Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 04:06:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549117.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_SRR1549117 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549117.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 04:06:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549117.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	11,940,785
Mapped reads	7,083,123 / 59.32%
Unmapped reads	4,857,662 / 40.68%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	343,617 / 2.88%
Duplication rate	3.76%
Clipped reads	647,373 / 5.42%

2.2. ACGT Content

Number/percentage of A's	80,877,398 / 28.93%
Number/percentage of C's	58,866,813 / 21.06%
Number/percentage of T's	80,960,339 / 28.96%
Number/percentage of G's	58,834,059 / 21.05%
Number/percentage of N's	11,019 / 0%
GC Percentage	42.1%

2.3. Coverage

Mean	0.0903
Standard Deviation	0.6329

2.4. Mapping Quality

Mean Mapping Quality	40.33

2.5. Mismatches and indels

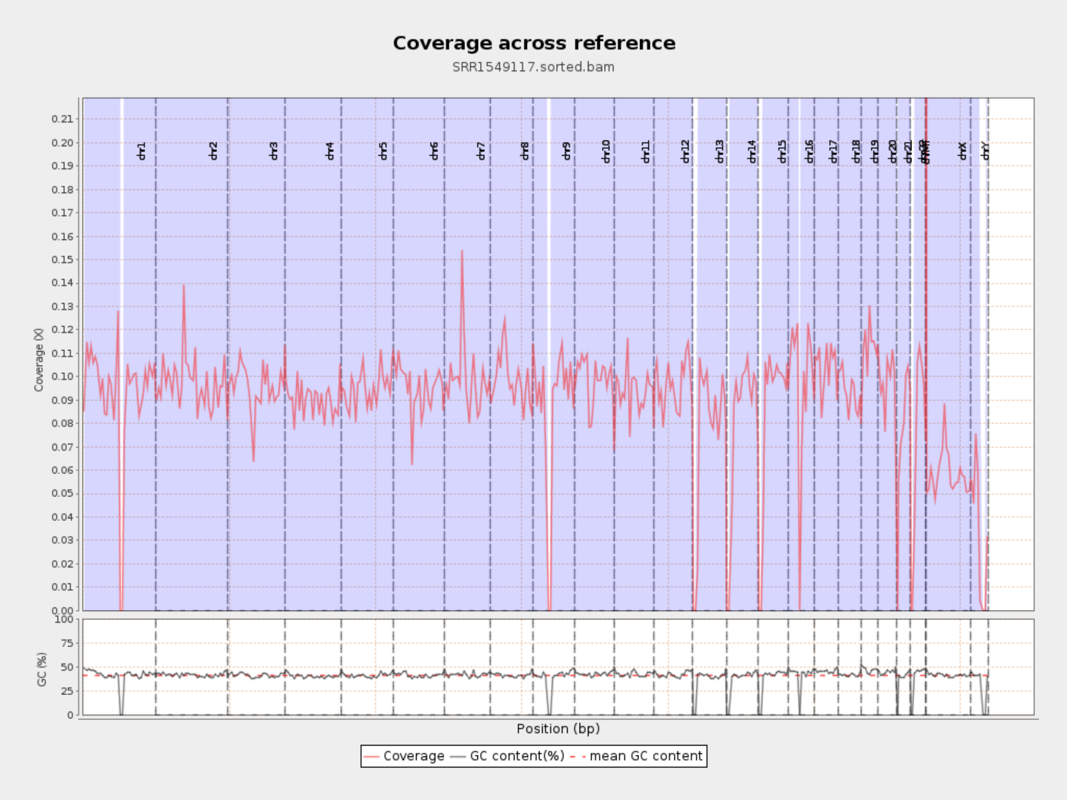
General error rate	0.37%
Mismatches	1,016,351
Insertions	10,383
Mapped reads with at least one insertion	0.15%
Deletions	27,226
Mapped reads with at least one deletion	0.38%
Homopolymer indels	45.08%

2.6. Chromosome stats

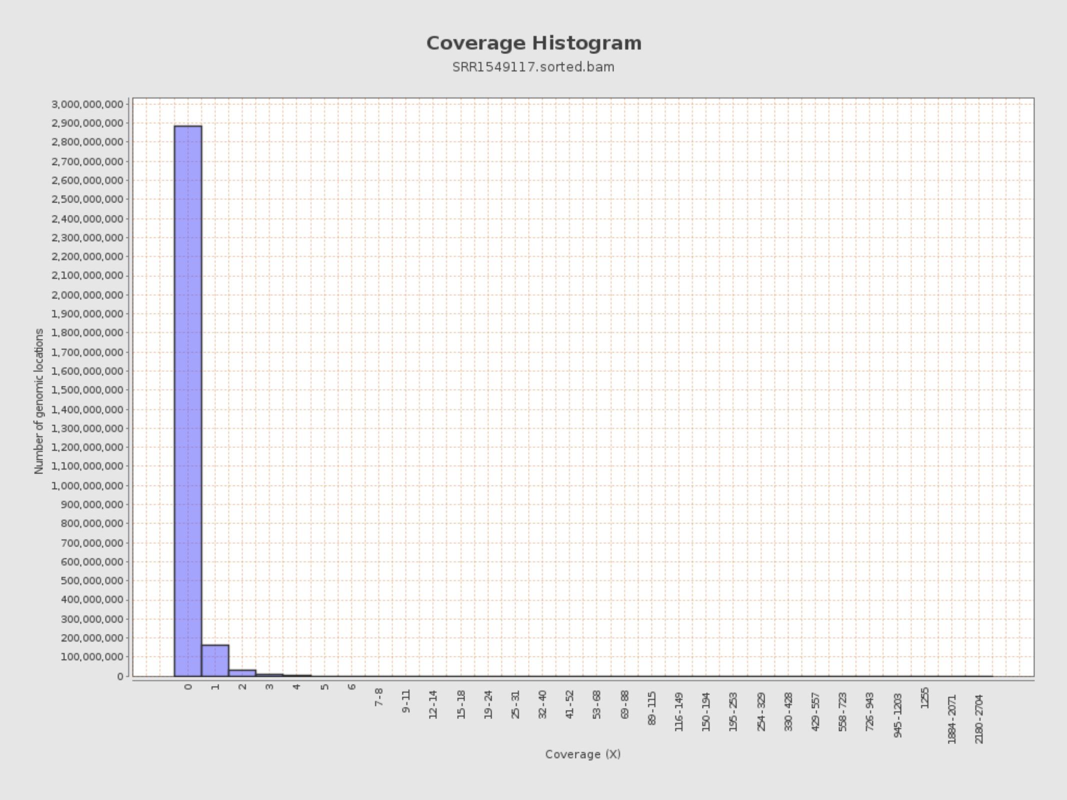
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	23067519	0.0925	0.9506
chr2	243199373	23745077	0.0976	0.5689
chr3	198022430	18844747	0.0952	0.4039
chr4	191154276	17215739	0.0901	0.3968
chr5	180915260	17264232	0.0954	0.412
chr6	171115067	16278382	0.0951	0.432
chr7	159138663	15842611	0.0996	0.7372
chr8	146364022	14417972	0.0985	1.3864

chr9	141213431	12109670	0.0858	0.5488
chr10	135534747	13437428	0.0991	0.5253
chr11	135006516	12652805	0.0937	0.477
chr12	133851895	13035022	0.0974	0.4281
chr13	115169878	8767525	0.0761	0.3573
chr14	107349540	8637223	0.0805	0.6141
chr15	102531392	8442251	0.0823	0.368
chr16	90354753	8640274	0.0956	0.4246
chr17	81195210	8513122	0.1048	0.4258
chr18	78077248	7330436	0.0939	1.0576
chr19	59128983	6673797	0.1129	1.0284
chr20	63025520	6148163	0.0976	0.4277
chr21	48129895	3666628	0.0762	0.4053
chr22	51304566	3673729	0.0716	0.3713
chrMT	16571	119659	7.221	10.4141
chrX	155270560	9095650	0.0586	0.3945
chrY	59373566	1964034	0.0331	0.2644

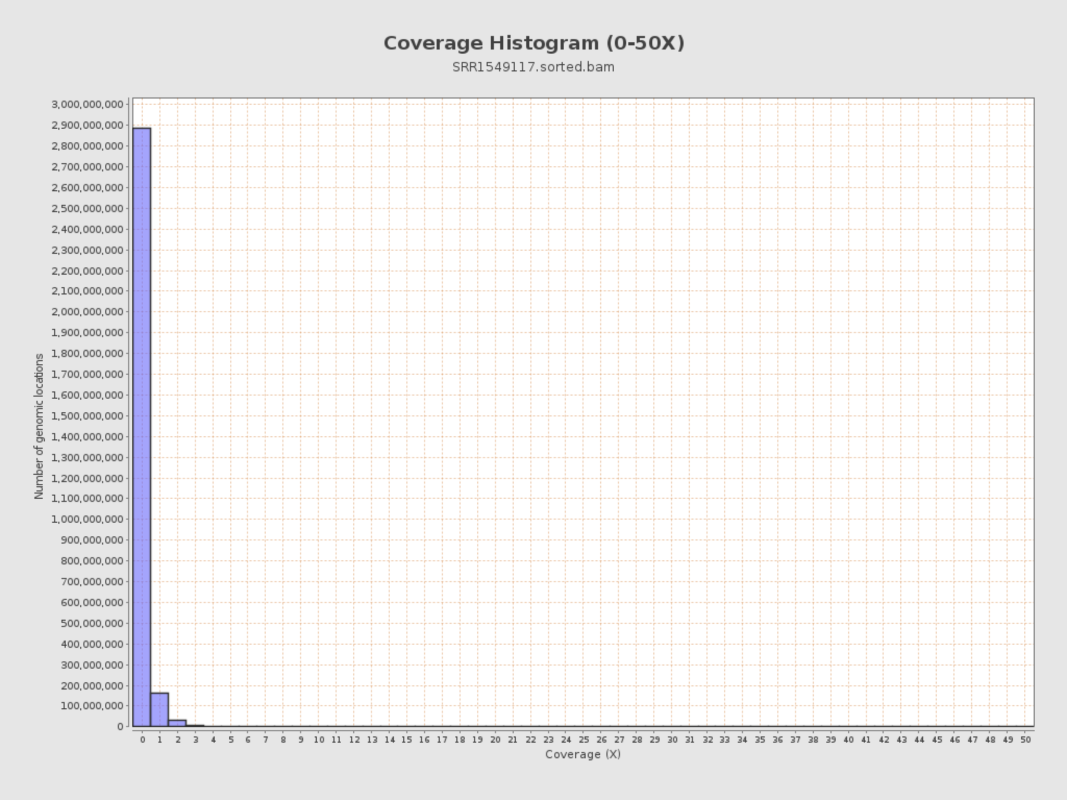
3. Results : Coverage across reference



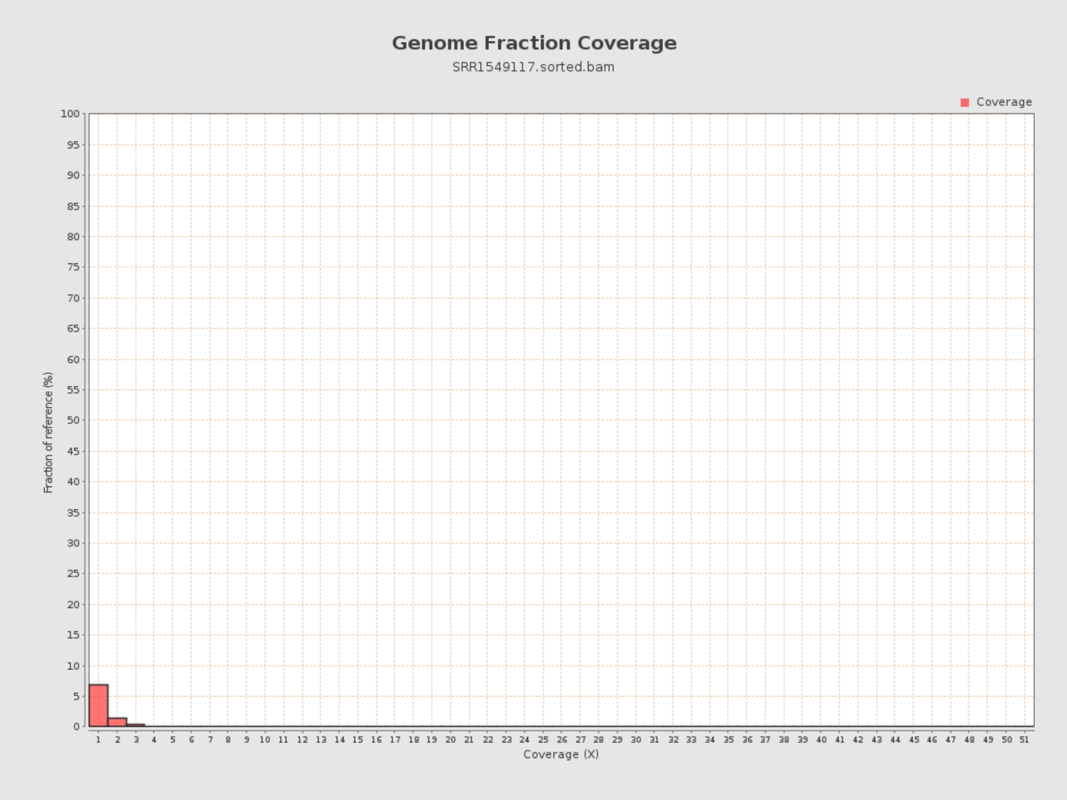
4. Results : Coverage Histogram



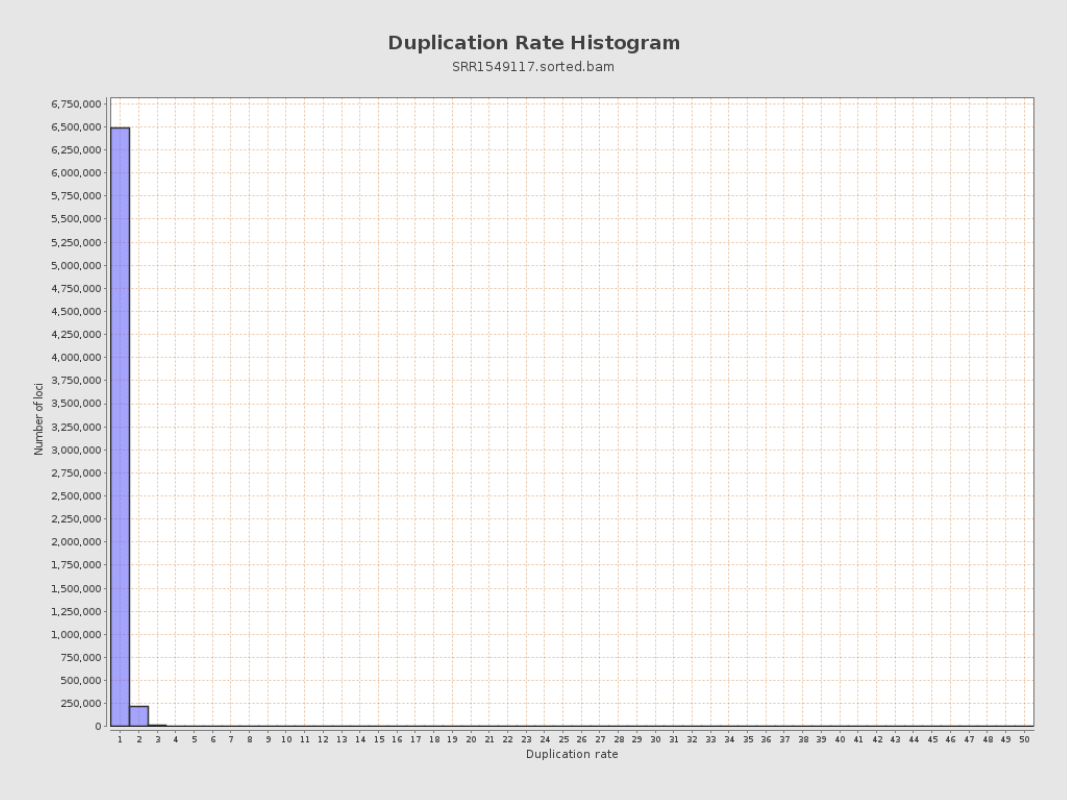
5. Results : Coverage Histogram (0-50X)



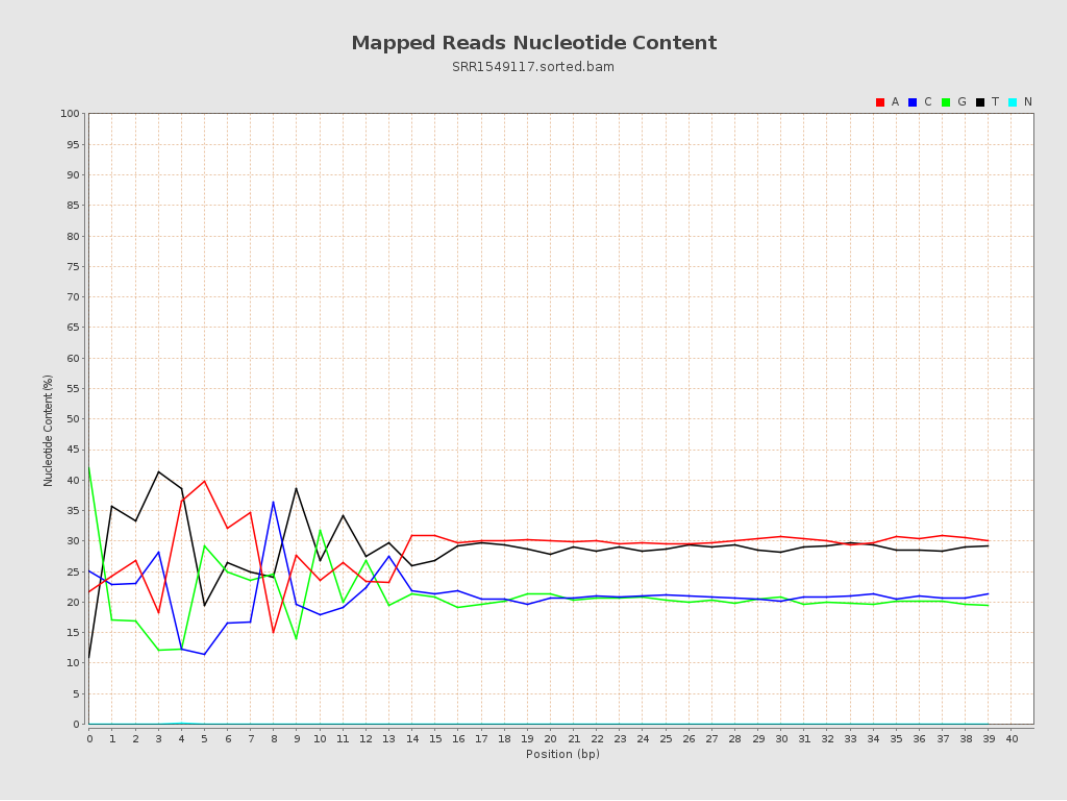
6. Results : Genome Fraction Coverage



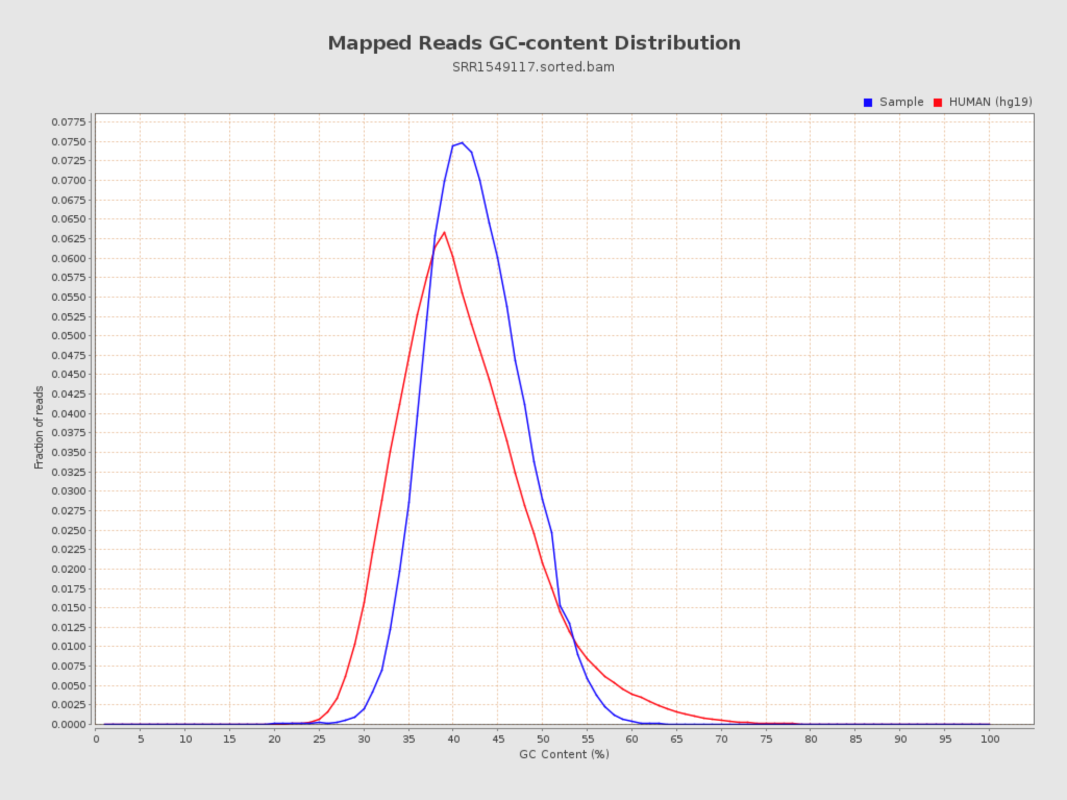
7. Results : Duplication Rate Histogram



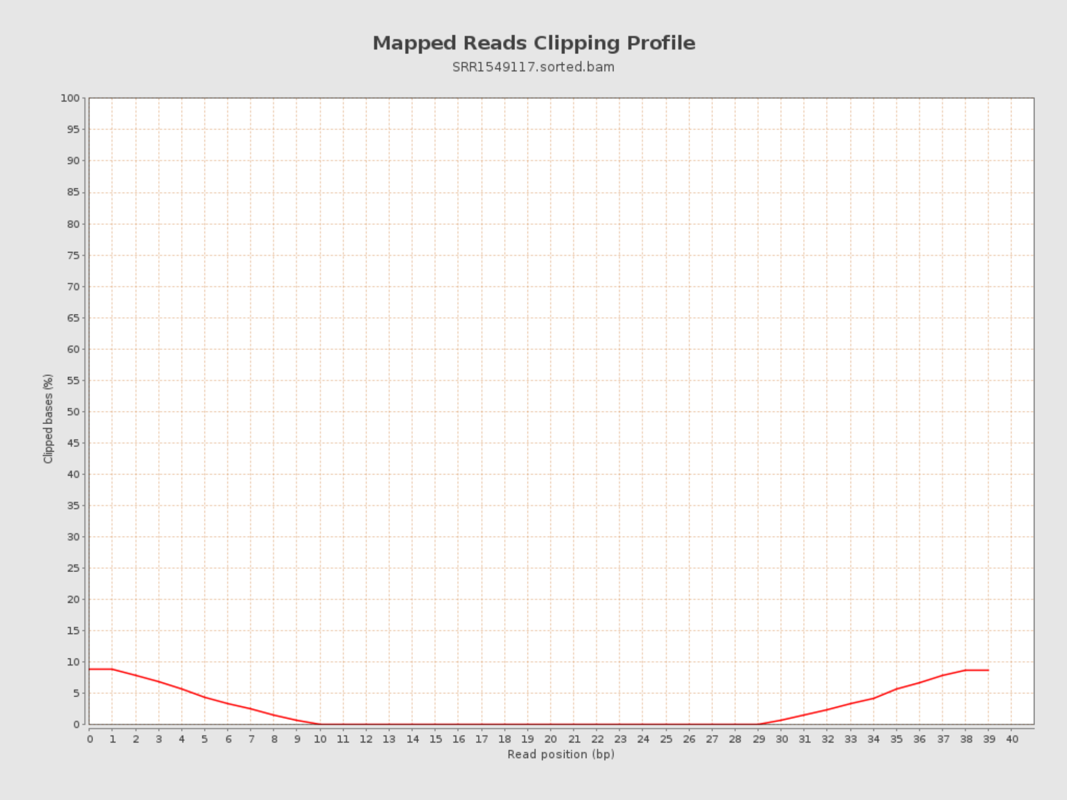
8. Results : Mapped Reads Nucleotide Content



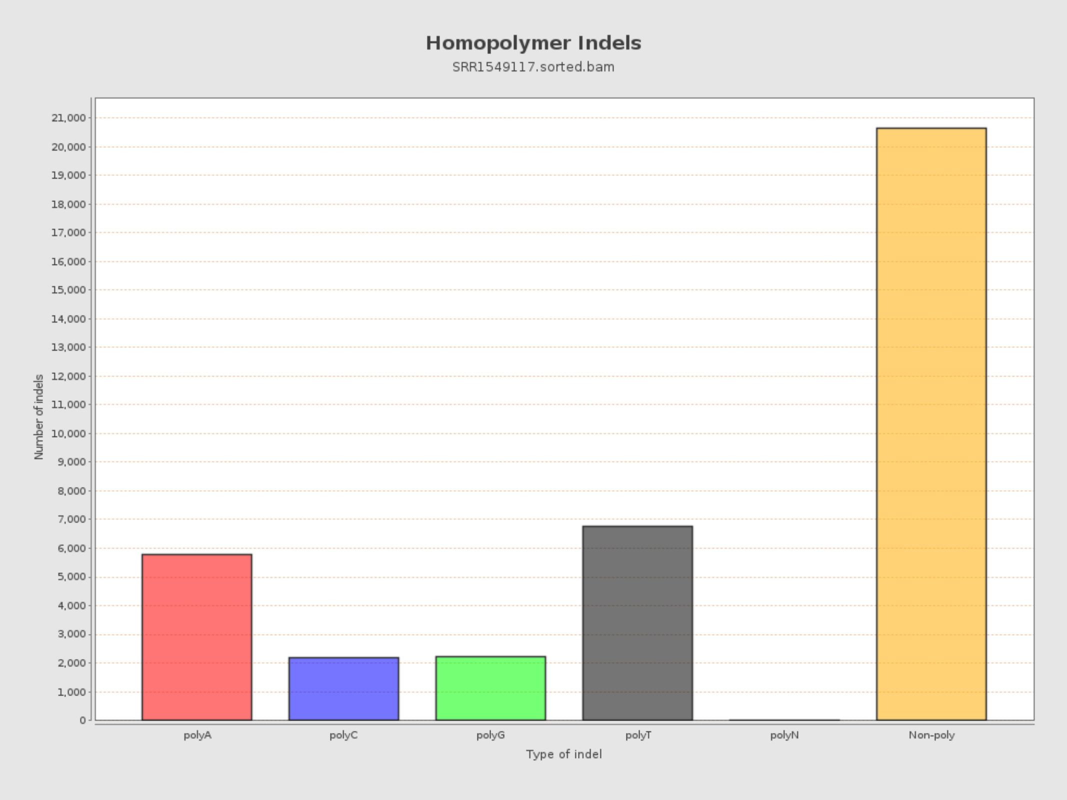
9. Results : Mapped Reads GC-content Distribution



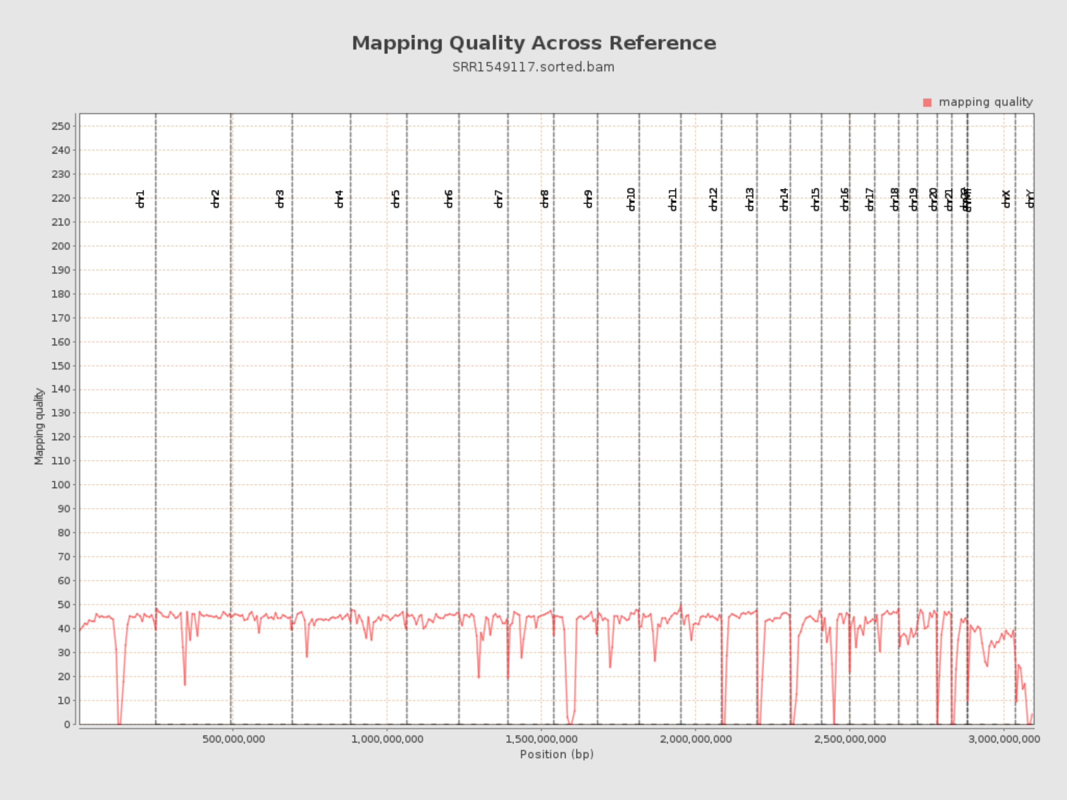
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram