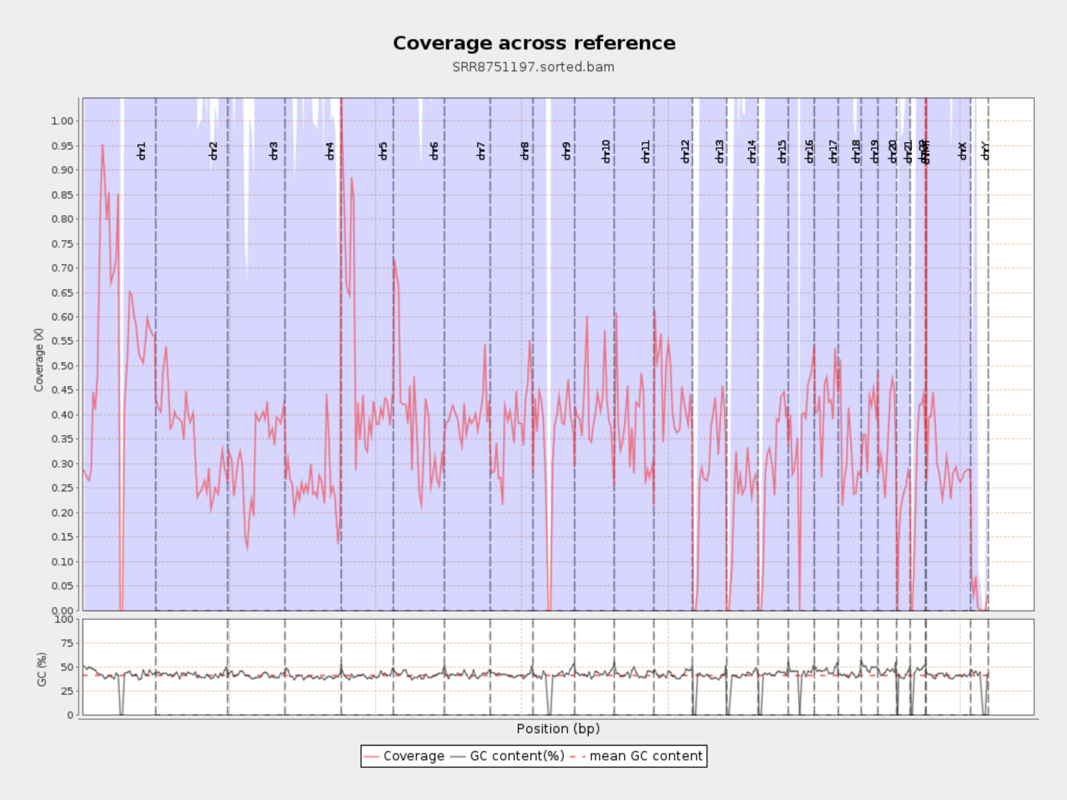
General error rate	0.76%
Mismatches	8,086,191
Insertions	239,473
Mapped reads with at least one insertion	3.02%
Deletions	137,669
Mapped reads with at least one deletion	1.74%
Homopolymer indels	49.56%

2.6. Chromosome stats

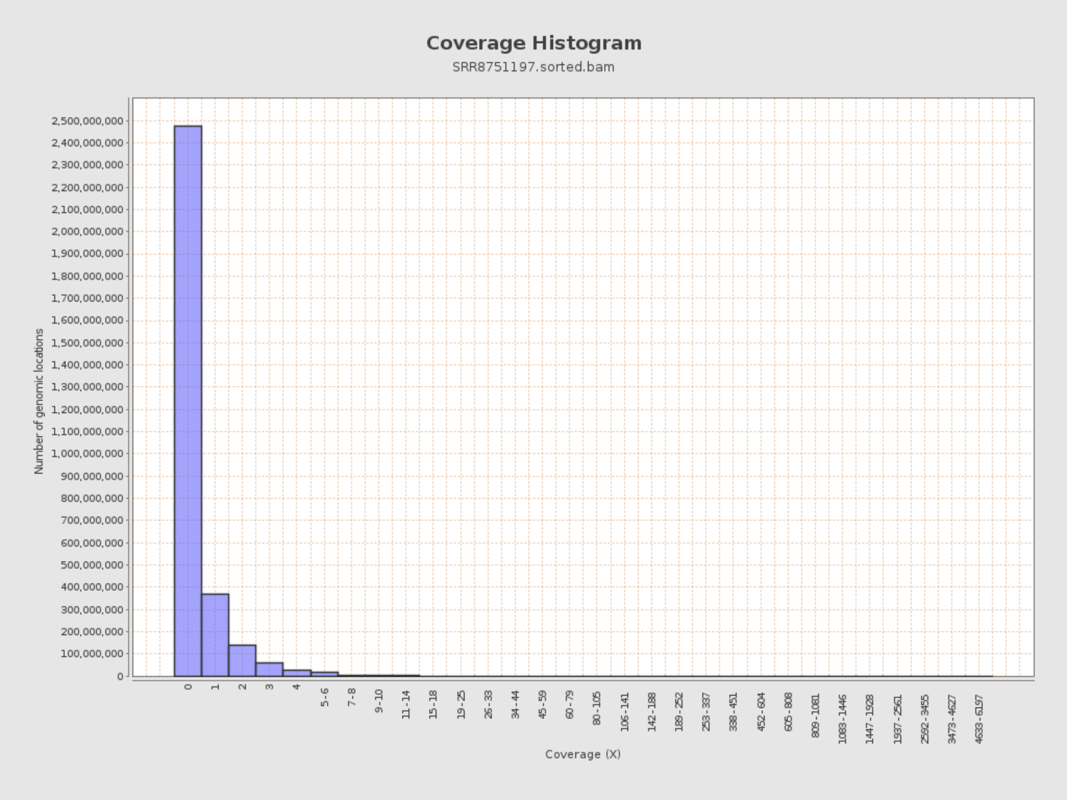
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	136299257	0.5468	5.6342
chr2	243199373	83639351	0.3439	1.1276
chr3	198022430	63480323	0.3206	0.883
chr4	191154276	49037015	0.2565	0.9763
chr5	180915260	90040567	0.4977	1.1017
chr6	171115067	65593085	0.3833	1.4547
chr7	159138663	63366419	0.3982	1.5241

chr8	146364022	54366426	0.3714	1.0119
chr9	141213431	49312919	0.3492	1.3135
chr10	135534747	56192883	0.4146	3.4726
chr11	135006516	49931878	0.3698	1.3041
chr12	133851895	60546346	0.4523	1.0621
chr13	115169878	33364827	0.2897	0.8408
chr14	107349540	23794674	0.2217	0.7528
chr15	102531392	29022610	0.2831	0.8529
chr16	90354753	32665515	0.3615	1.2424
chr17	81195210	34658029	0.4268	1.5206
chr18	78077248	24464645	0.3133	1.6515
chr19	59128983	22778515	0.3852	3.7063
chr20	63025520	22214486	0.3525	0.9581
chr21	48129895	10102262	0.2099	0.7722
chr22	51304566	14244799	0.2777	0.8528
chrMT	16571	693902	41.8745	19.0501
chrX	155270560	46715176	0.3009	0.9271
chrY	59373566	1406765	0.0237	0.5524

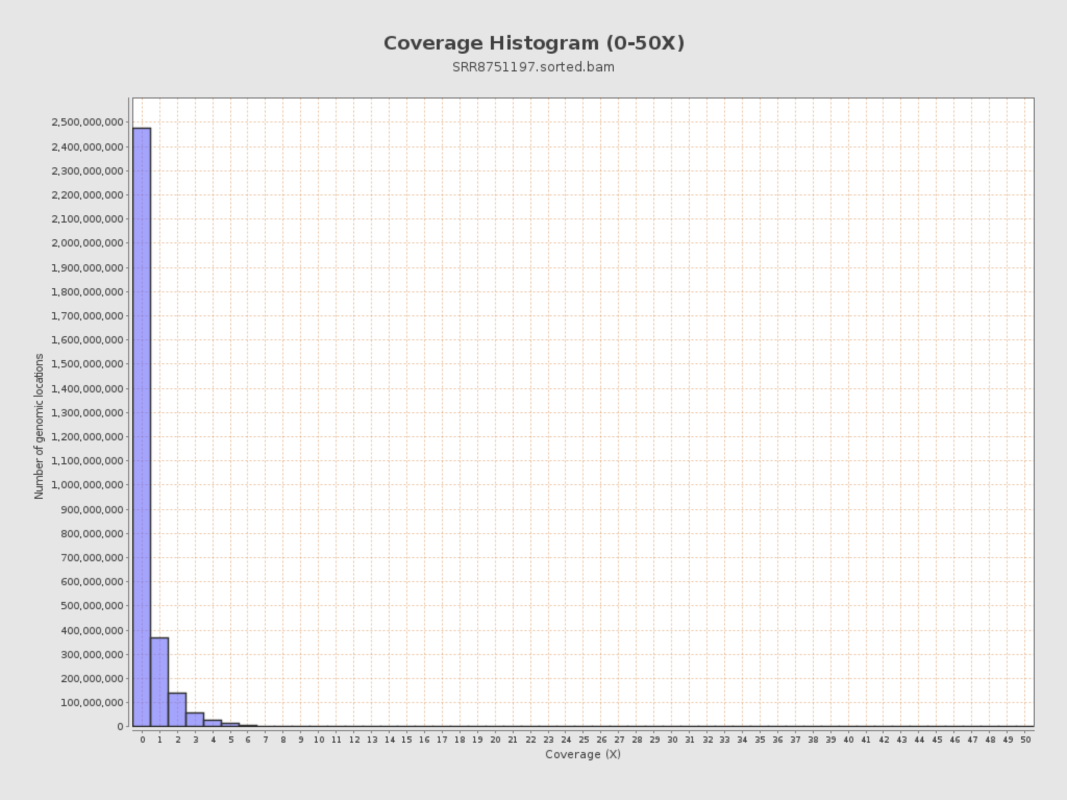
3. Results : Coverage across reference



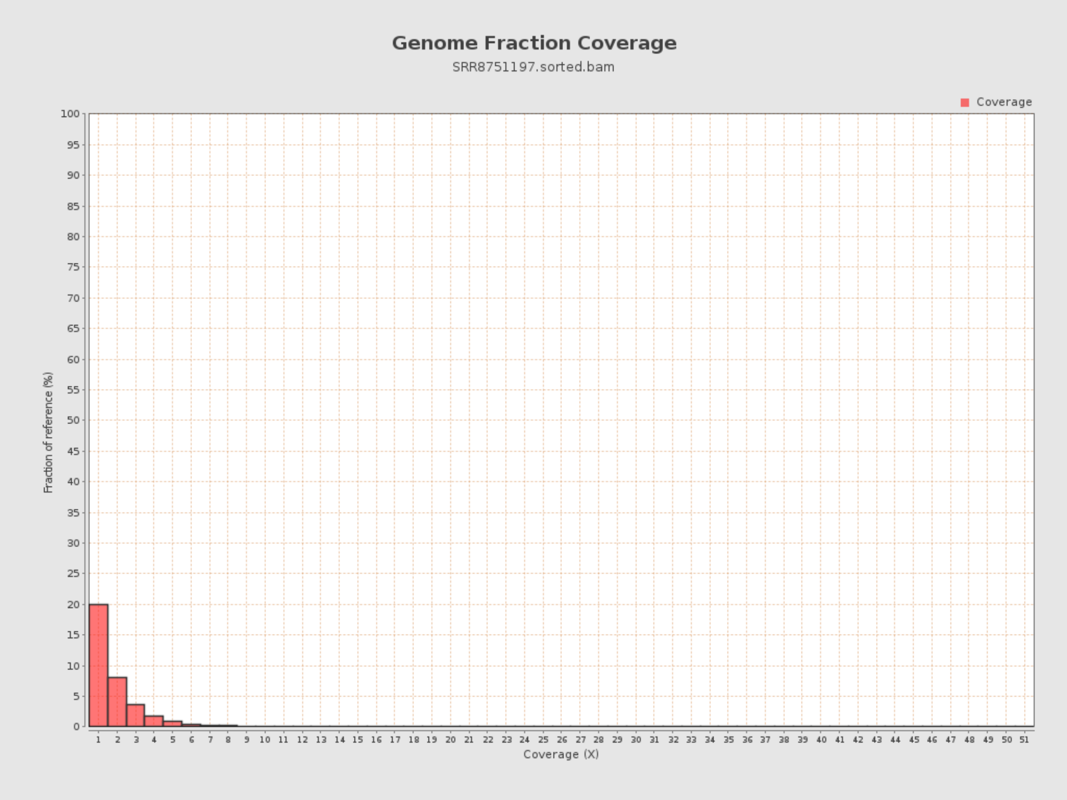
4. Results : Coverage Histogram



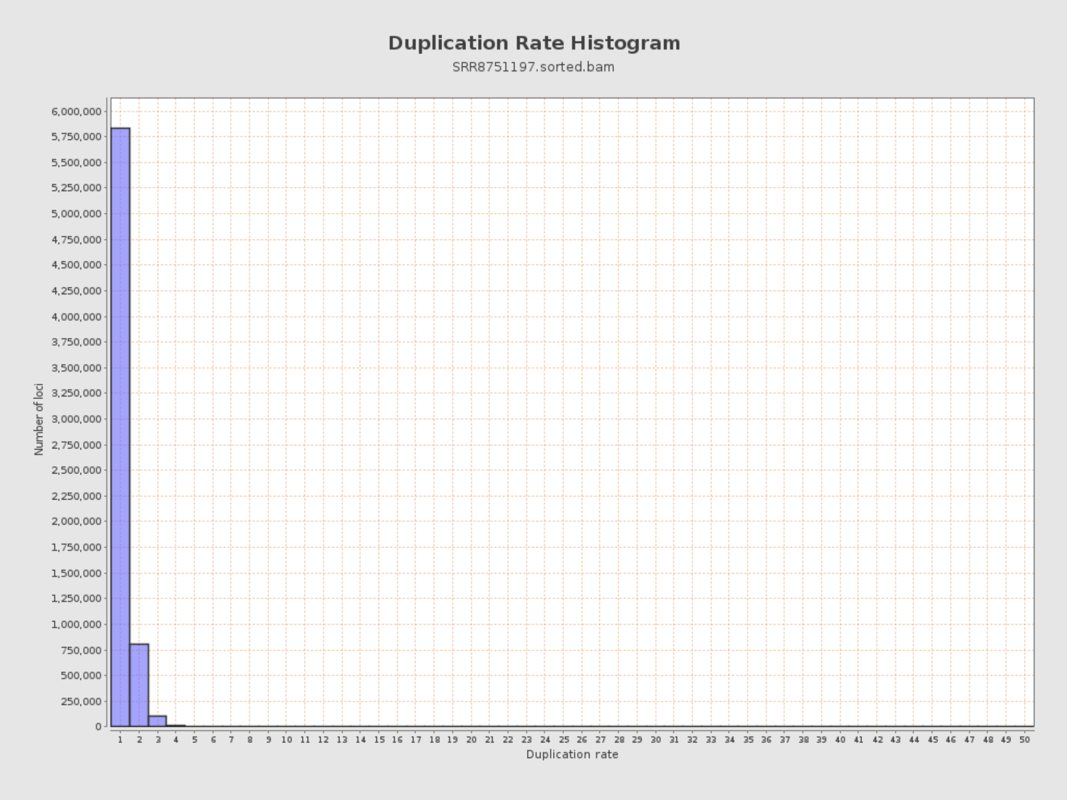
5. Results : Coverage Histogram (0-50X)



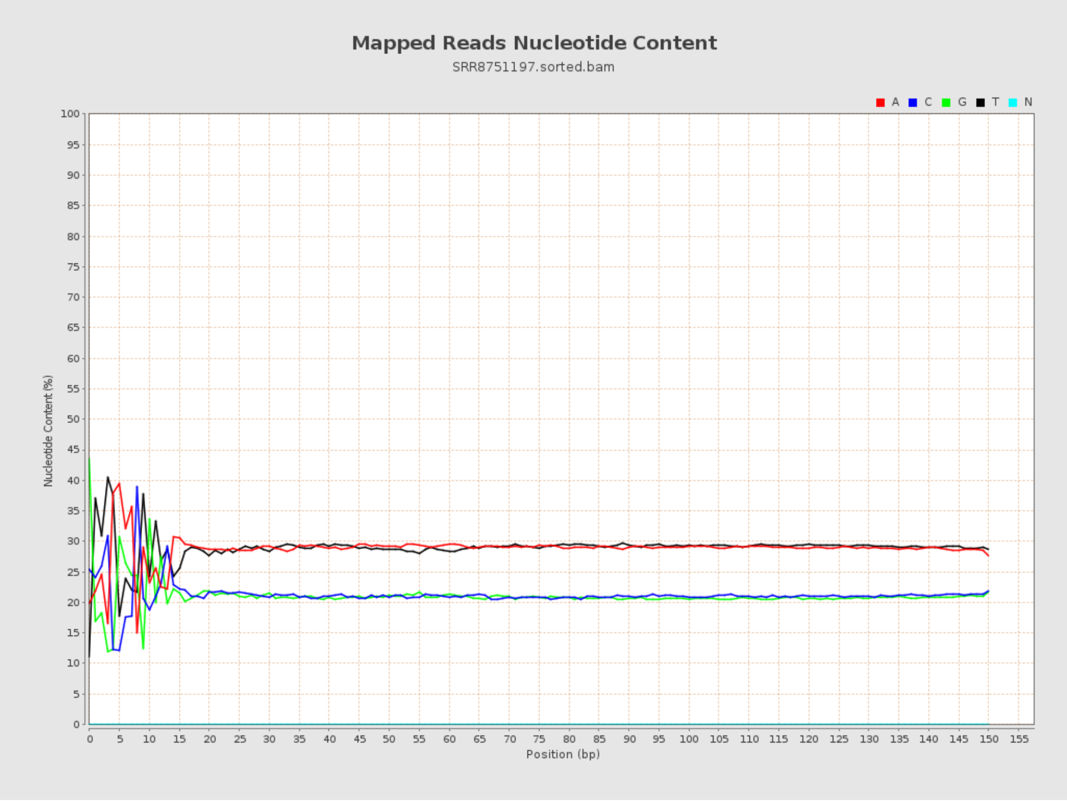
6. Results : Genome Fraction Coverage



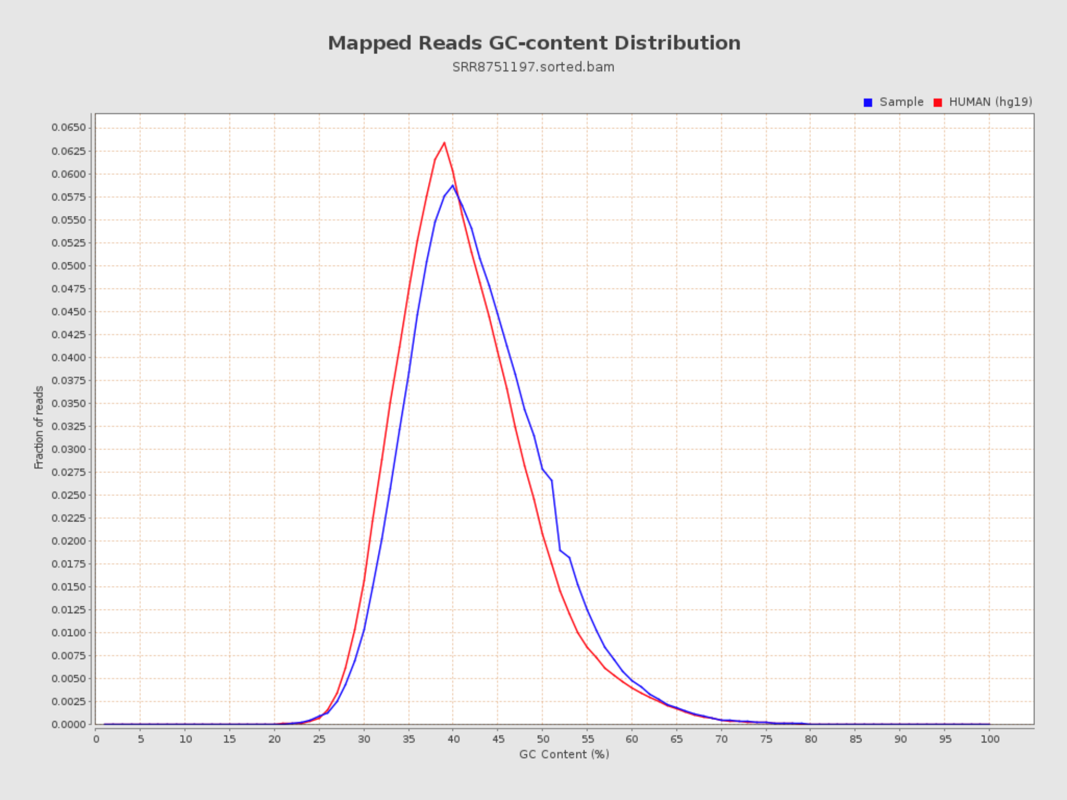
7. Results : Duplication Rate Histogram



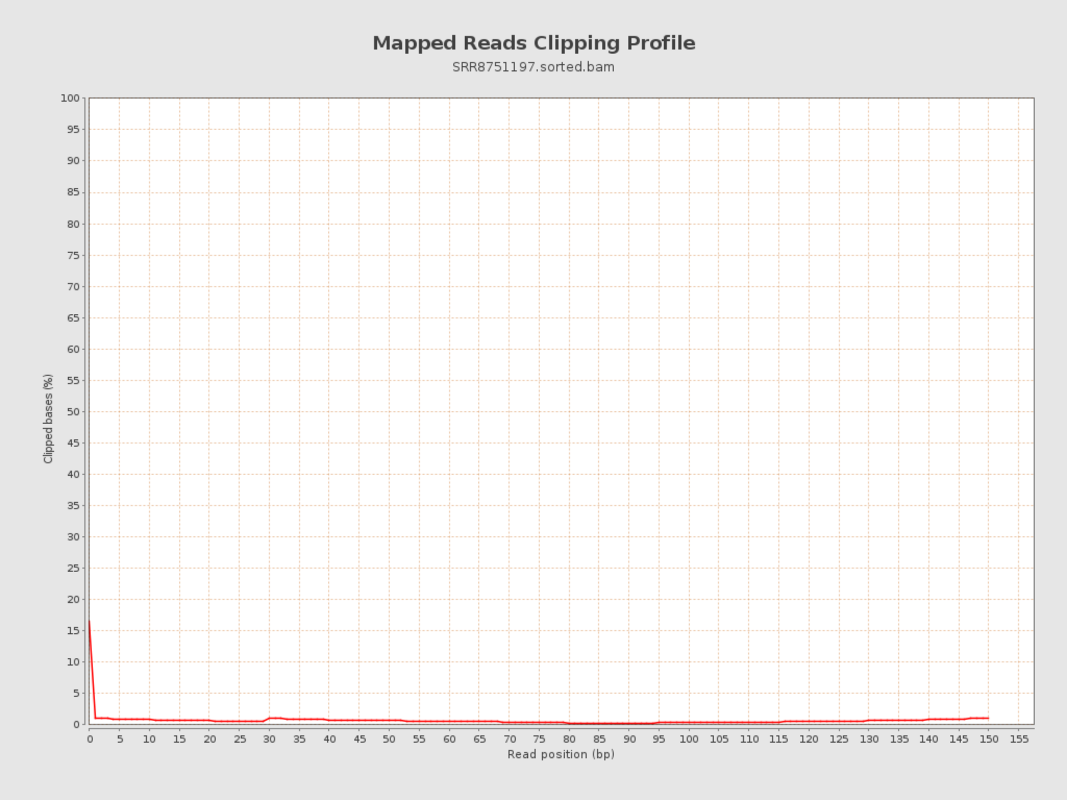
8. Results : Mapped Reads Nucleotide Content



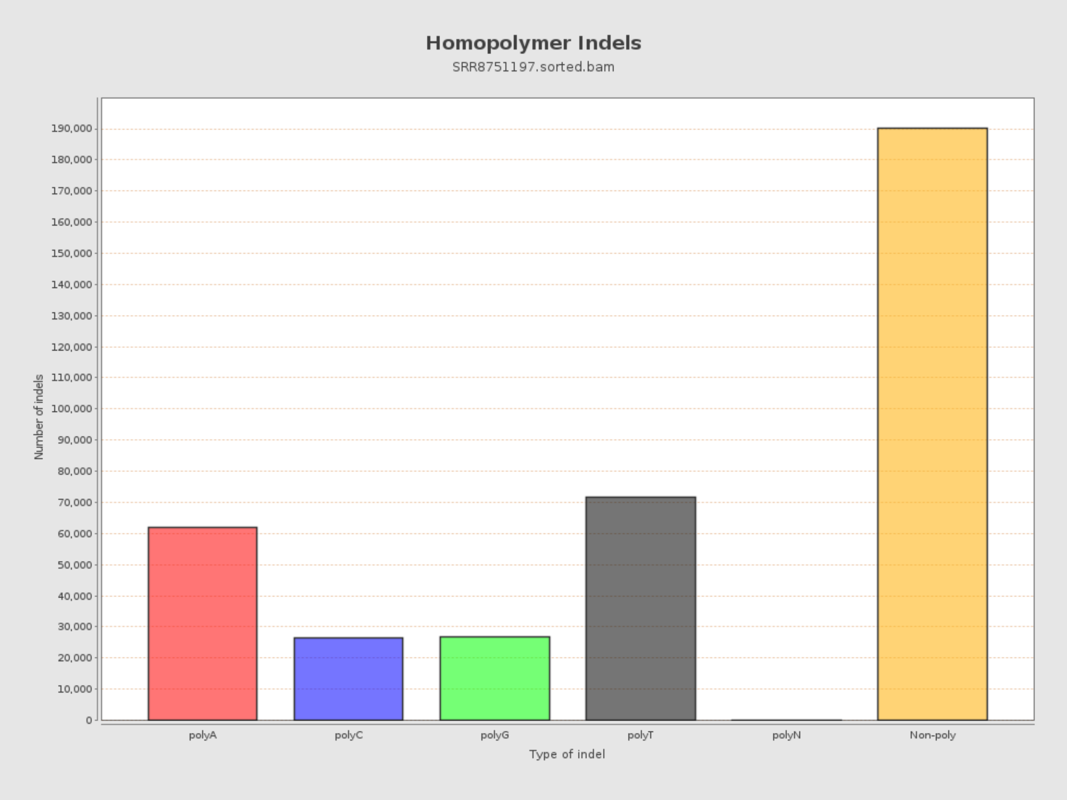
9. Results : Mapped Reads GC-content Distribution



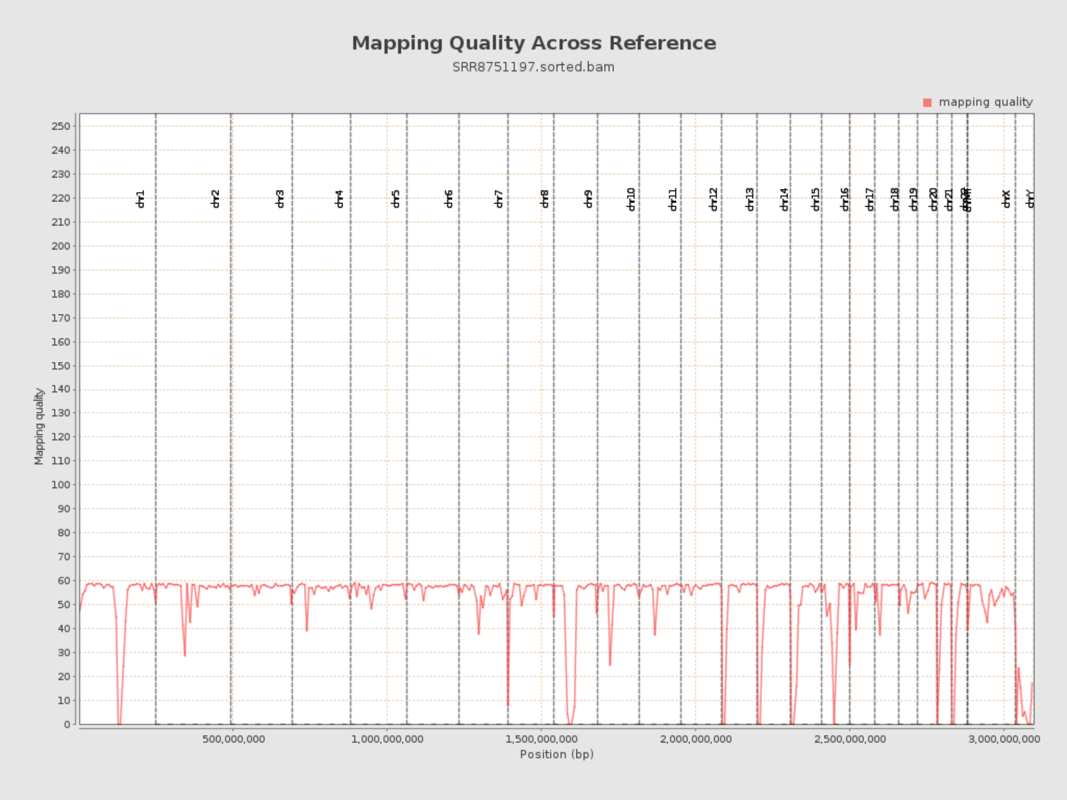
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram