Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 03:10:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549111.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_SRR1549111 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549111.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 03:10:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549111.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	11,807,440
Mapped reads	10,072,563 / 85.31%
Unmapped reads	1,734,877 / 14.69%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	905,991 / 7.67%
Duplication rate	6.82%
Clipped reads	1,268,214 / 10.74%

2.2. ACGT Content

Number/percentage of A's	116,830,113 / 29.53%
Number/percentage of C's	80,267,020 / 20.29%
Number/percentage of T's	117,449,414 / 29.69%
Number/percentage of G's	81,055,801 / 20.49%
Number/percentage of N's	1,543 / 0%
GC Percentage	40.78%

2.3. Coverage

Mean	0.1278
Standard Deviation	1.3056

2.4. Mapping Quality

Mean Mapping Quality	39.55

2.5. Mismatches and indels

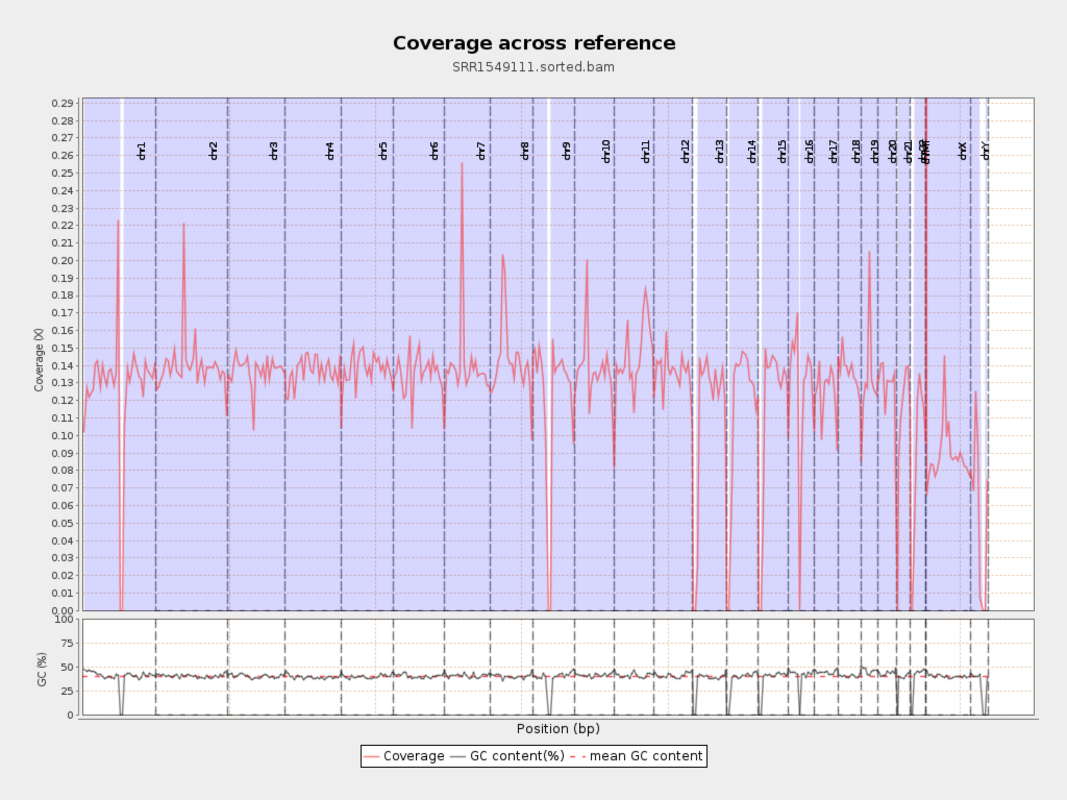
General error rate	0.42%
Mismatches	1,648,491
Insertions	16,854
Mapped reads with at least one insertion	0.17%
Deletions	38,815
Mapped reads with at least one deletion	0.39%
Homopolymer indels	41.41%

2.6. Chromosome stats

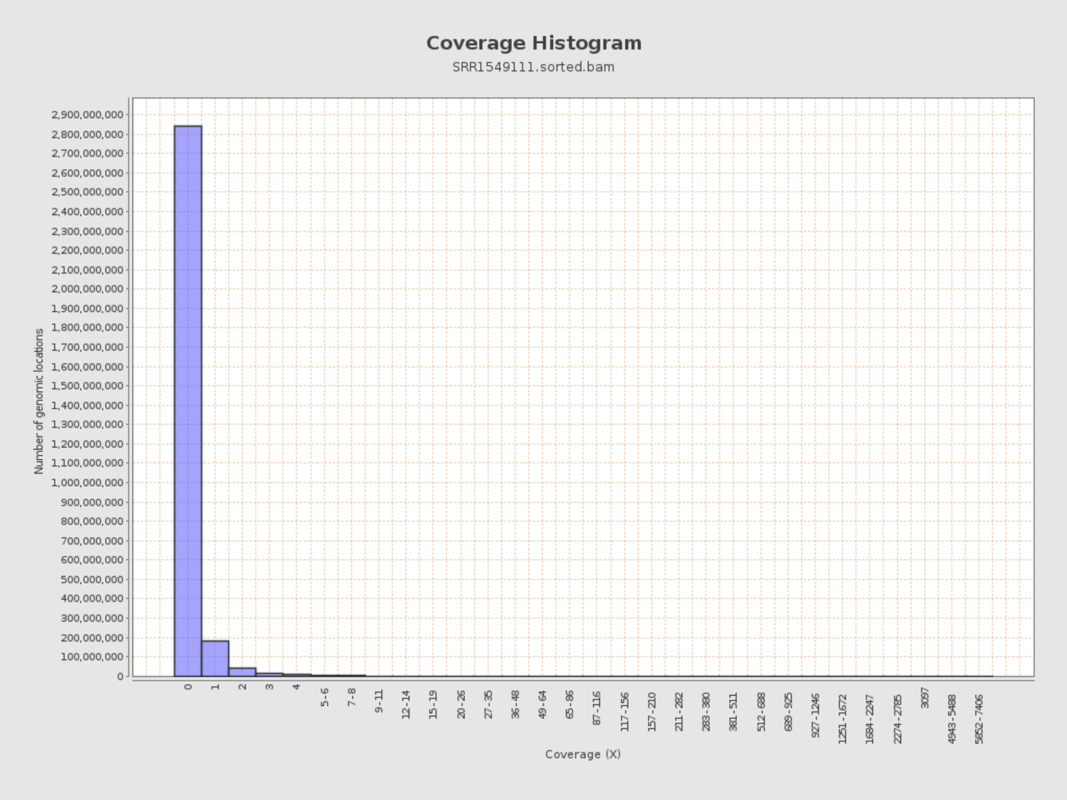
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	31596480	0.1268	2.0981
chr2	243199373	34122545	0.1403	0.9256
chr3	198022430	27117491	0.1369	0.5748
chr4	191154276	26168990	0.1369	0.6073
chr5	180915260	24978543	0.1381	0.5985
chr6	171115067	23263617	0.136	0.6446
chr7	159138663	22439438	0.141	1.3539
chr8	146364022	20875984	0.1426	3.6272

chr9	141213431	16955050	0.1201	0.9847
chr10	135534747	18628935	0.1374	0.9388
chr11	135006516	19697454	0.1459	0.8188
chr12	133851895	18284768	0.1366	0.6341
chr13	115169878	12708151	0.1103	0.5116
chr14	107349540	12268839	0.1143	1.537
chr15	102531392	11559831	0.1127	0.5029
chr16	90354753	11080801	0.1226	0.6283
chr17	81195210	10228938	0.126	0.5732
chr18	78077248	10693996	0.137	1.9025
chr19	59128983	7976952	0.1349	2.1964
chr20	63025520	8139141	0.1291	0.6168
chr21	48129895	5219098	0.1084	0.5933
chr22	51304566	4375182	0.0853	0.5014
chrMT	16571	183334	11.0635	13.5559
chrX	155270560	13812107	0.089	0.6579
chrY	59373566	3275638	0.0552	0.4915

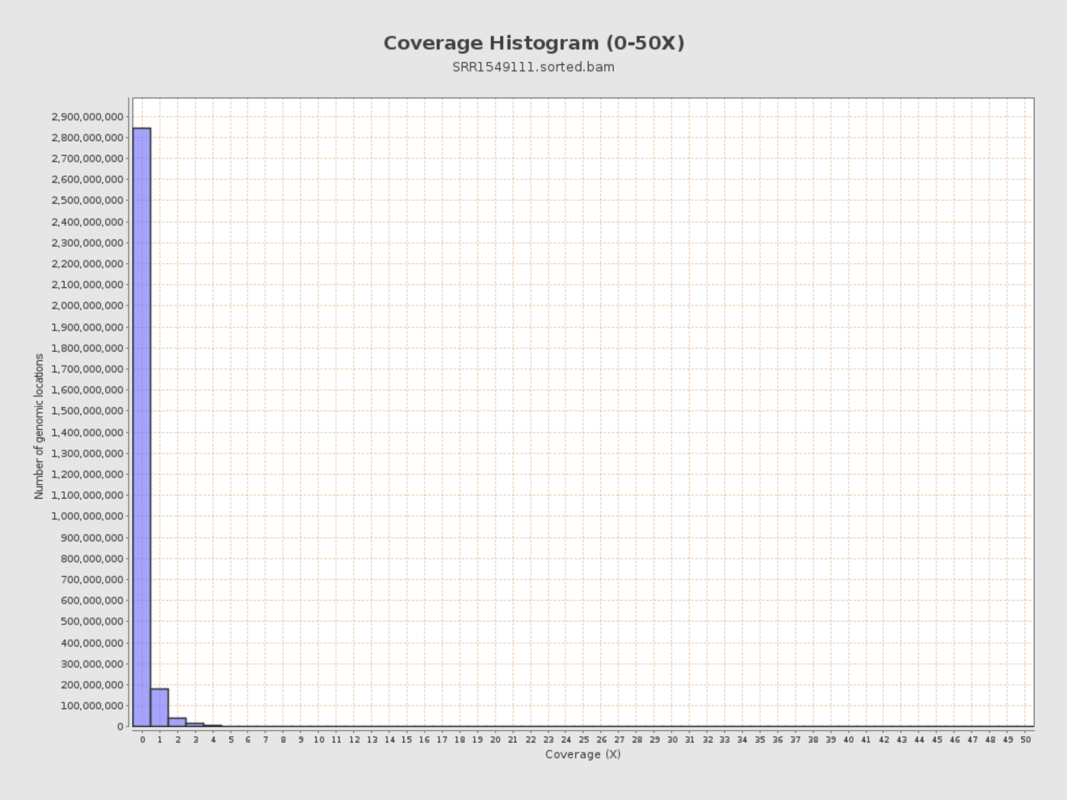
3. Results : Coverage across reference



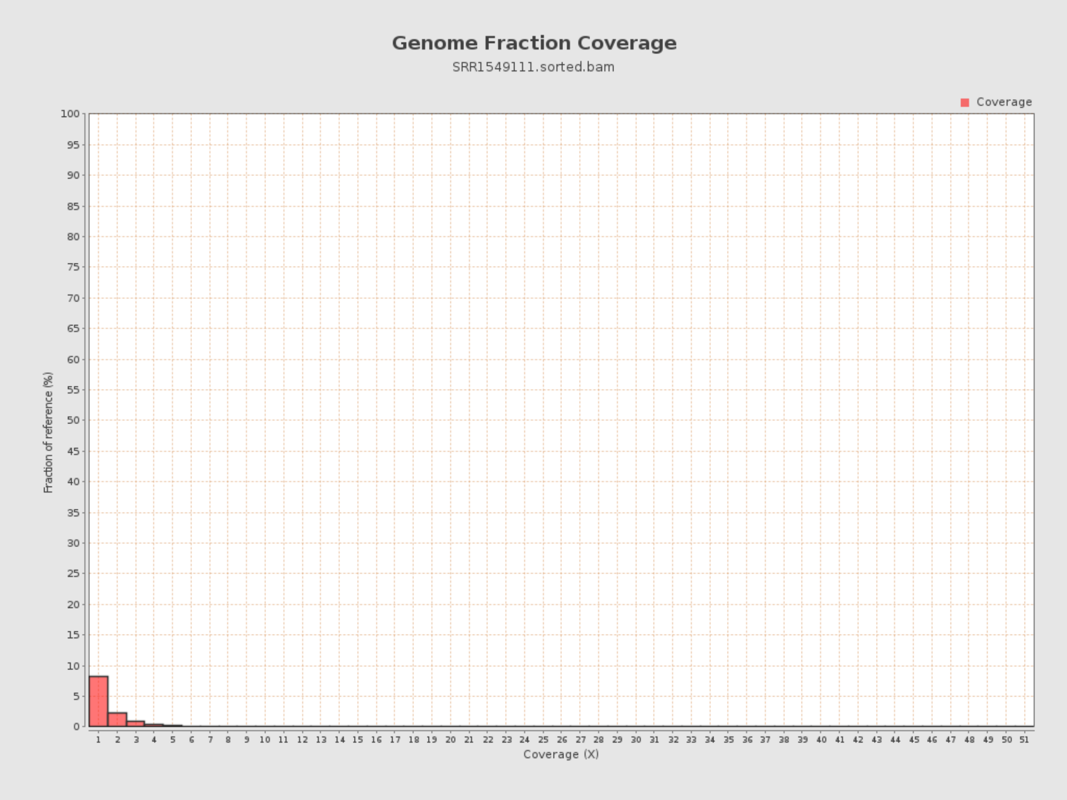
4. Results : Coverage Histogram



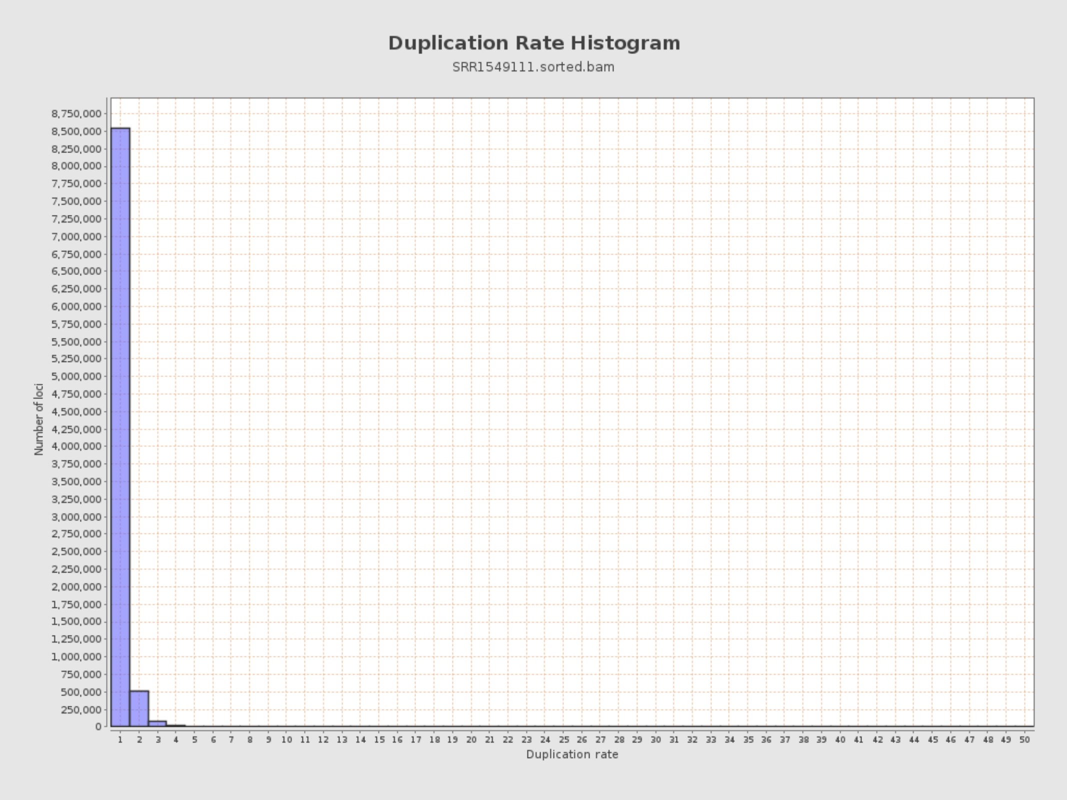
5. Results : Coverage Histogram (0-50X)



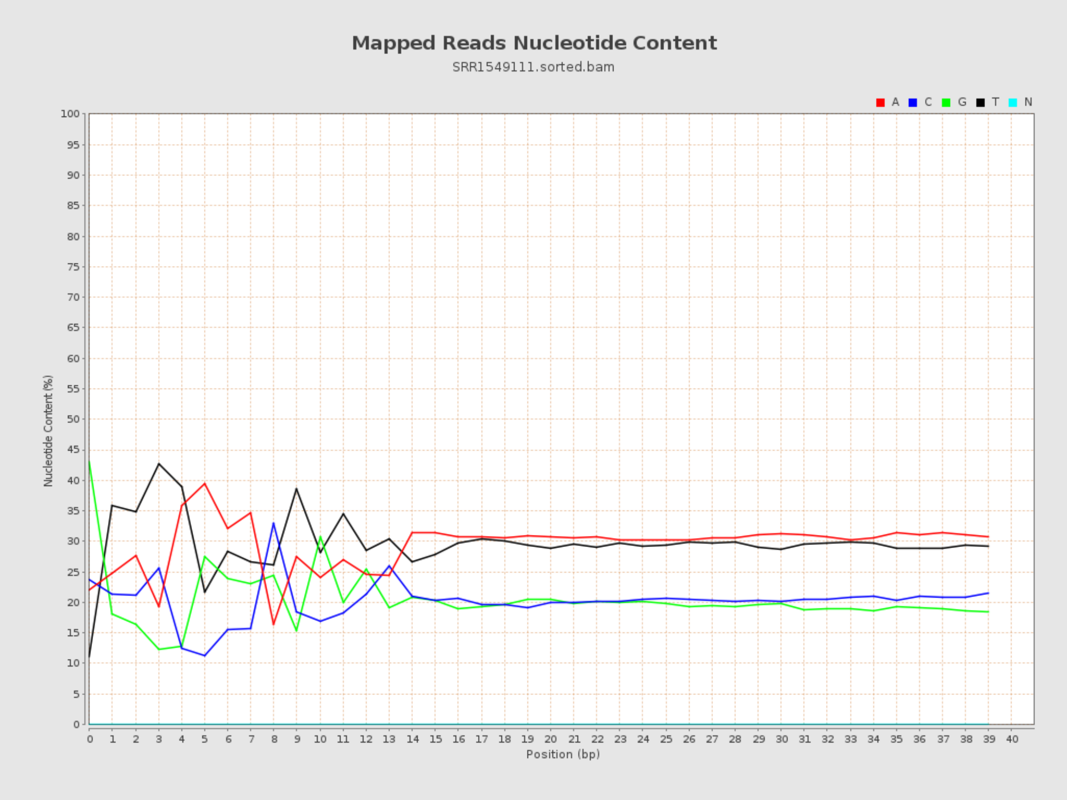
6. Results : Genome Fraction Coverage



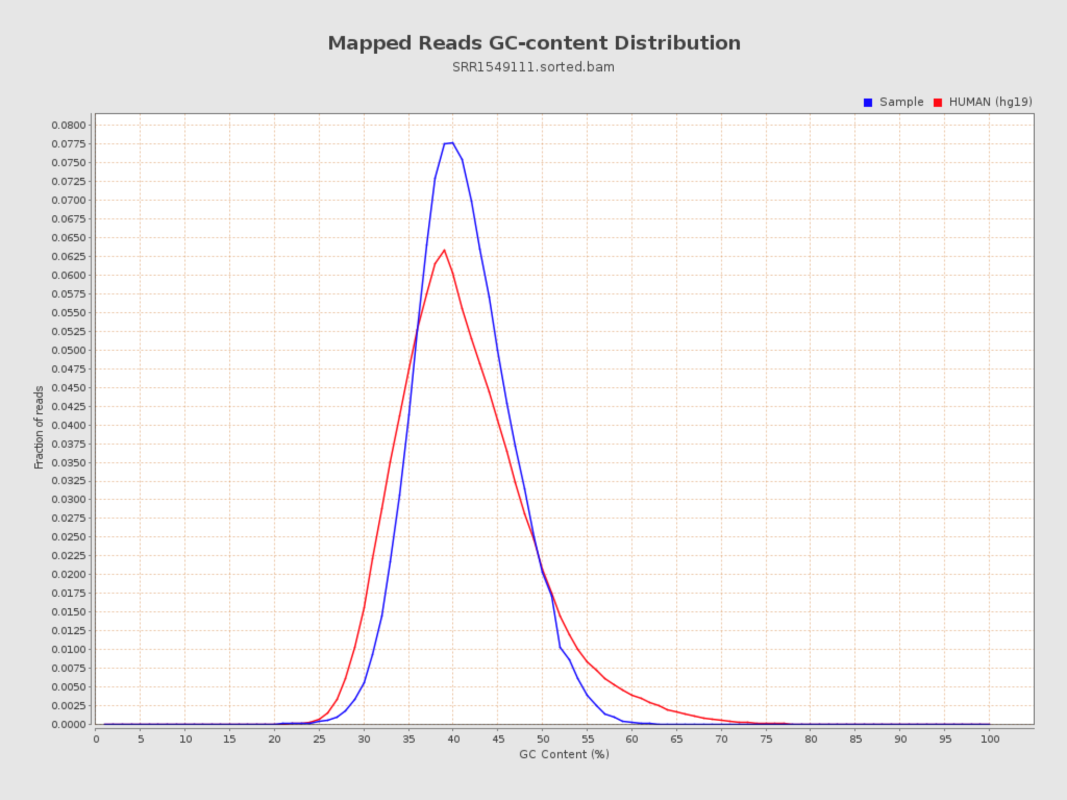
7. Results : Duplication Rate Histogram



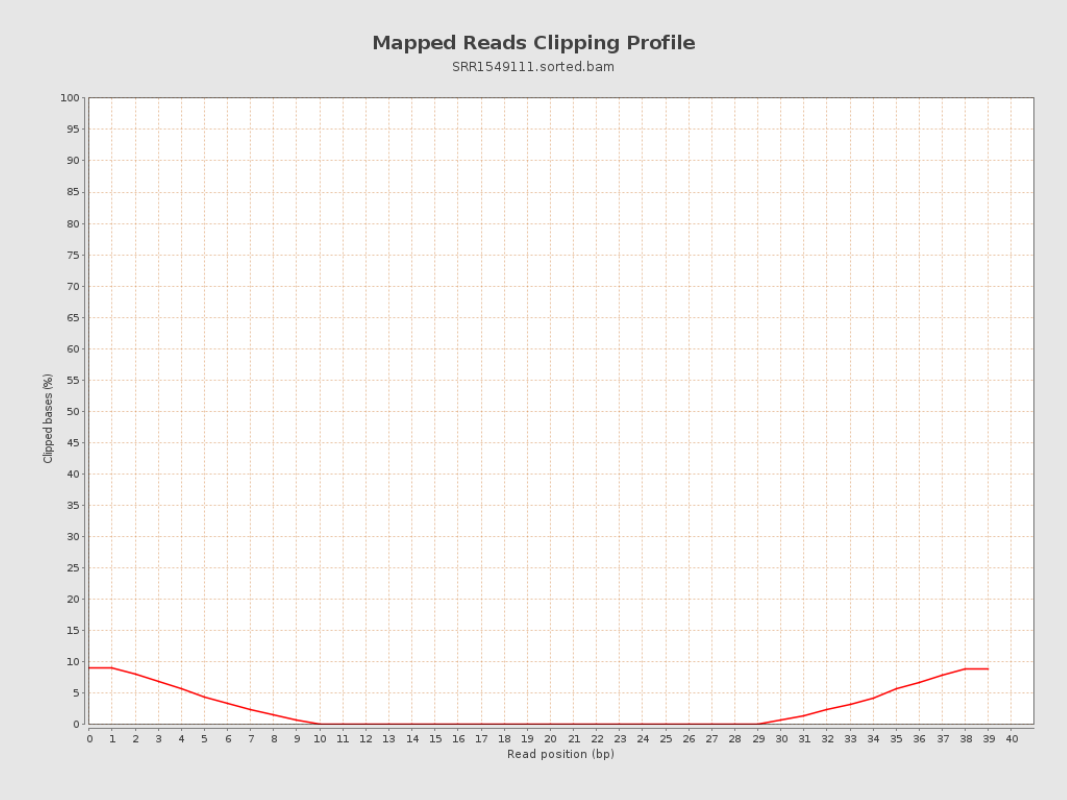
8. Results : Mapped Reads Nucleotide Content



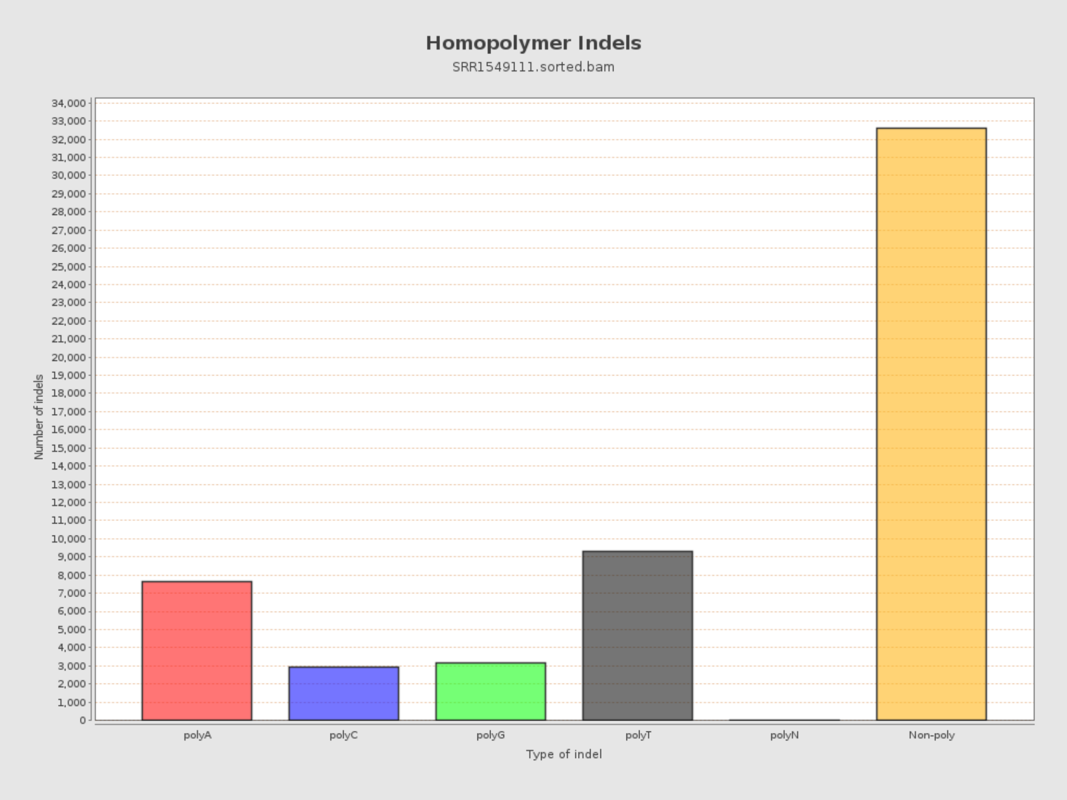
9. Results : Mapped Reads GC-content Distribution



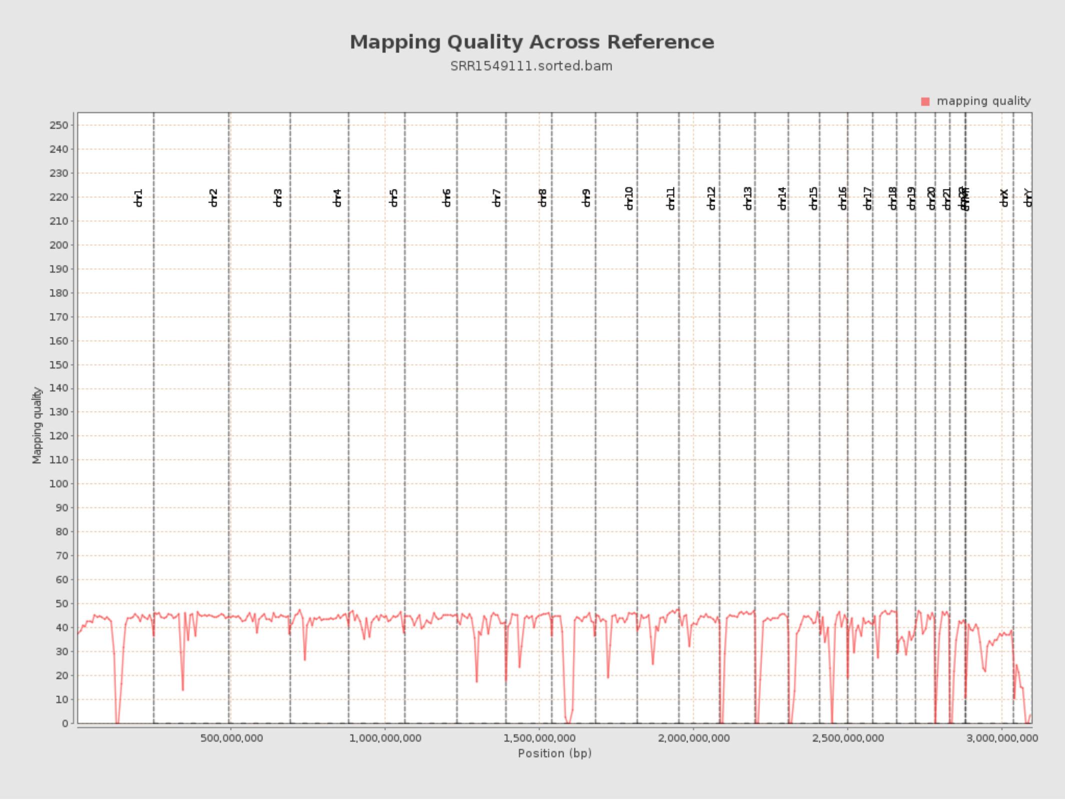
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram