Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 09:28:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549144.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_SRR1549144 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549144.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 09:28:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549144.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	12,589,379
Mapped reads	11,017,746 / 87.52%
Unmapped reads	1,571,633 / 12.48%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	570,621 / 4.53%
Duplication rate	4.13%
Clipped reads	569,180 / 4.52%

2.2. ACGT Content

Number/percentage of A's	126,847,994 / 29.01%
Number/percentage of C's	90,530,521 / 20.7%
Number/percentage of T's	128,904,262 / 29.48%
Number/percentage of G's	90,898,912 / 20.79%
Number/percentage of N's	85,686 / 0.02%
GC Percentage	41.49%

2.3. Coverage

Mean	0.1413
Standard Deviation	0.7963

2.4. Mapping Quality

Mean Mapping Quality	43.67

2.5. Mismatches and indels

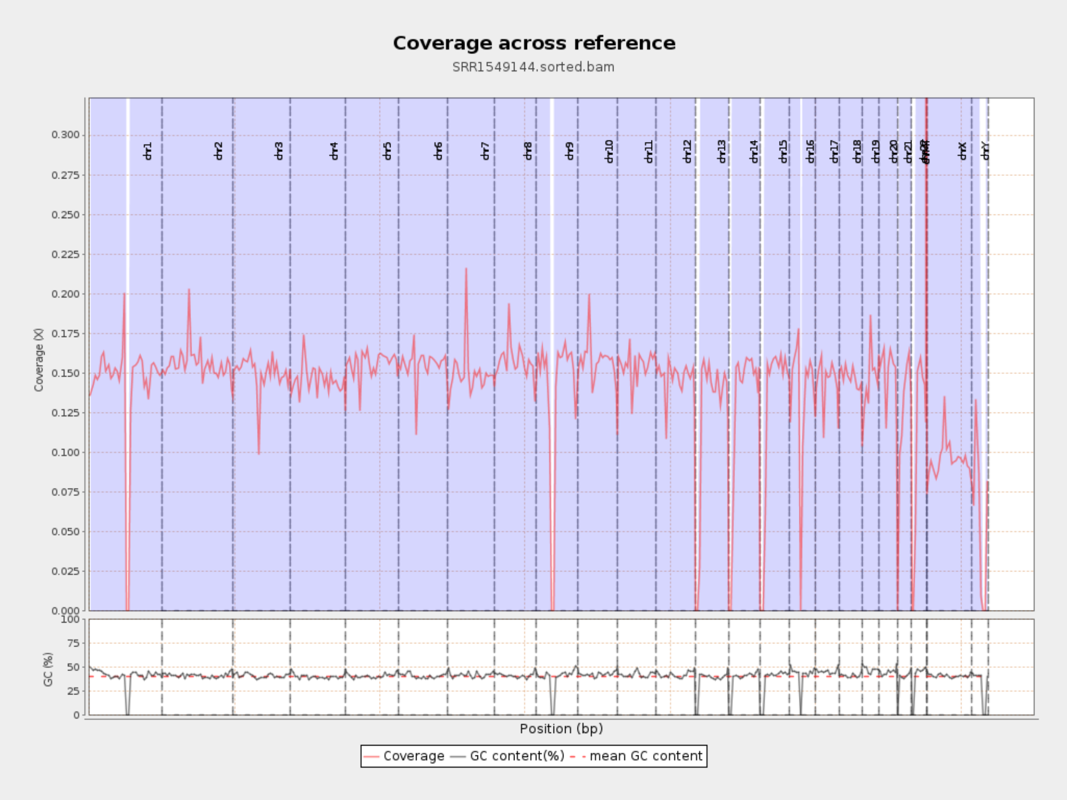
General error rate	0.31%
Mismatches	1,340,707
Insertions	10,920
Mapped reads with at least one insertion	0.1%
Deletions	35,295
Mapped reads with at least one deletion	0.32%
Homopolymer indels	45.56%

2.6. Chromosome stats

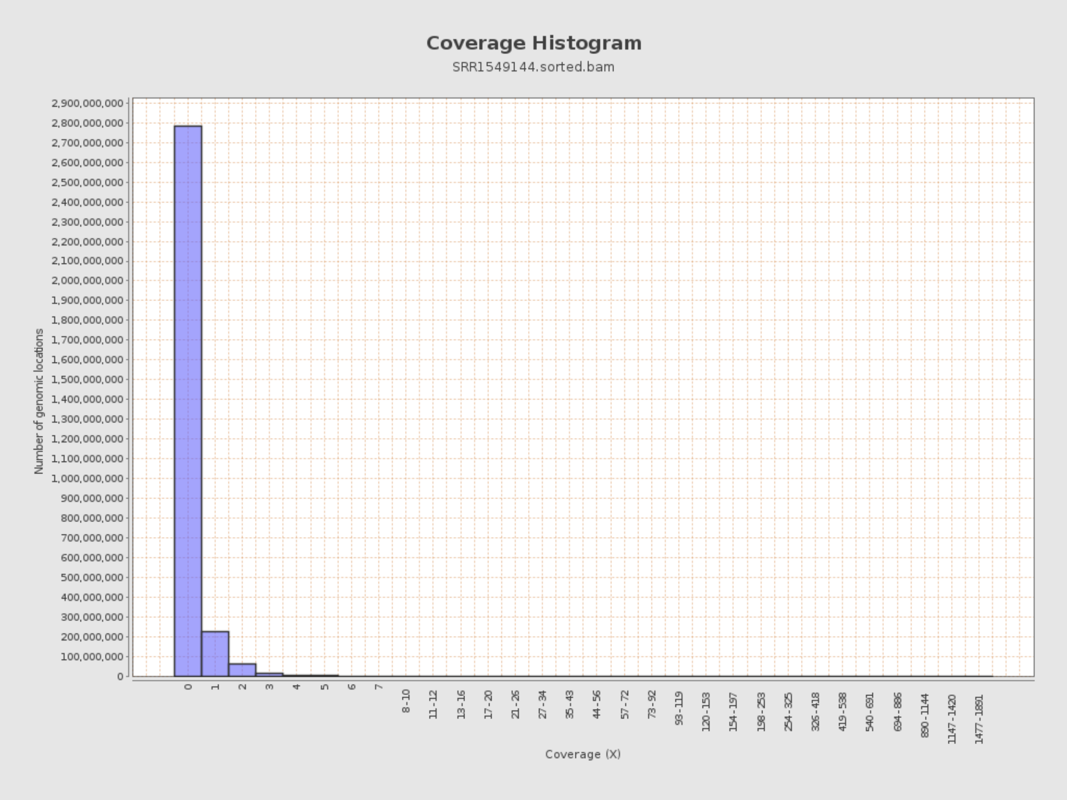
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	35461449	0.1423	1.4648
chr2	243199373	38040079	0.1564	0.7609
chr3	198022430	29629956	0.1496	0.5083
chr4	191154276	27830639	0.1456	0.5475
chr5	180915260	28223318	0.156	0.5362
chr6	171115067	26532333	0.1551	0.5726
chr7	159138663	23885028	0.1501	1.0922
chr8	146364022	23036513	0.1574	1.0064

chr9	141213431	19318328	0.1368	0.7034
chr10	135534747	21426307	0.1581	0.7807
chr11	135006516	20817748	0.1542	0.6996
chr12	133851895	19677602	0.147	0.5295
chr13	115169878	13986202	0.1214	0.4601
chr14	107349540	13531669	0.1261	0.5948
chr15	102531392	12928033	0.1261	0.4597
chr16	90354753	12256331	0.1356	0.5418
chr17	81195210	11660424	0.1436	0.537
chr18	78077248	11514294	0.1475	1.3643
chr19	59128983	8625100	0.1459	1.2196
chr20	63025520	9488365	0.1505	0.5453
chr21	48129895	5821321	0.121	0.5505
chr22	51304566	5250650	0.1023	0.4455
chrMT	16571	230494	13.9095	16.5857
chrX	155270560	14825597	0.0955	0.5215
chrY	59373566	3314743	0.0558	0.4996

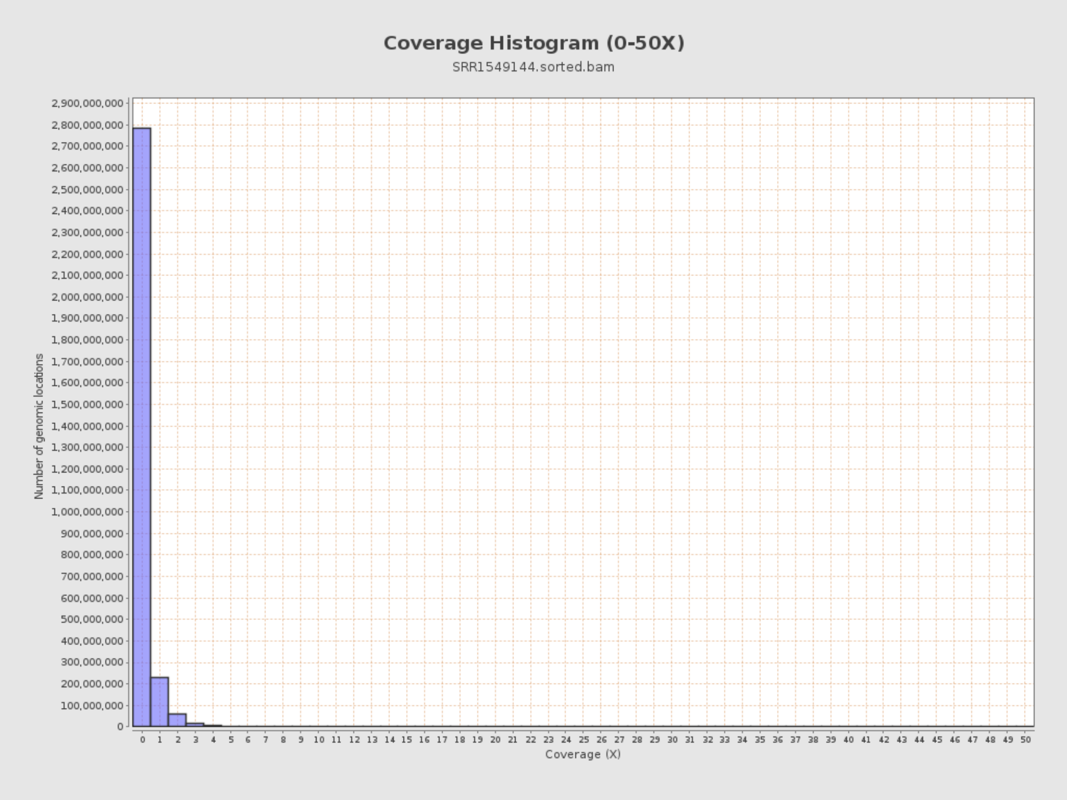
3. Results : Coverage across reference



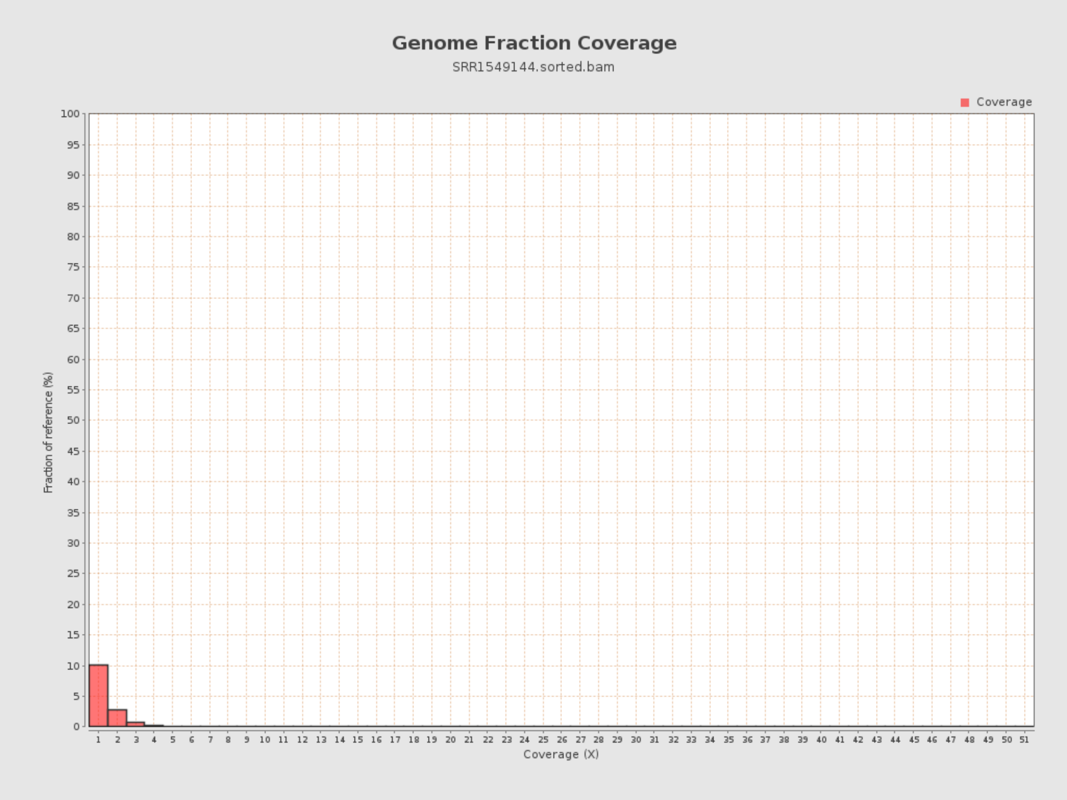
4. Results : Coverage Histogram



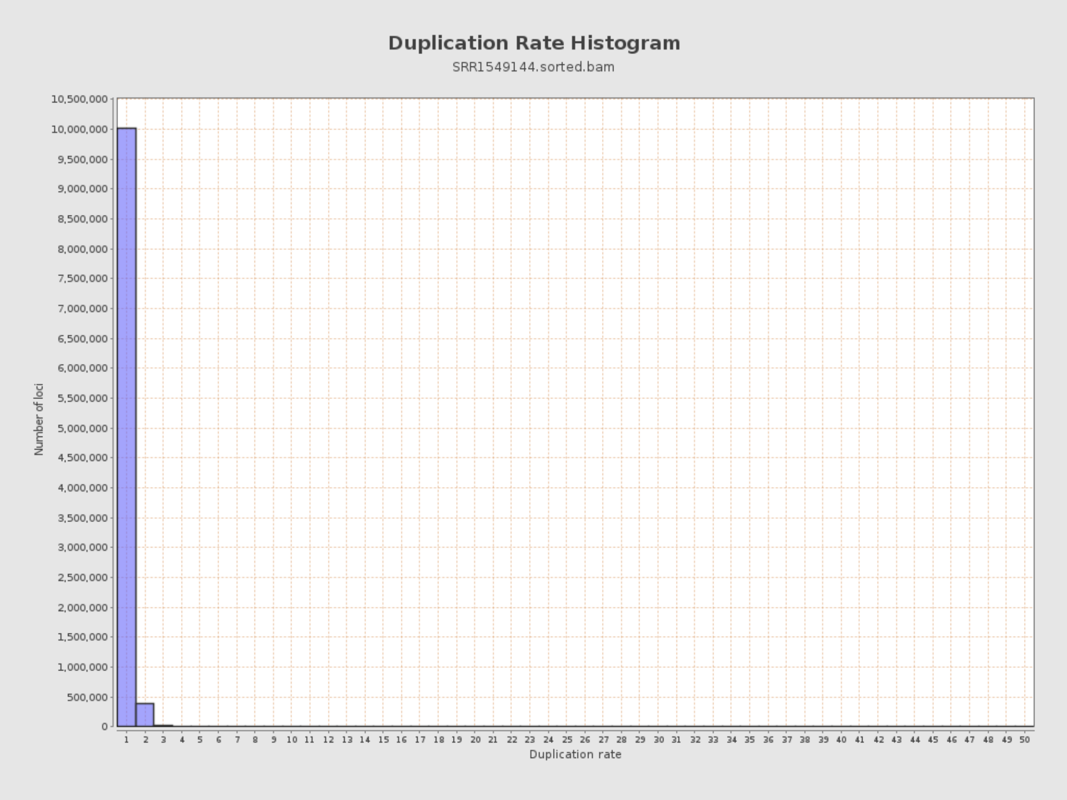
5. Results : Coverage Histogram (0-50X)



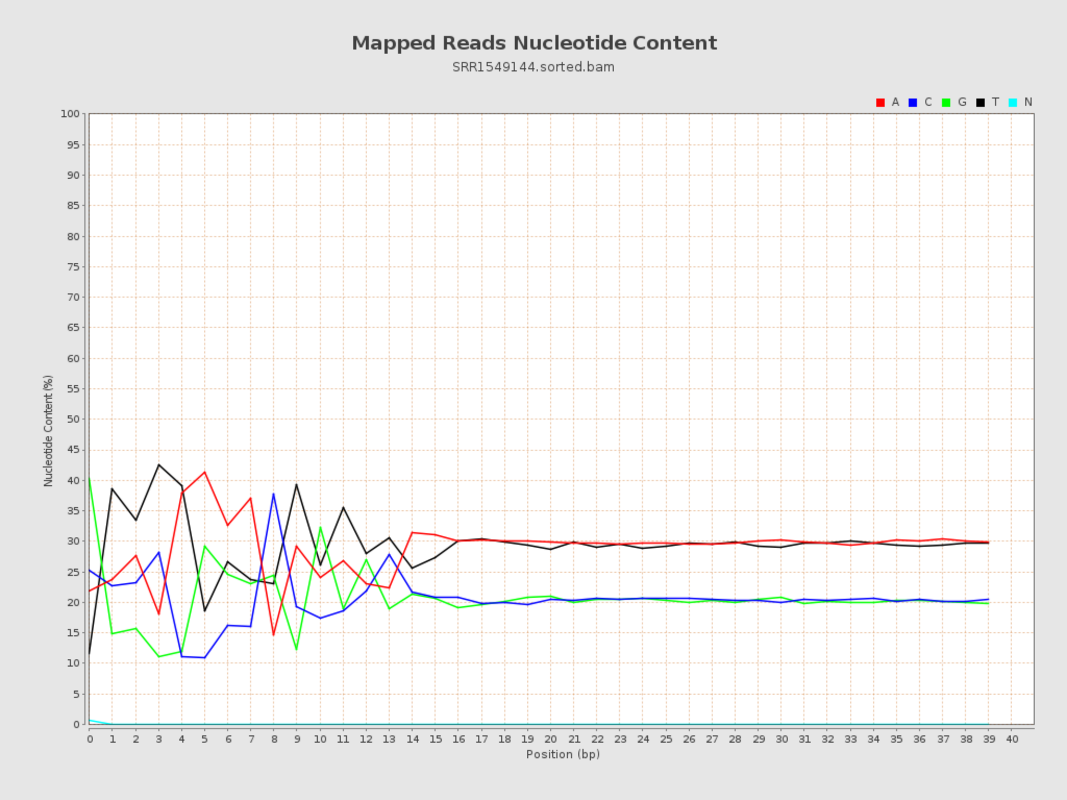
6. Results : Genome Fraction Coverage



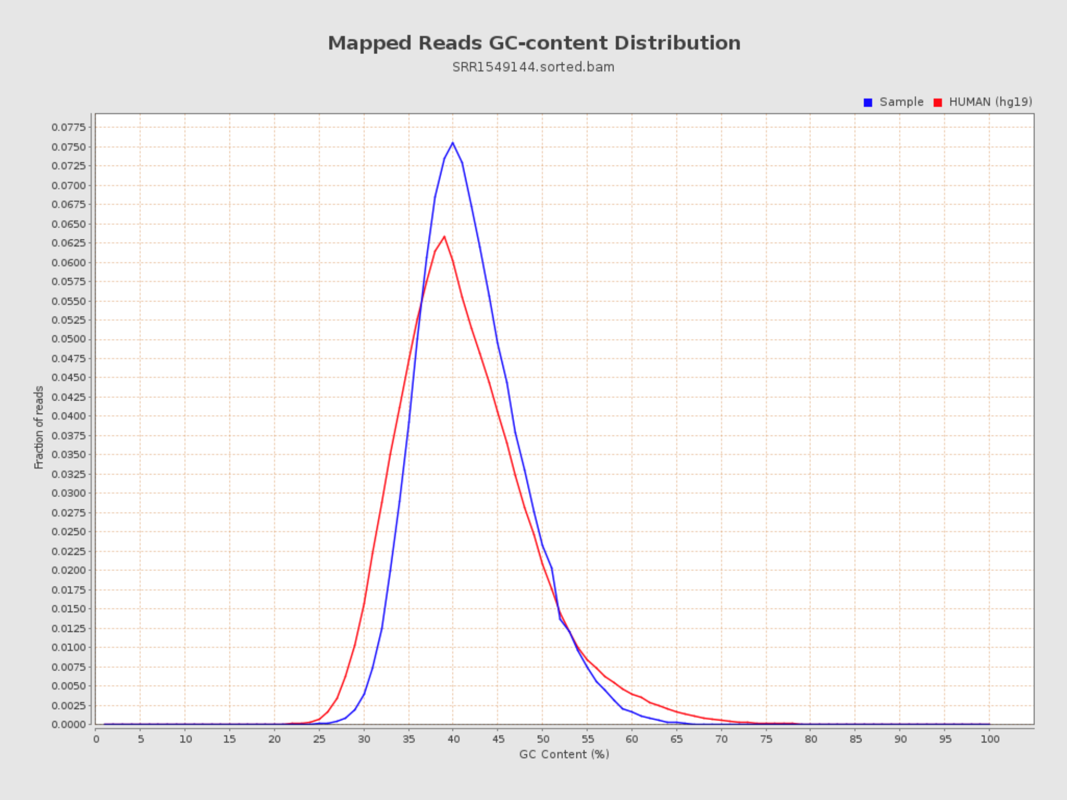
7. Results : Duplication Rate Histogram



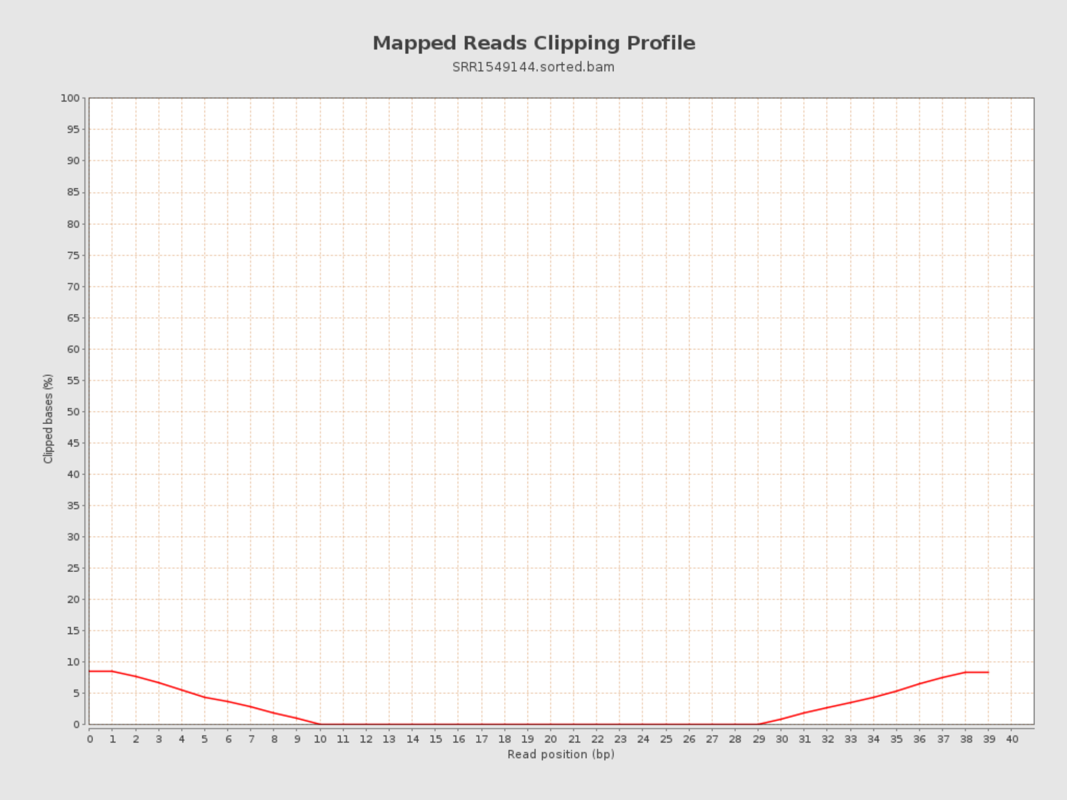
8. Results : Mapped Reads Nucleotide Content



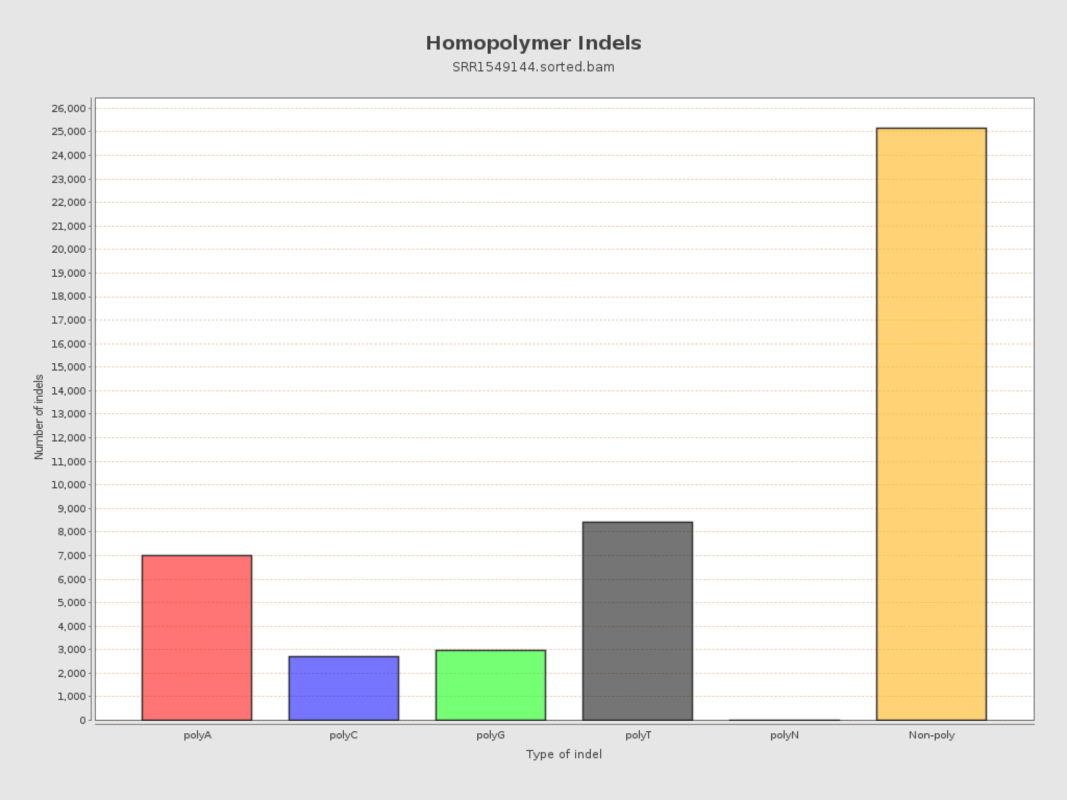
9. Results : Mapped Reads GC-content Distribution



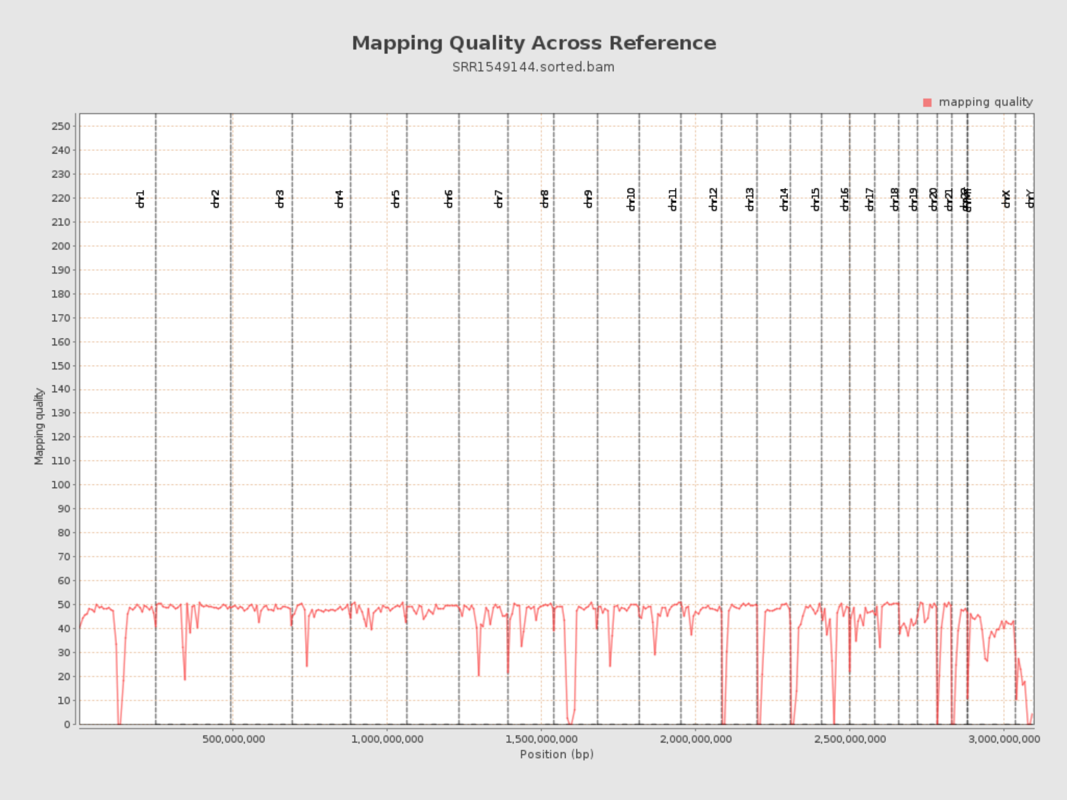
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram