Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 06:57:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549133.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_SRR1549133 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549133.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 06:57:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549133.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	13,629,696
Mapped reads	11,973,963 / 87.85%
Unmapped reads	1,655,733 / 12.15%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	599,700 / 4.4%
Duplication rate	3.97%
Clipped reads	597,496 / 4.38%

2.2. ACGT Content

Number/percentage of A's	137,782,948 / 28.98%
Number/percentage of C's	99,306,768 / 20.89%
Number/percentage of T's	139,240,870 / 29.29%
Number/percentage of G's	98,976,490 / 20.82%
Number/percentage of N's	110,622 / 0.02%
GC Percentage	41.71%

2.3. Coverage

Mean	0.1536
Standard Deviation	0.8749

2.4. Mapping Quality

Mean Mapping Quality	43.52

2.5. Mismatches and indels

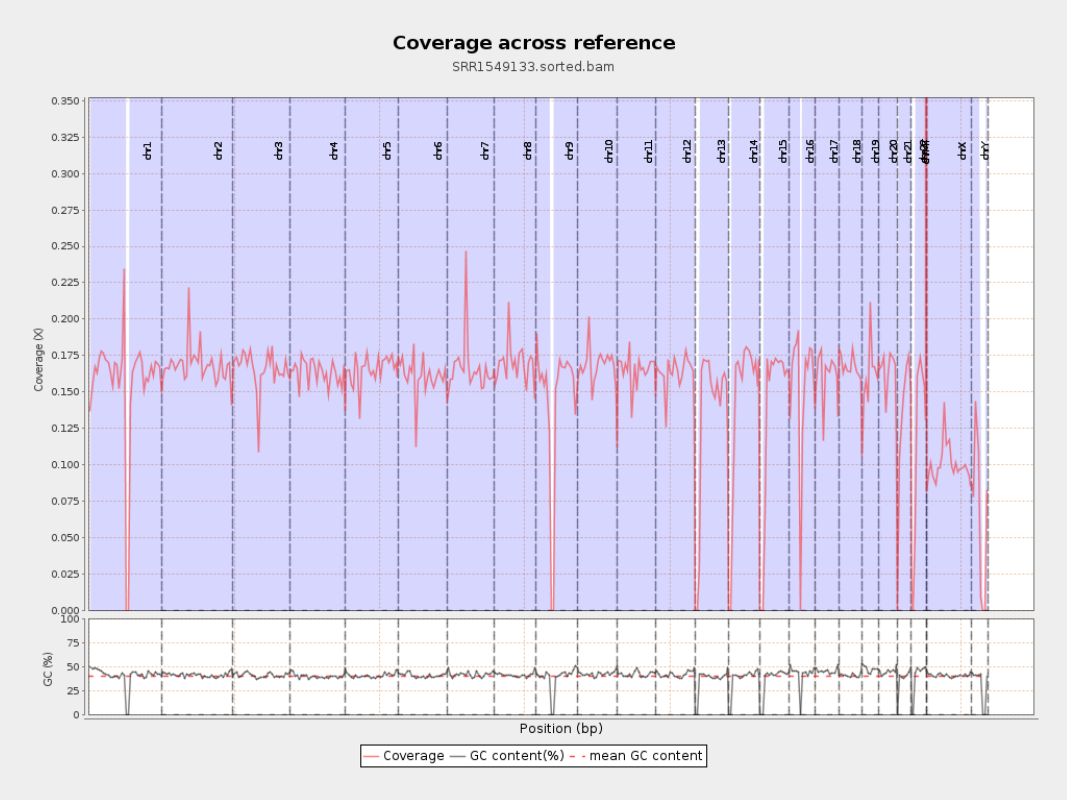
General error rate	0.32%
Mismatches	1,529,765
Insertions	11,685
Mapped reads with at least one insertion	0.1%
Deletions	35,467
Mapped reads with at least one deletion	0.3%
Homopolymer indels	46.14%

2.6. Chromosome stats

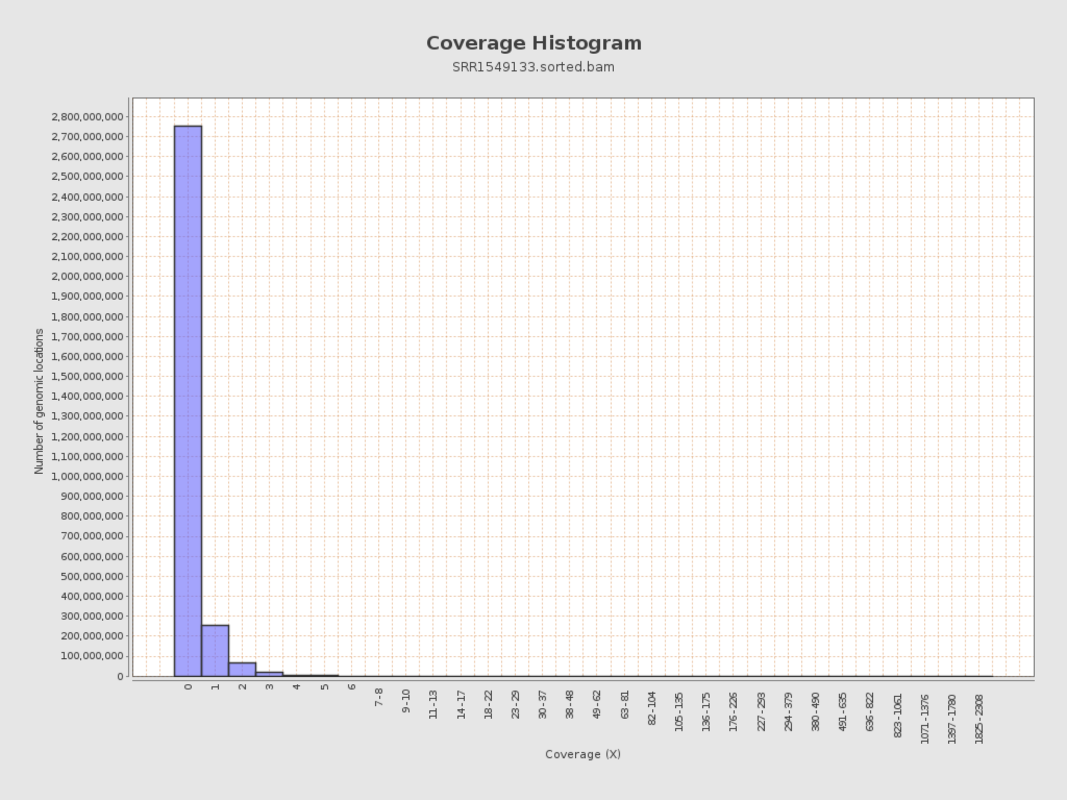
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	39021333	0.1566	1.8005
chr2	243199373	41004901	0.1686	0.8007
chr3	198022430	32771938	0.1655	0.5311
chr4	191154276	31235007	0.1634	0.548
chr5	180915260	29931727	0.1654	0.5451
chr6	171115067	27554696	0.161	0.6001
chr7	159138663	26543219	0.1668	1.2445
chr8	146364022	24769404	0.1692	0.7711

chr9	141213431	20071576	0.1421	0.7446
chr10	135534747	22870846	0.1687	0.7768
chr11	135006516	22210158	0.1645	0.7203
chr12	133851895	21826505	0.1631	0.5556
chr13	115169878	15240796	0.1323	0.4651
chr14	107349540	15114972	0.1408	0.6374
chr15	102531392	14000794	0.1366	0.4761
chr16	90354753	13851522	0.1533	0.574
chr17	81195210	13038520	0.1606	0.5805
chr18	78077248	13109555	0.1679	1.5669
chr19	59128983	9598936	0.1623	1.4505
chr20	63025520	10266756	0.1629	0.5626
chr21	48129895	6347632	0.1319	0.556
chr22	51304566	5706911	0.1112	0.476
chrMT	16571	96983	5.8526	7.2547
chrX	155270560	15567584	0.1003	0.5395
chrY	59373566	3709910	0.0625	0.4631

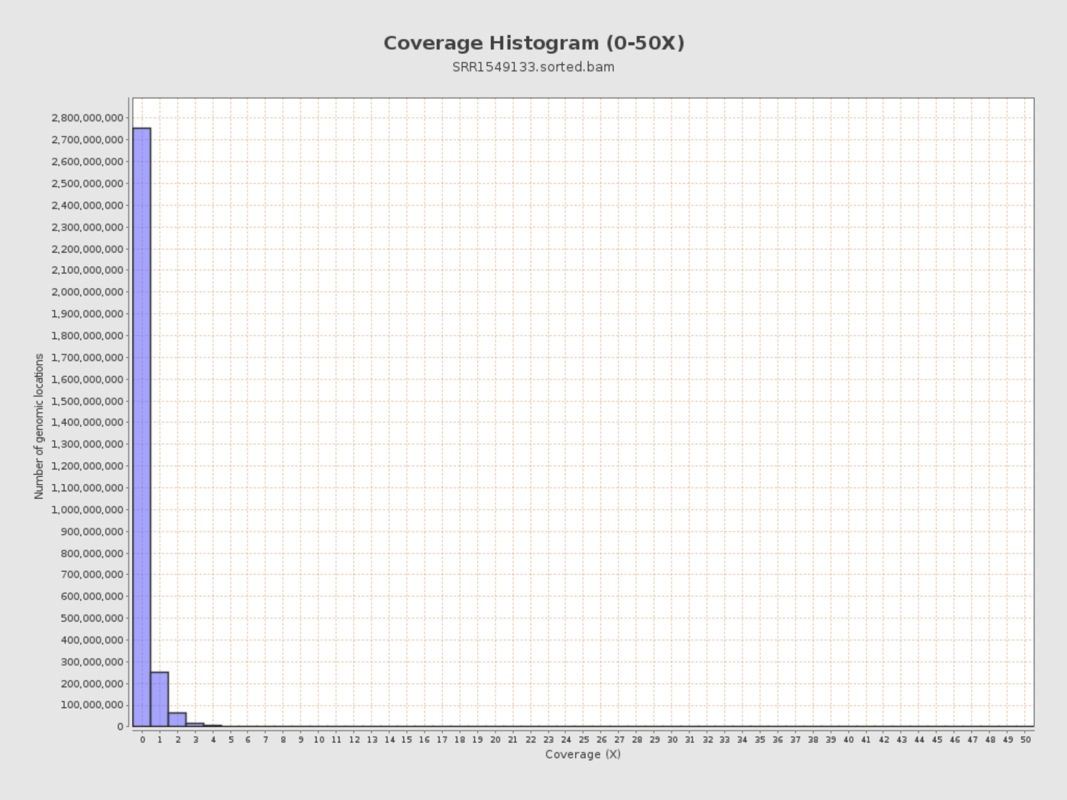
3. Results : Coverage across reference



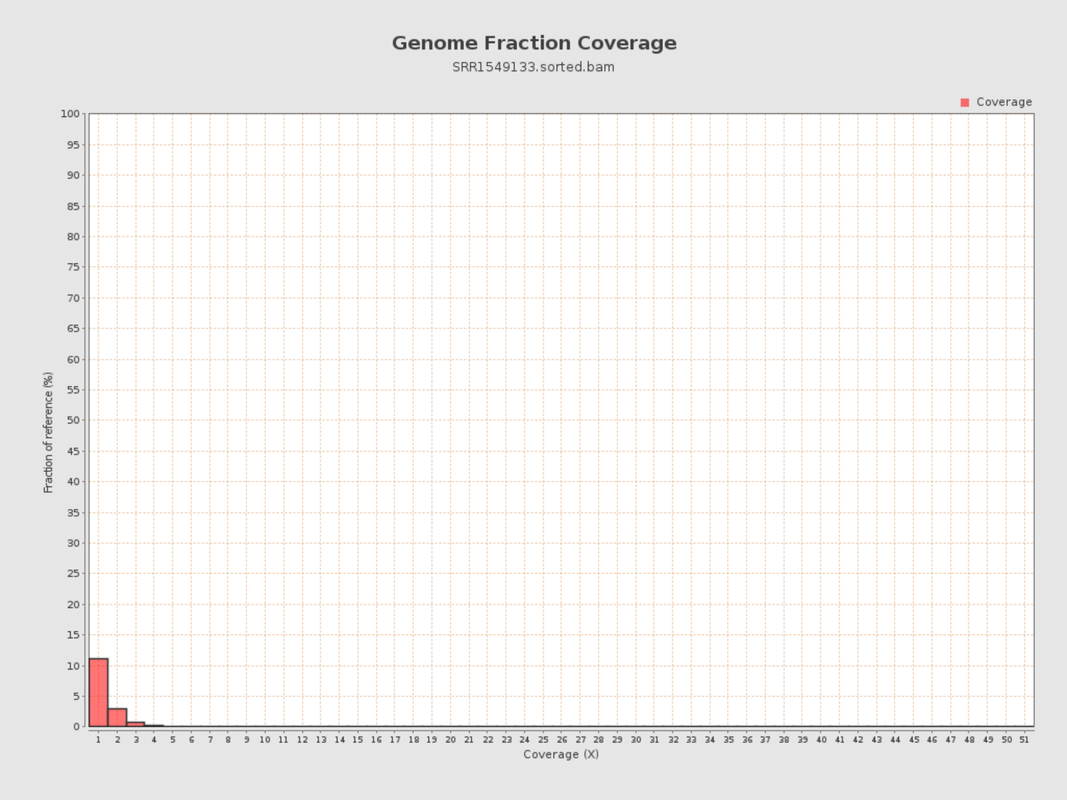
4. Results : Coverage Histogram



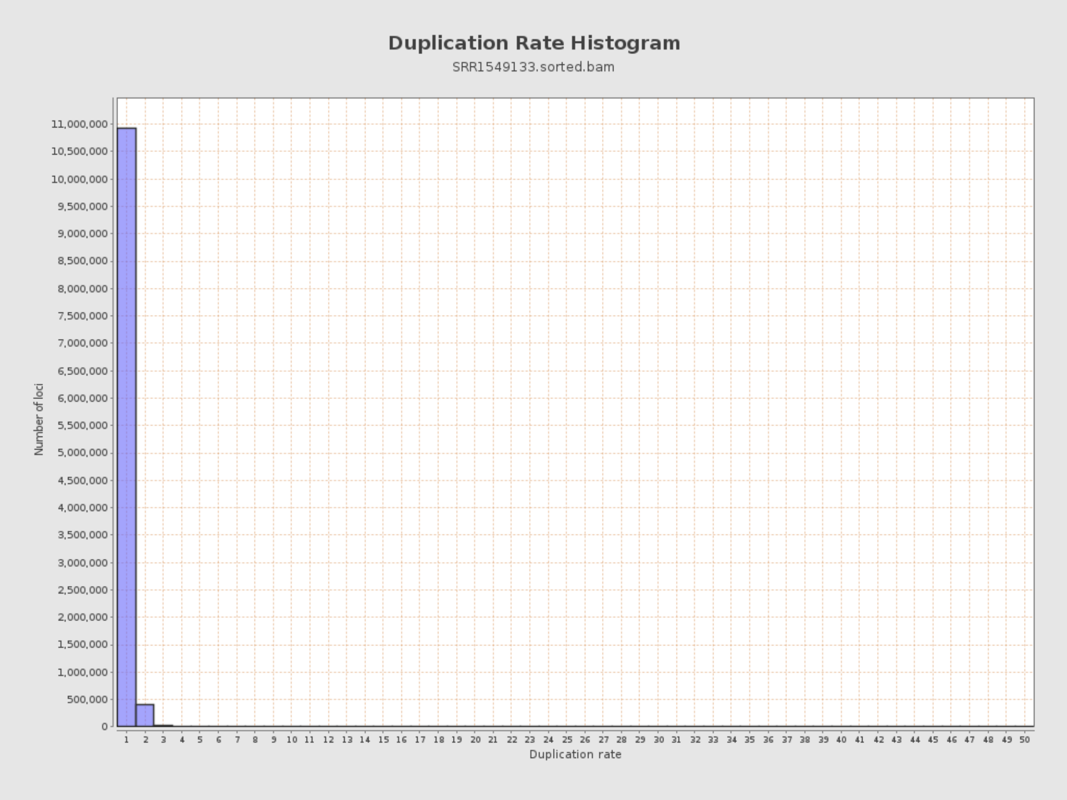
5. Results : Coverage Histogram (0-50X)



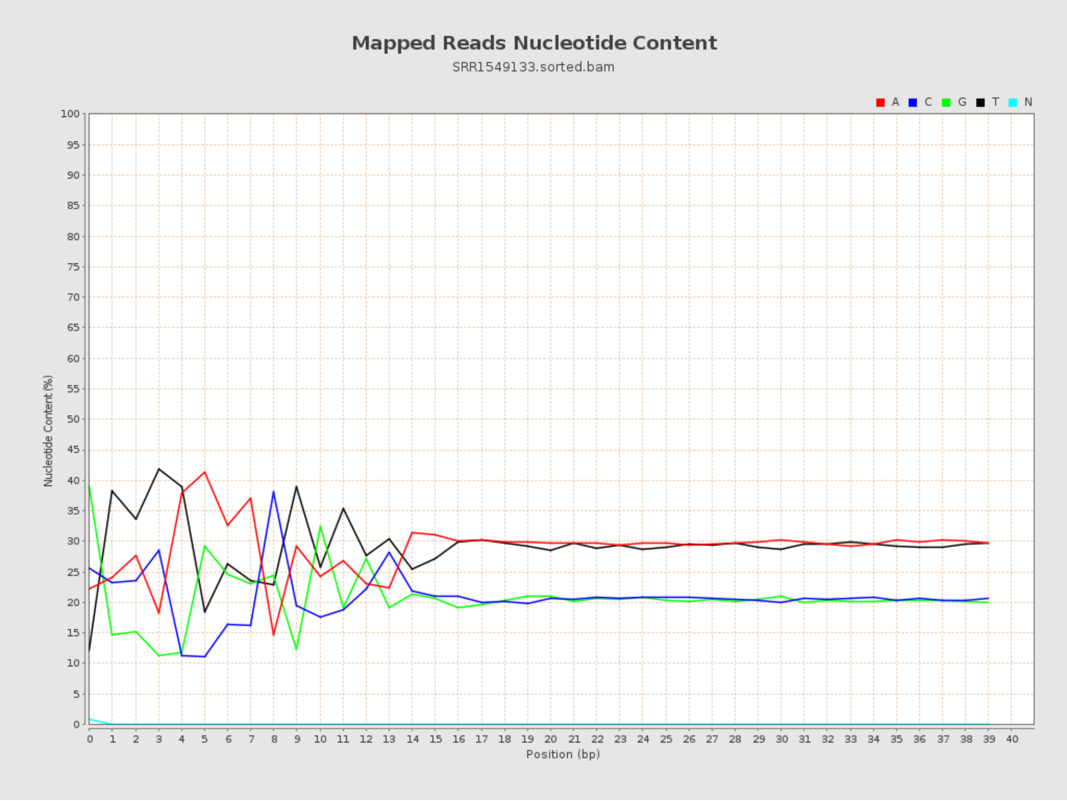
6. Results : Genome Fraction Coverage



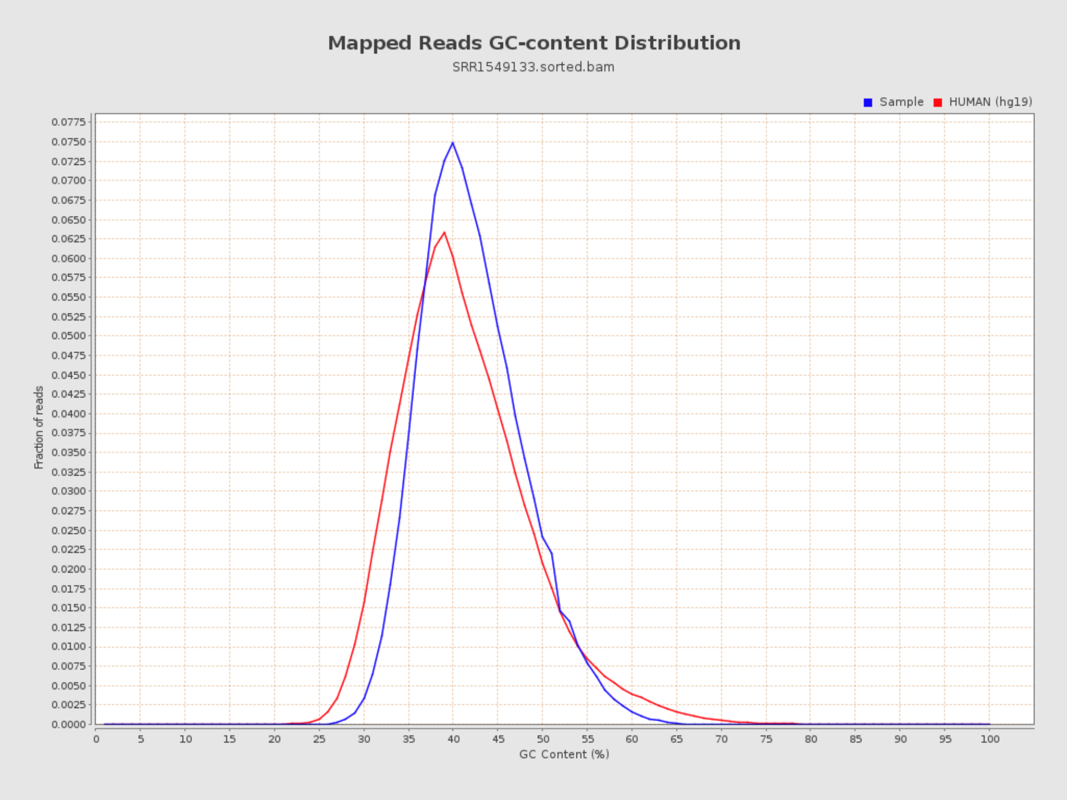
7. Results : Duplication Rate Histogram



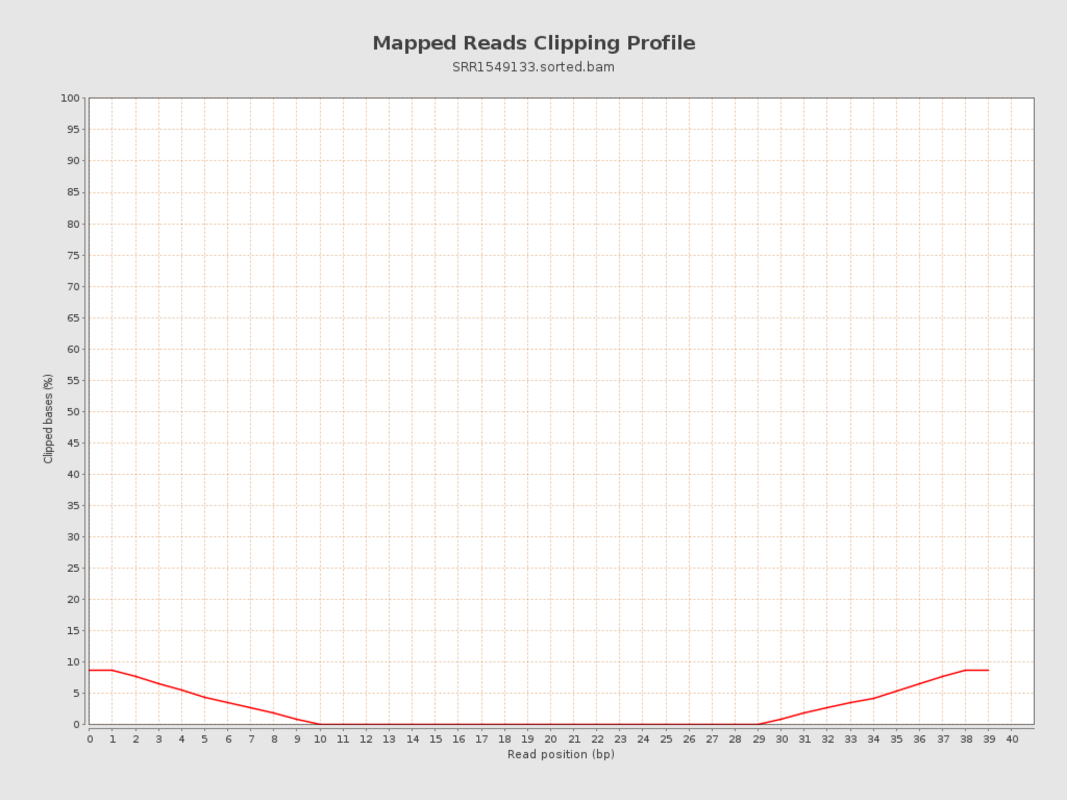
8. Results : Mapped Reads Nucleotide Content



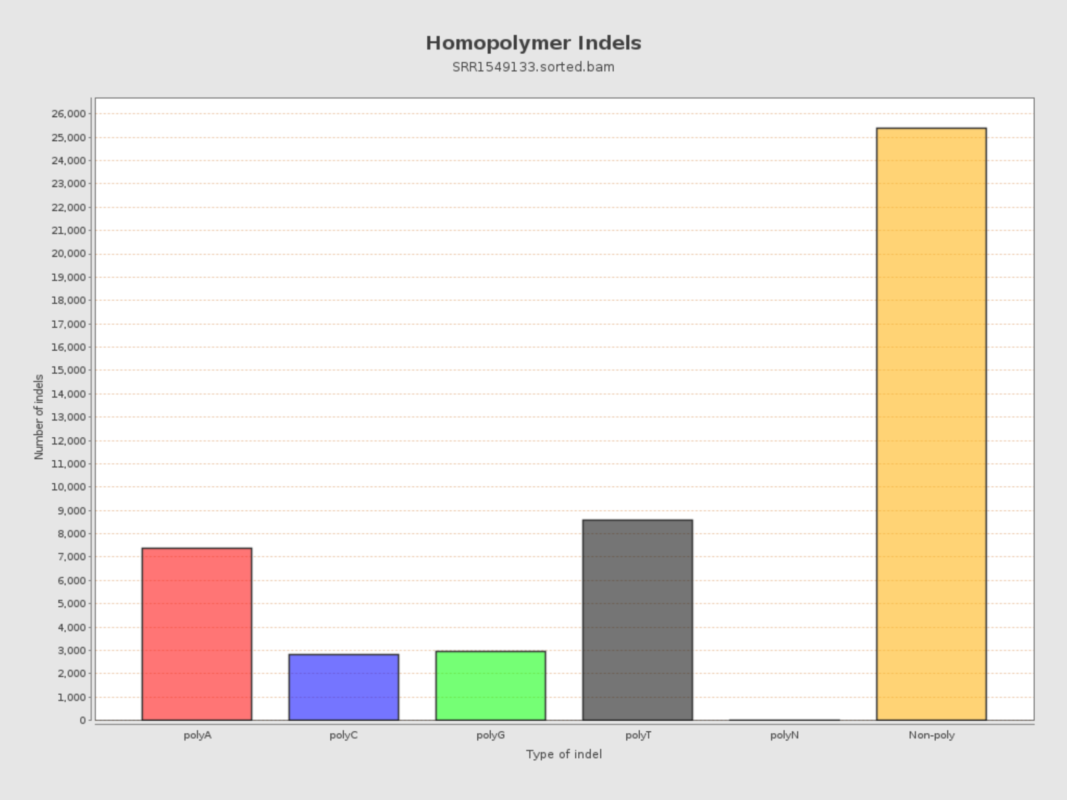
9. Results : Mapped Reads GC-content Distribution



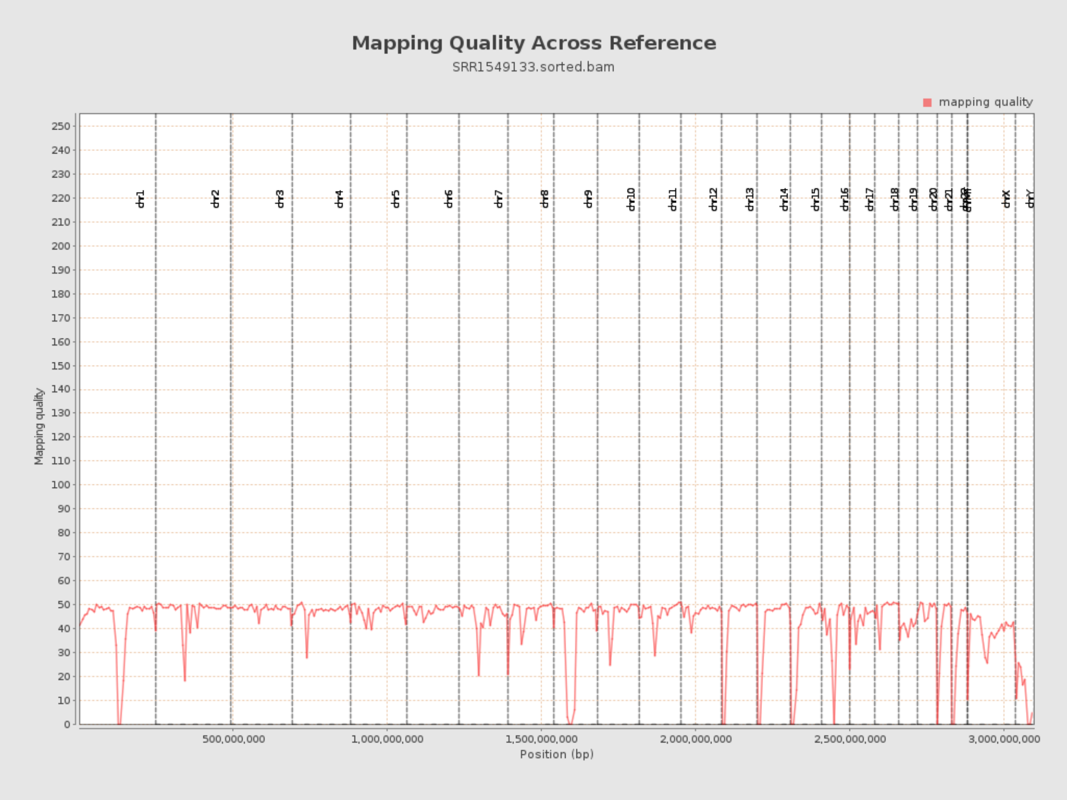
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram