Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 07:33:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549136.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_SRR1549136 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549136.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 07:33:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549136.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	13,649,303
Mapped reads	12,038,981 / 88.2%
Unmapped reads	1,610,322 / 11.8%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	637,735 / 4.67%
Duplication rate	4.08%
Clipped reads	675,681 / 4.95%

2.2. ACGT Content

Number/percentage of A's	133,973,618 / 28.05%
Number/percentage of C's	104,236,924 / 21.83%
Number/percentage of T's	135,483,798 / 28.37%
Number/percentage of G's	103,774,208 / 21.73%
Number/percentage of N's	100,589 / 0.02%
GC Percentage	43.56%

2.3. Coverage

Mean	0.1543
Standard Deviation	0.9196

2.4. Mapping Quality

Mean Mapping Quality	42.4

2.5. Mismatches and indels

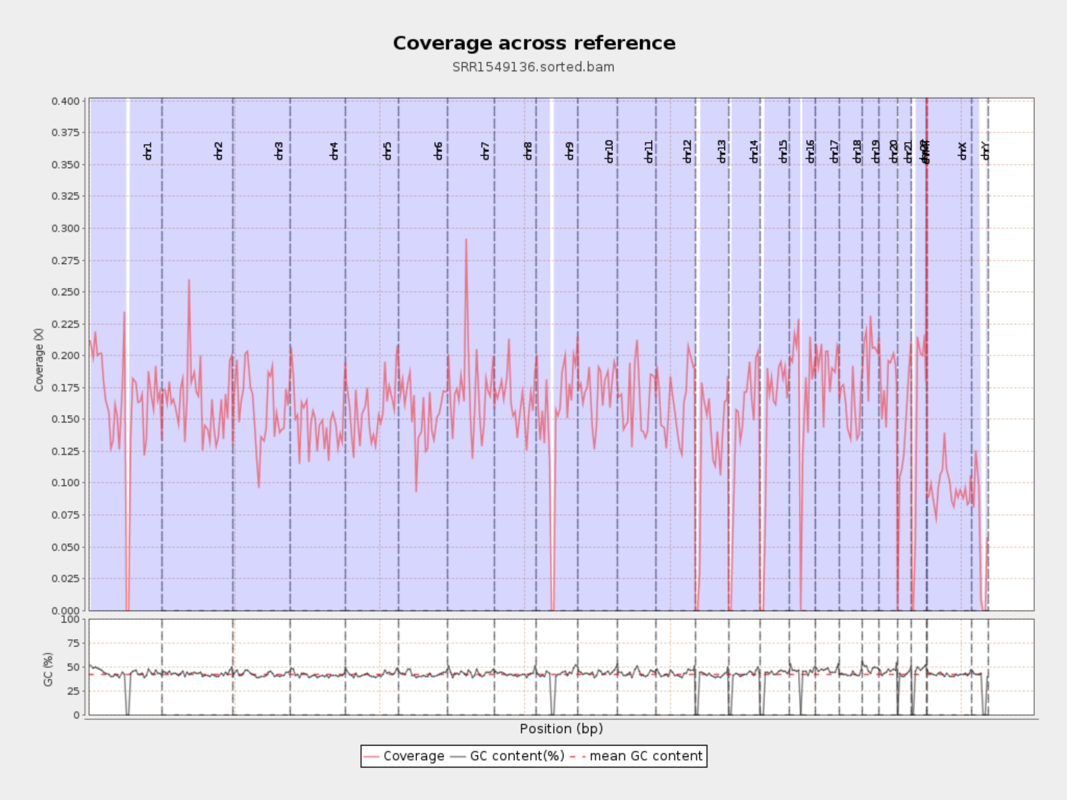
General error rate	0.33%
Mismatches	1,556,675
Insertions	13,154
Mapped reads with at least one insertion	0.11%
Deletions	38,049
Mapped reads with at least one deletion	0.32%
Homopolymer indels	46.34%

2.6. Chromosome stats

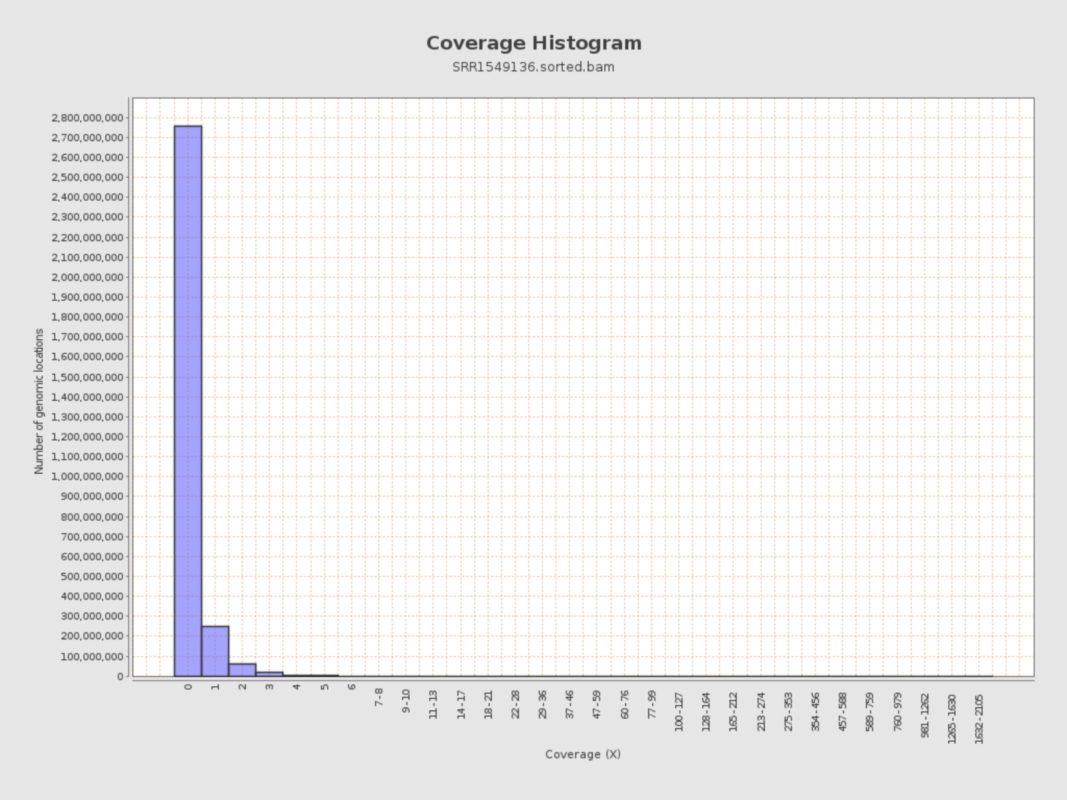
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	39959757	0.1603	1.6188
chr2	243199373	40007526	0.1645	0.9116
chr3	198022430	31537382	0.1593	0.5412
chr4	191154276	28246806	0.1478	0.538
chr5	180915260	28436887	0.1572	0.5497
chr6	171115067	26698984	0.156	0.6159
chr7	159138663	27451101	0.1725	1.5245
chr8	146364022	24122731	0.1648	1.0854

chr9	141213431	20728855	0.1468	0.8623
chr10	135534747	23291577	0.1718	0.8164
chr11	135006516	22219879	0.1646	0.7727
chr12	133851895	21878445	0.1635	0.5811
chr13	115169878	14122797	0.1226	0.4523
chr14	107349540	14956466	0.1393	0.6947
chr15	102531392	14971286	0.146	0.504
chr16	90354753	15621271	0.1729	0.6229
chr17	81195210	15609186	0.1922	0.627
chr18	78077248	12438383	0.1593	1.7812
chr19	59128983	12144817	0.2054	1.4775
chr20	63025520	11380218	0.1806	0.6178
chr21	48129895	6397390	0.1329	0.615
chr22	51304566	7244789	0.1412	0.5762
chrMT	16571	10368	0.6257	1.2588
chrX	155270560	14820999	0.0955	0.5745
chrY	59373566	3319236	0.0559	0.3838

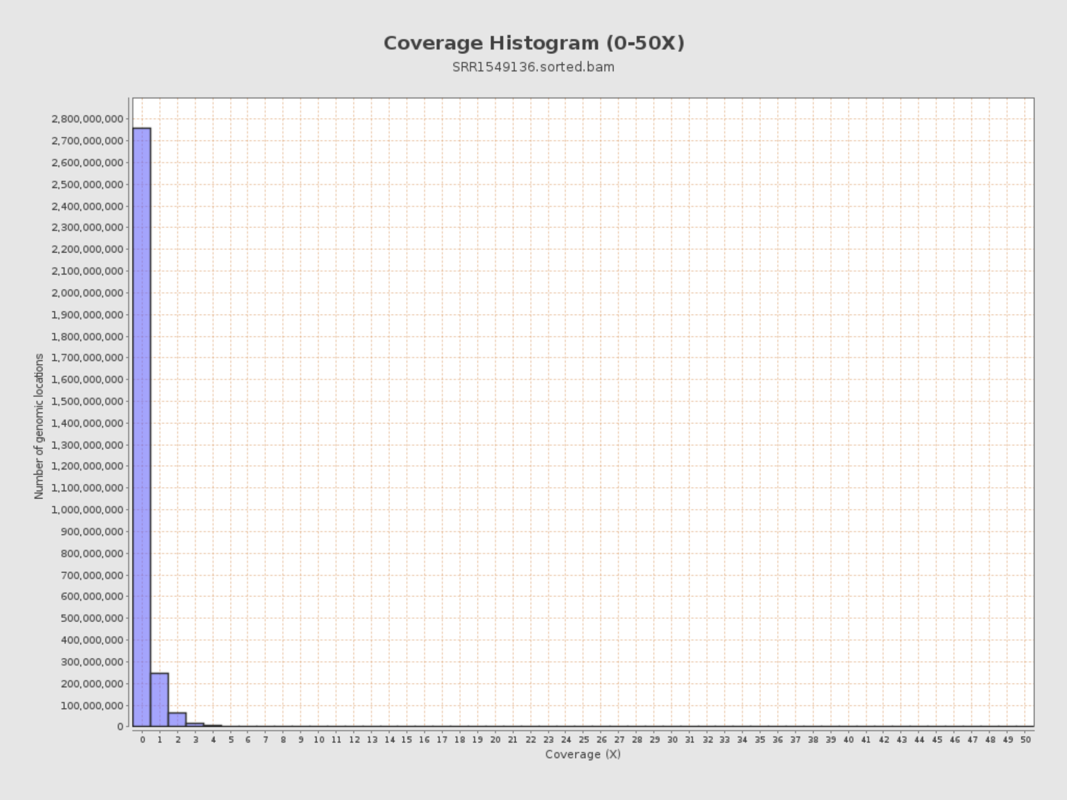
3. Results : Coverage across reference



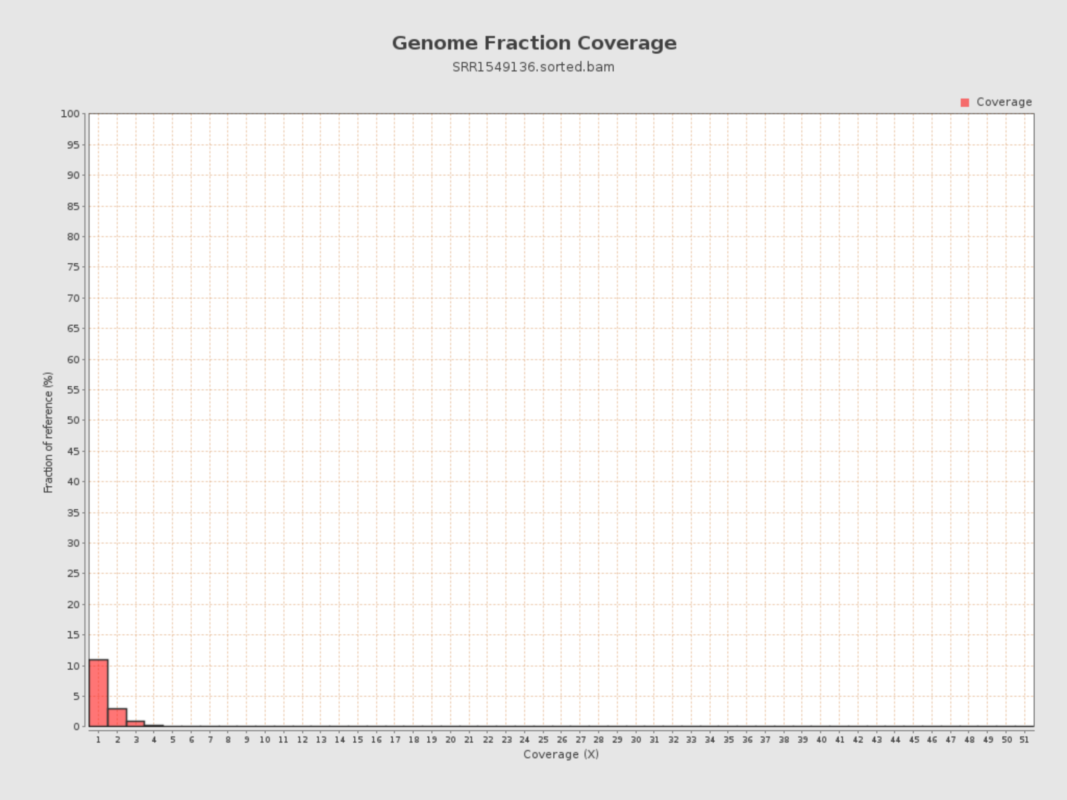
4. Results : Coverage Histogram



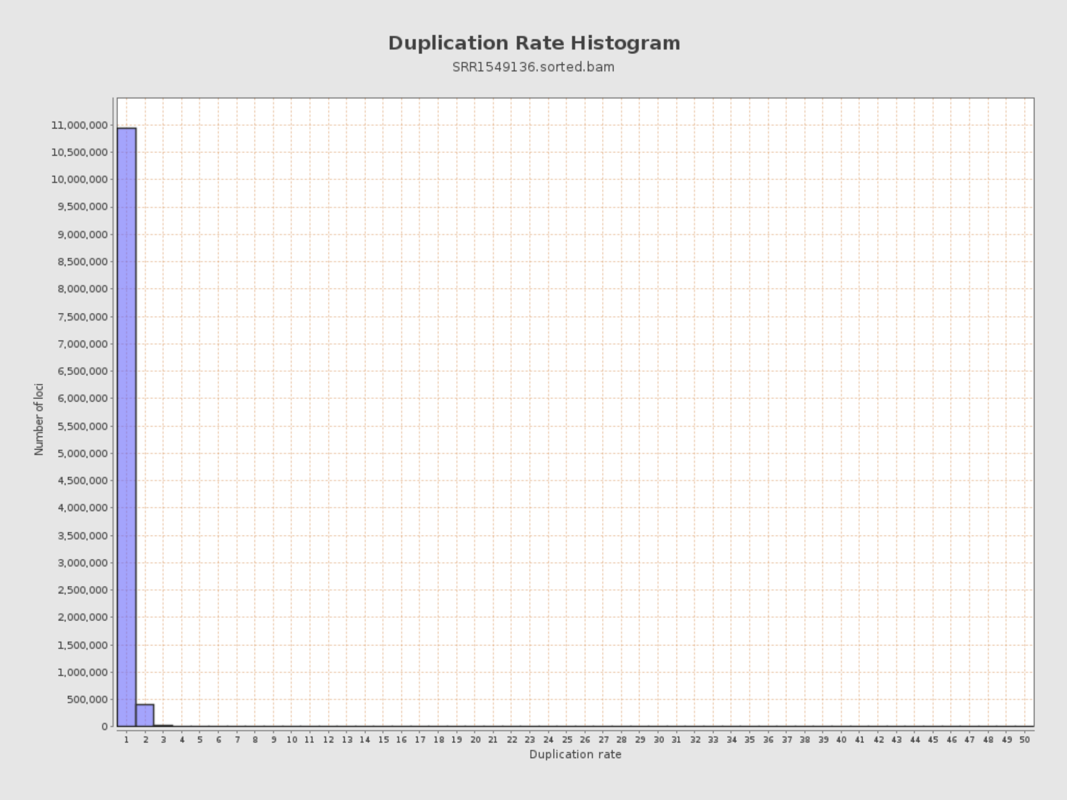
5. Results : Coverage Histogram (0-50X)



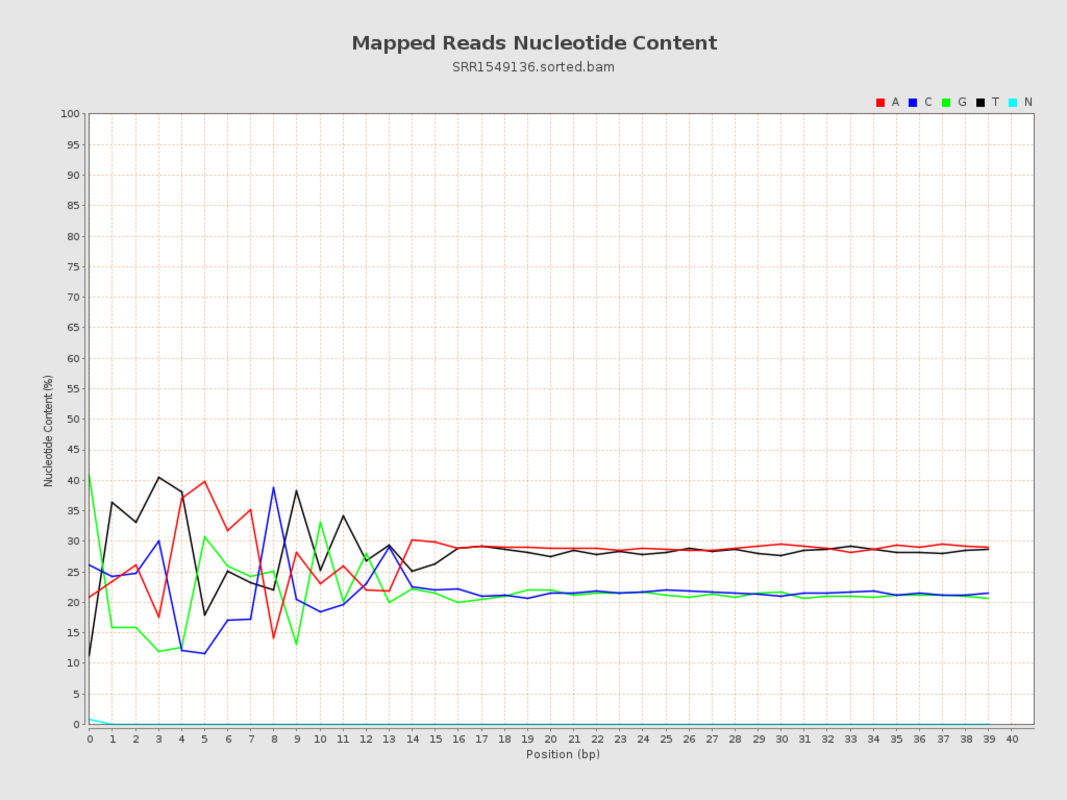
6. Results : Genome Fraction Coverage



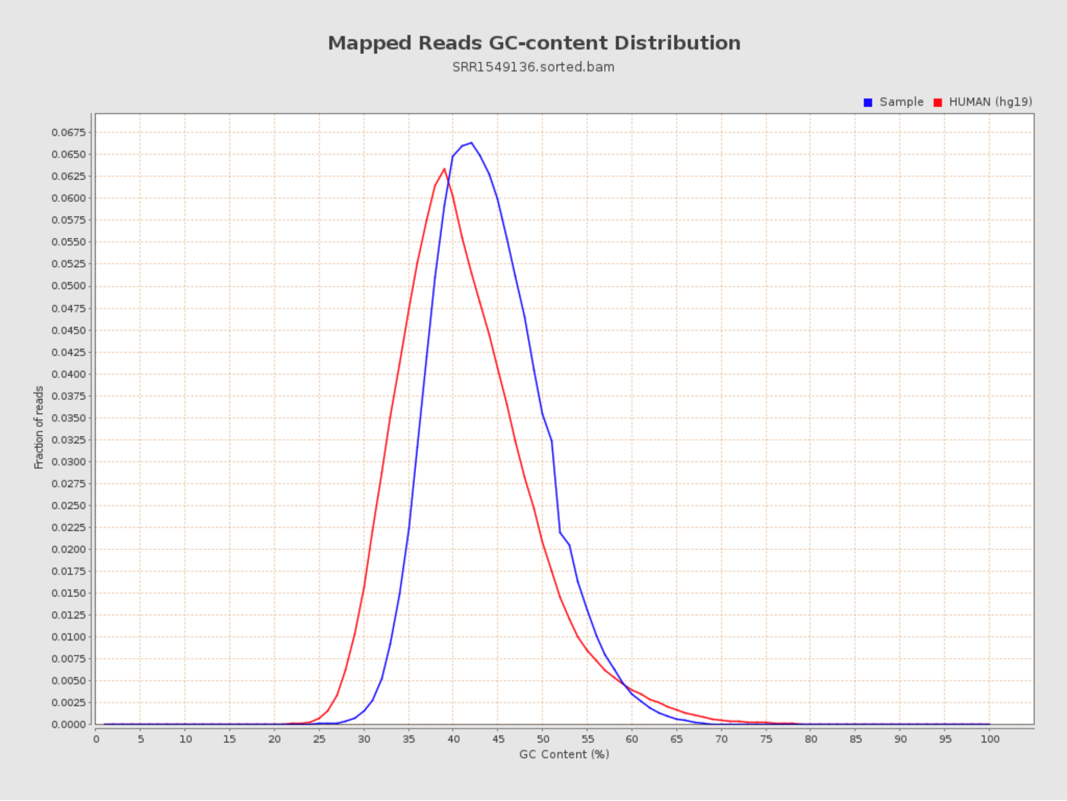
7. Results : Duplication Rate Histogram



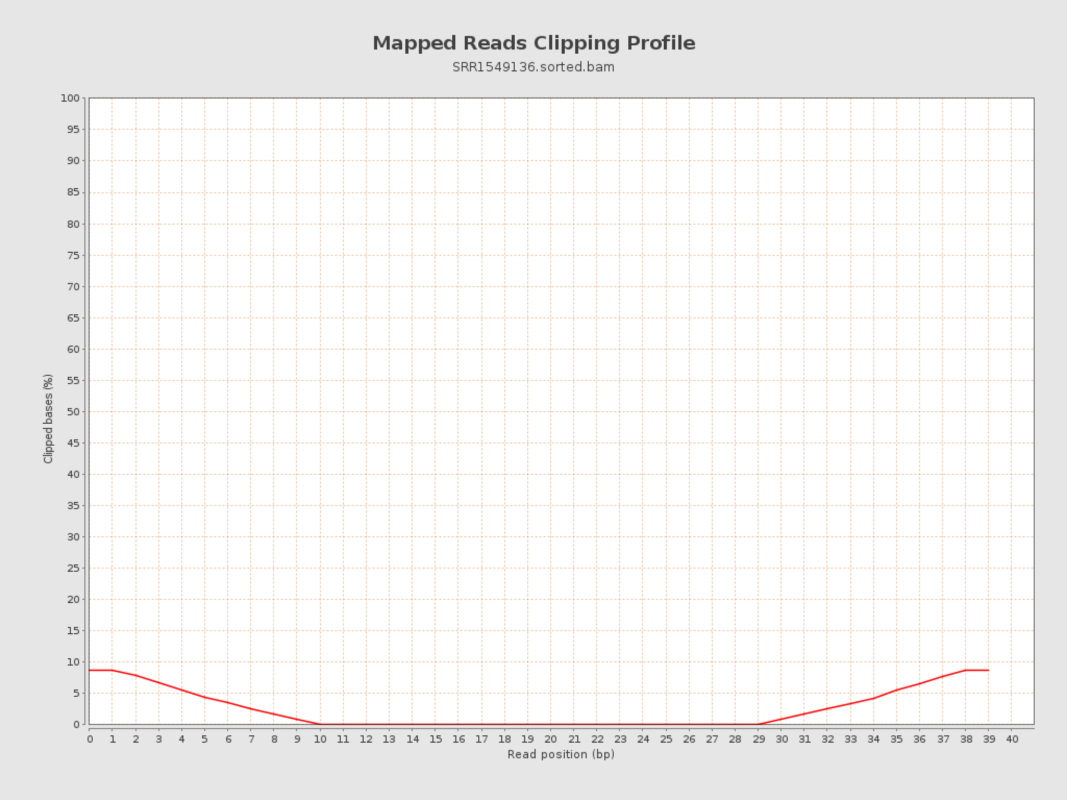
8. Results : Mapped Reads Nucleotide Content



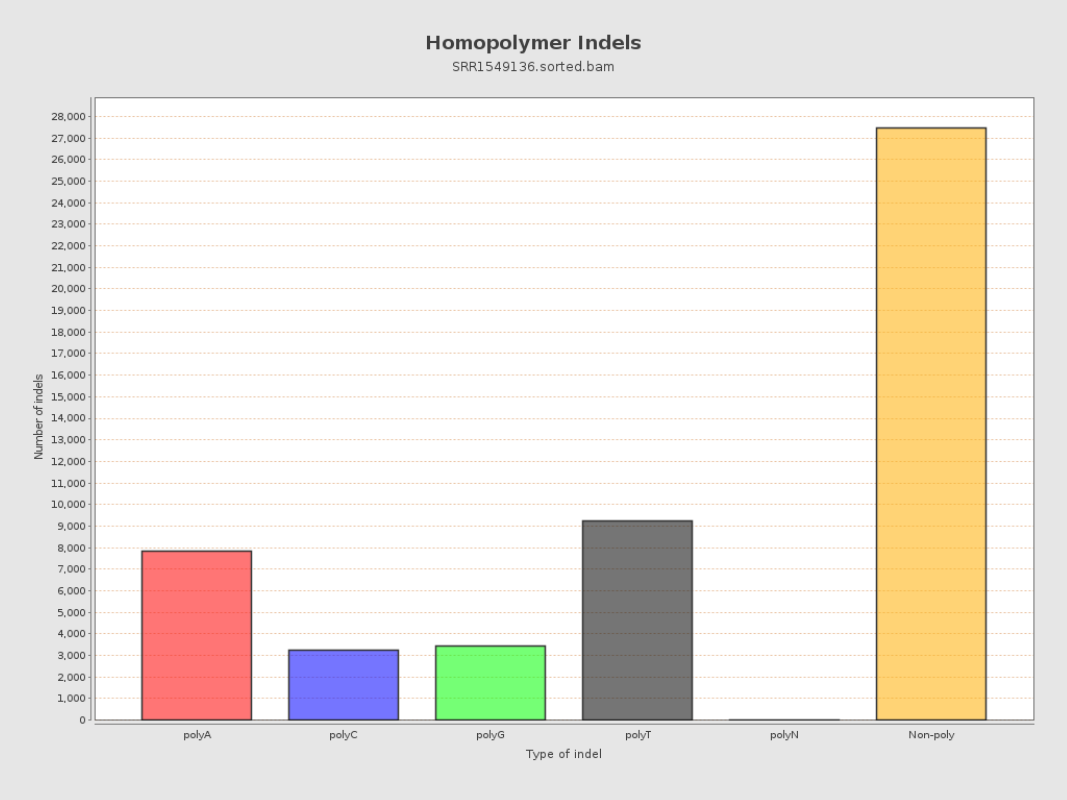
9. Results : Mapped Reads GC-content Distribution



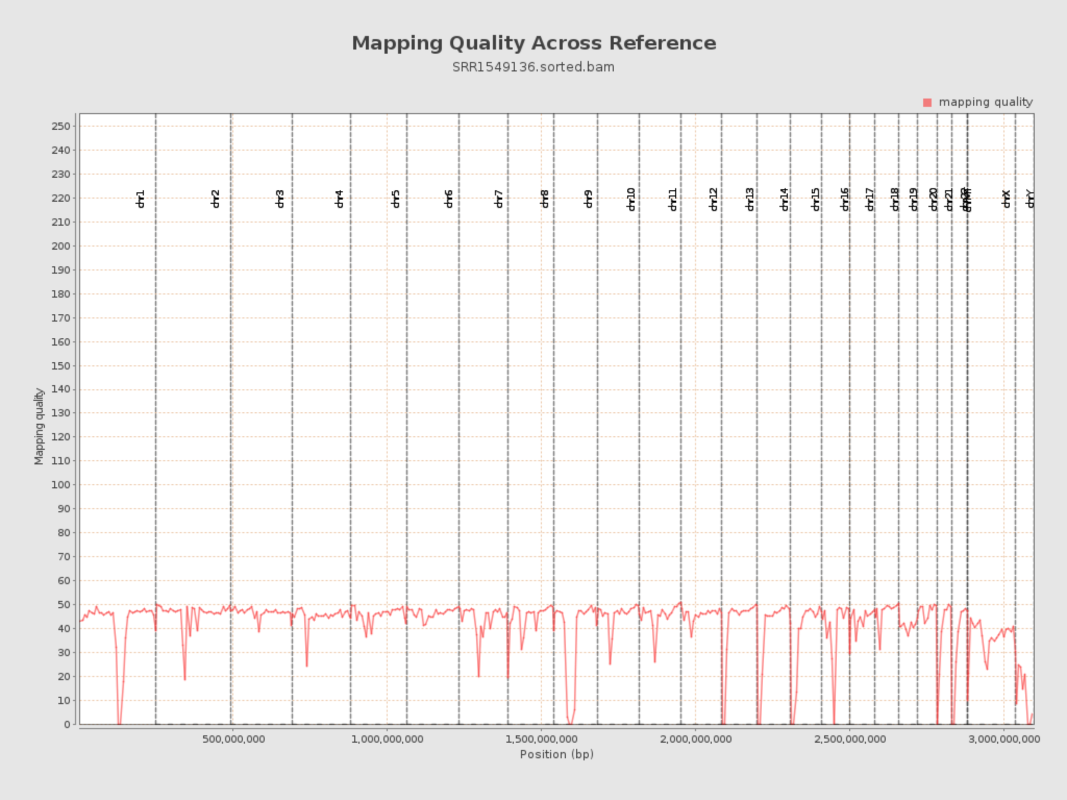
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram