Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 09:18:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549143.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_SRR1549143 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549143.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 09:18:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549143.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	13,420,015
Mapped reads	11,782,554 / 87.8%
Unmapped reads	1,637,461 / 12.2%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	641,594 / 4.78%
Duplication rate	4.29%
Clipped reads	654,760 / 4.88%

2.2. ACGT Content

Number/percentage of A's	132,158,892 / 28.28%
Number/percentage of C's	100,302,173 / 21.46%
Number/percentage of T's	134,158,439 / 28.71%
Number/percentage of G's	100,645,126 / 21.53%
Number/percentage of N's	93,698 / 0.02%
GC Percentage	43%

2.3. Coverage

Mean	0.151
Standard Deviation	0.8722

2.4. Mapping Quality

Mean Mapping Quality	42.61

2.5. Mismatches and indels

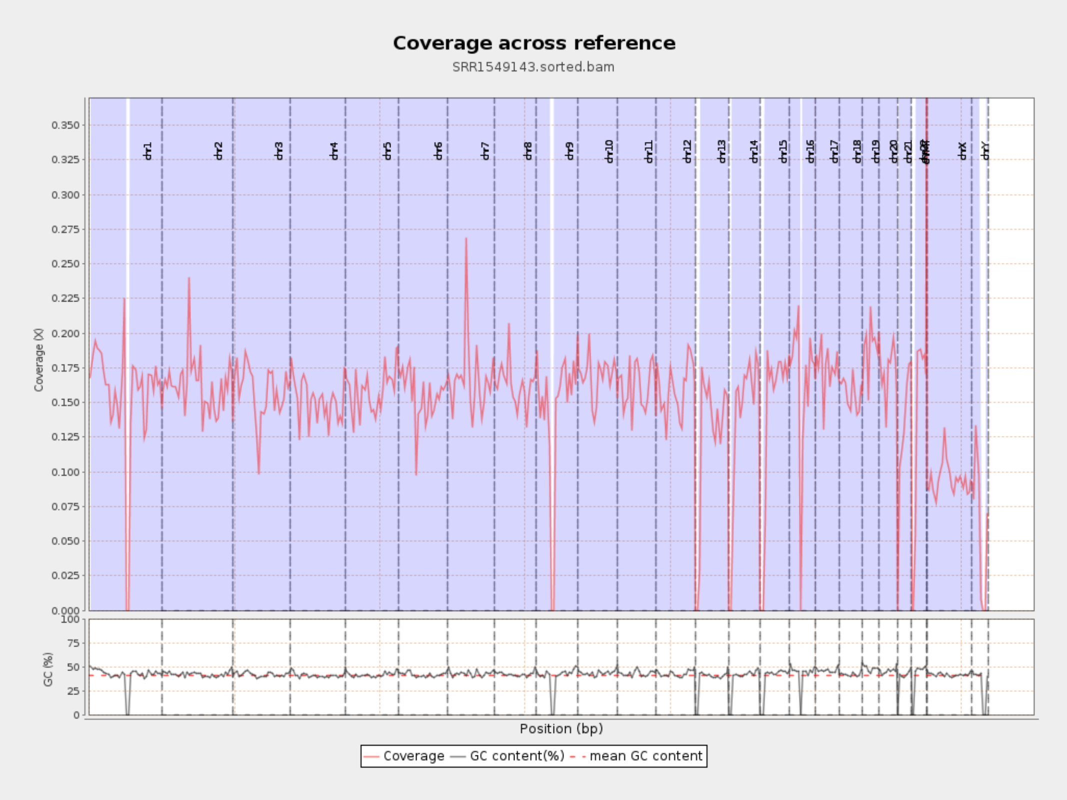
General error rate	0.32%
Mismatches	1,469,825
Insertions	12,369
Mapped reads with at least one insertion	0.1%
Deletions	37,482
Mapped reads with at least one deletion	0.32%
Homopolymer indels	45.83%

2.6. Chromosome stats

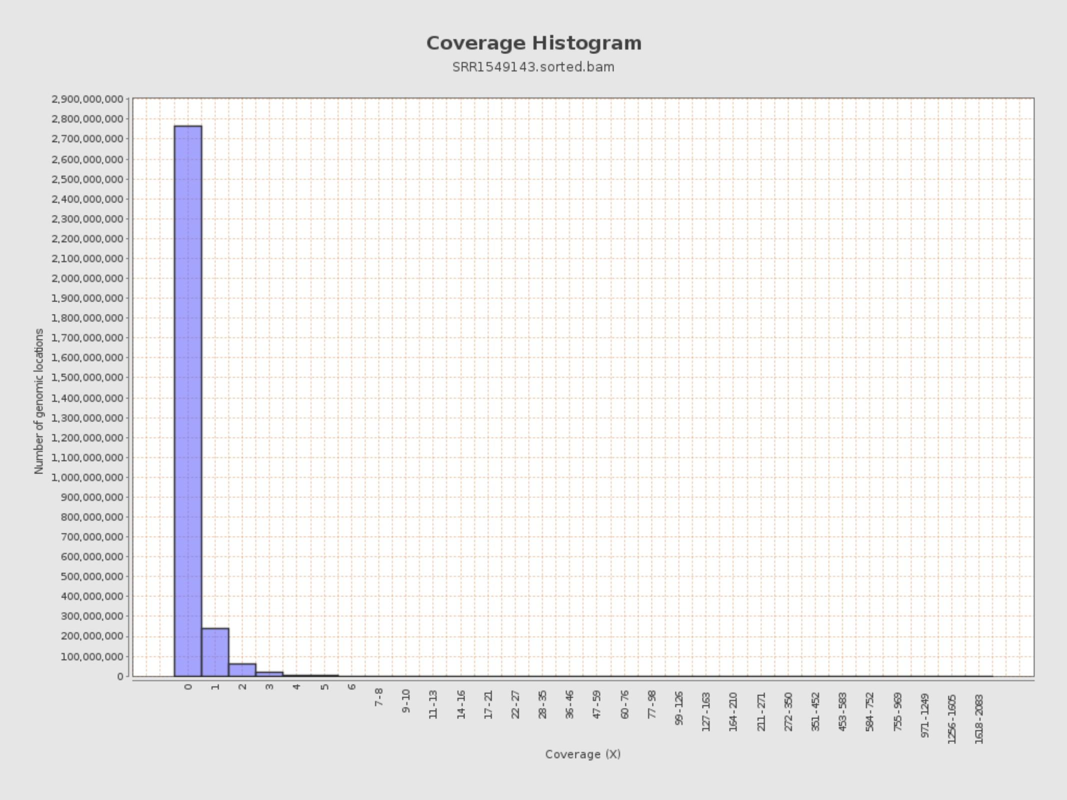
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	38583540	0.1548	1.602
chr2	243199373	39579372	0.1627	0.8582
chr3	198022430	31142151	0.1573	0.5294
chr4	191154276	28810827	0.1507	0.5455
chr5	180915260	28581544	0.158	0.5436
chr6	171115067	26644922	0.1557	0.6052
chr7	159138663	26598373	0.1671	1.348
chr8	146364022	23769550	0.1624	0.7753

chr9	141213431	19930003	0.1411	0.8105
chr10	135534747	22882871	0.1688	0.804
chr11	135006516	21829983	0.1617	0.7547
chr12	133851895	21420307	0.16	0.5699
chr13	115169878	14253531	0.1238	0.4579
chr14	107349540	14653006	0.1365	0.7243
chr15	102531392	14407107	0.1405	0.4974
chr16	90354753	14902308	0.1649	0.6114
chr17	81195210	14199524	0.1749	0.6254
chr18	78077248	12241076	0.1568	1.6884
chr19	59128983	11214502	0.1897	1.4531
chr20	63025520	10846016	0.1721	0.5939
chr21	48129895	6201262	0.1288	0.588
chr22	51304566	6505153	0.1268	0.5215
chrMT	16571	7631	0.4605	0.8166
chrX	155270560	14720066	0.0948	0.5413
chrY	59373566	3481178	0.0586	0.4314

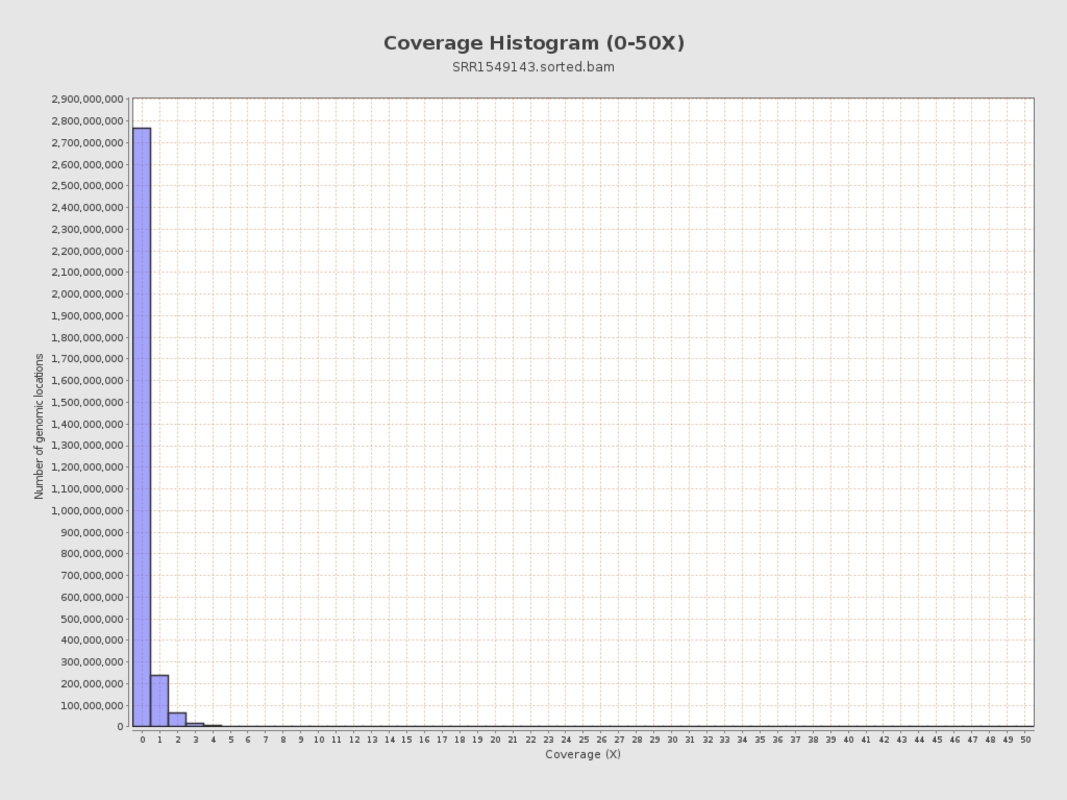
3. Results : Coverage across reference



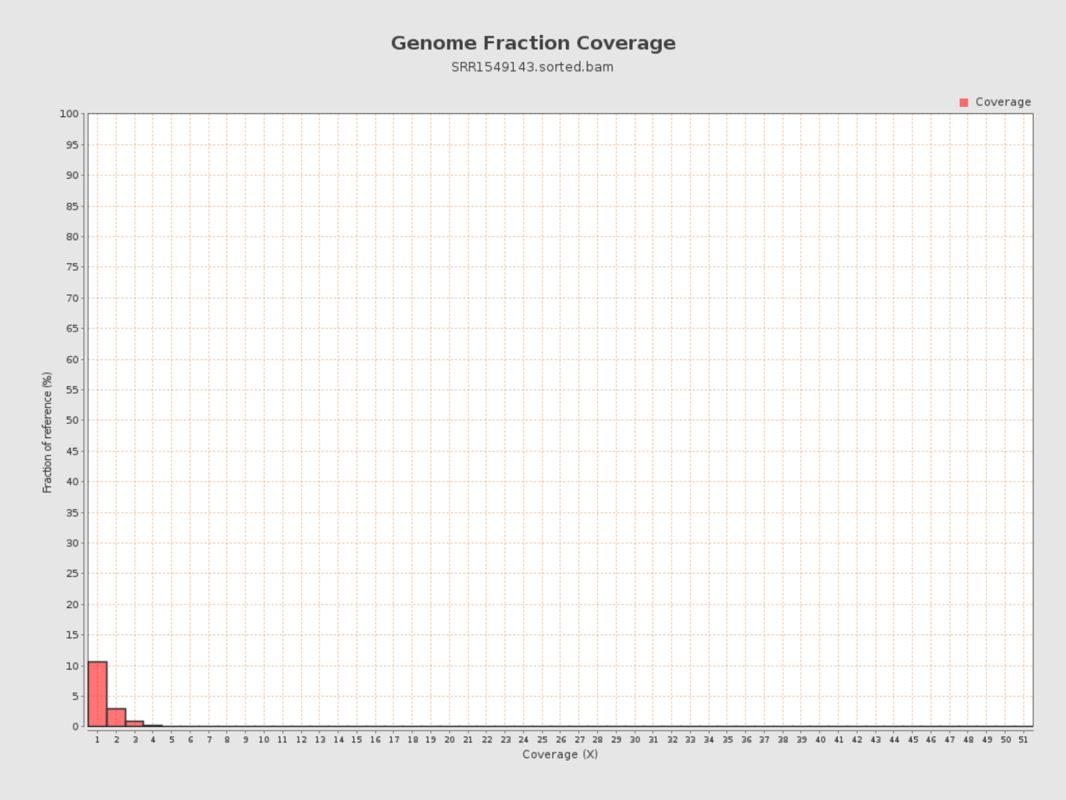
4. Results : Coverage Histogram



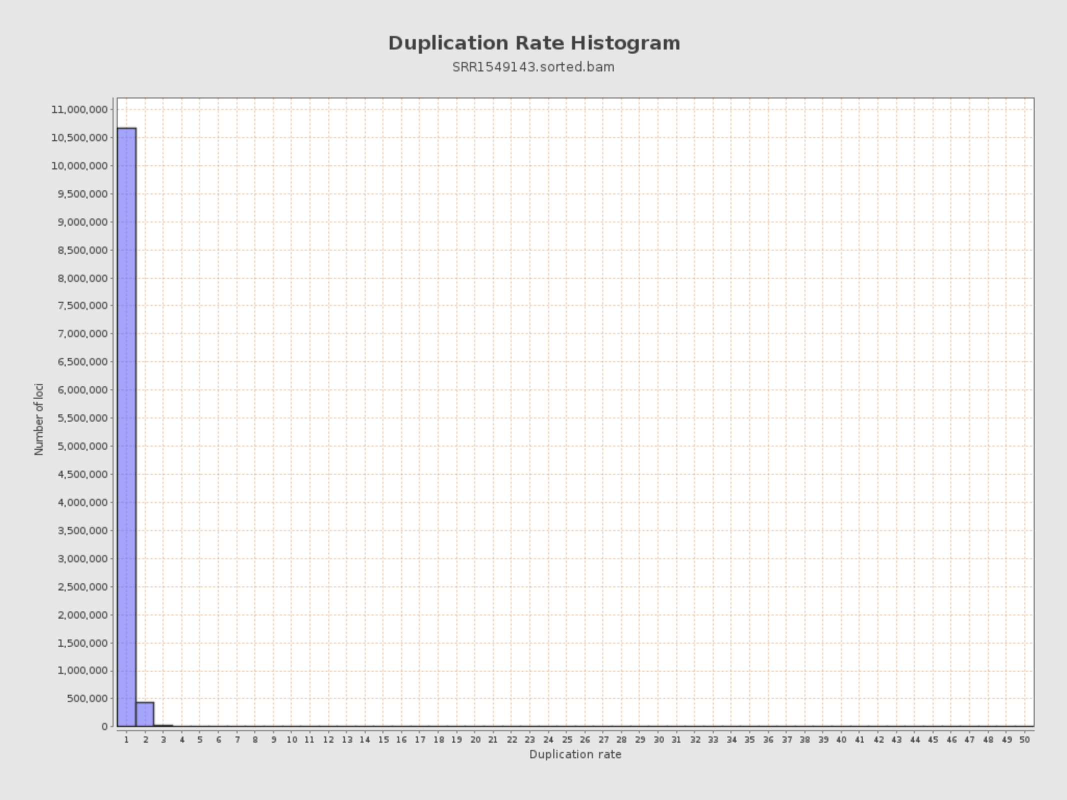
5. Results : Coverage Histogram (0-50X)



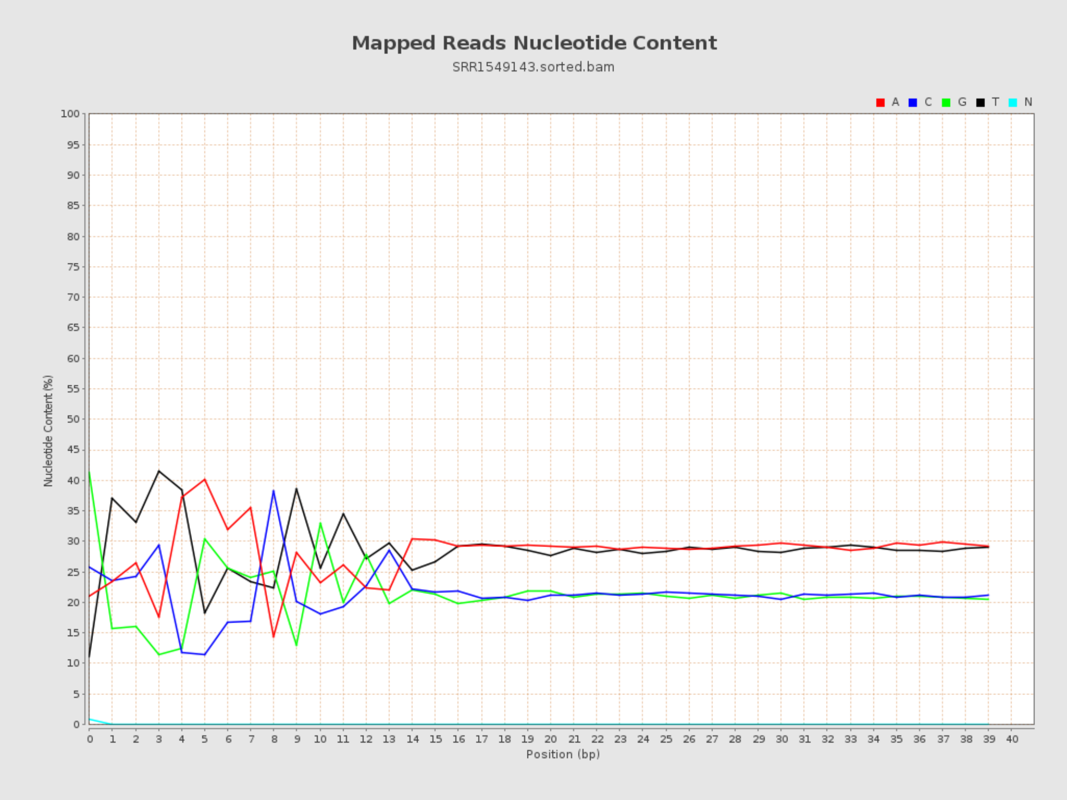
6. Results : Genome Fraction Coverage



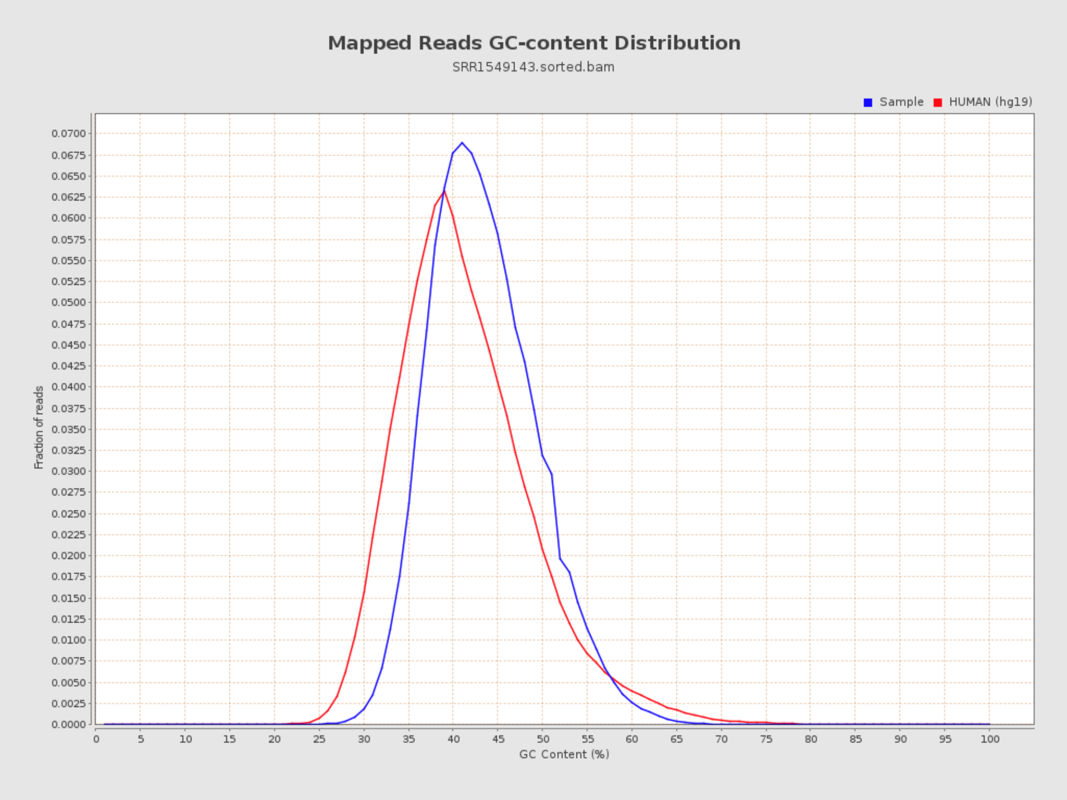
7. Results : Duplication Rate Histogram



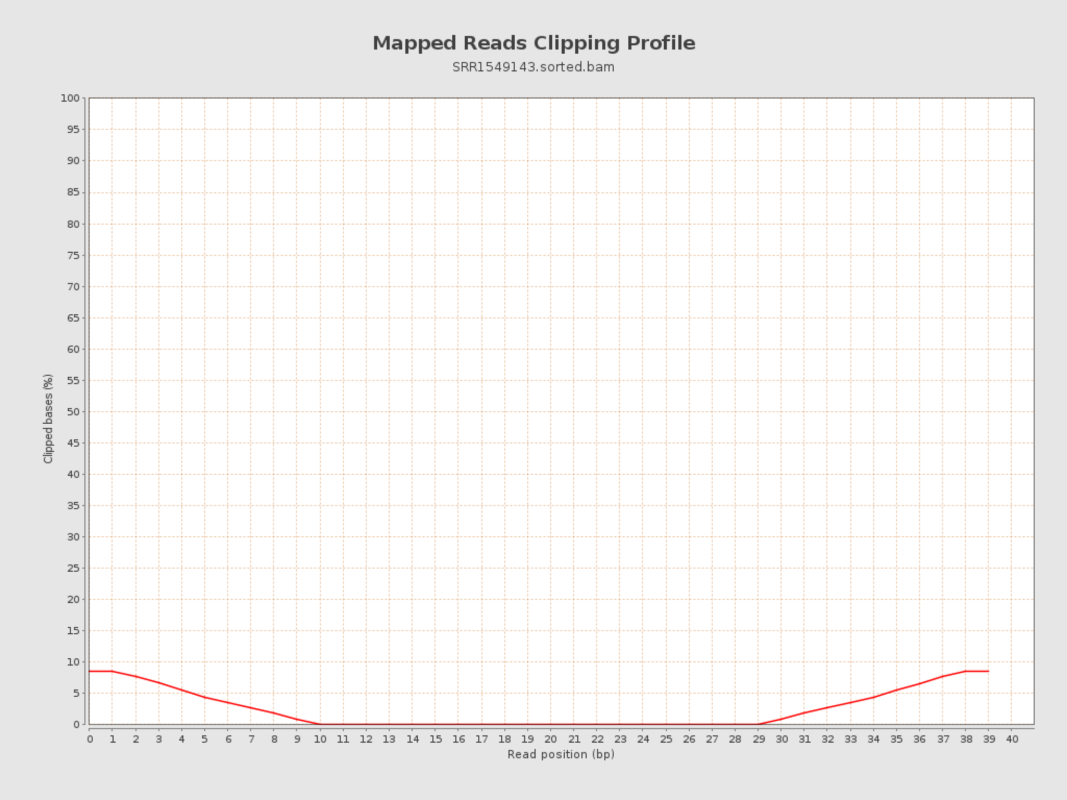
8. Results : Mapped Reads Nucleotide Content



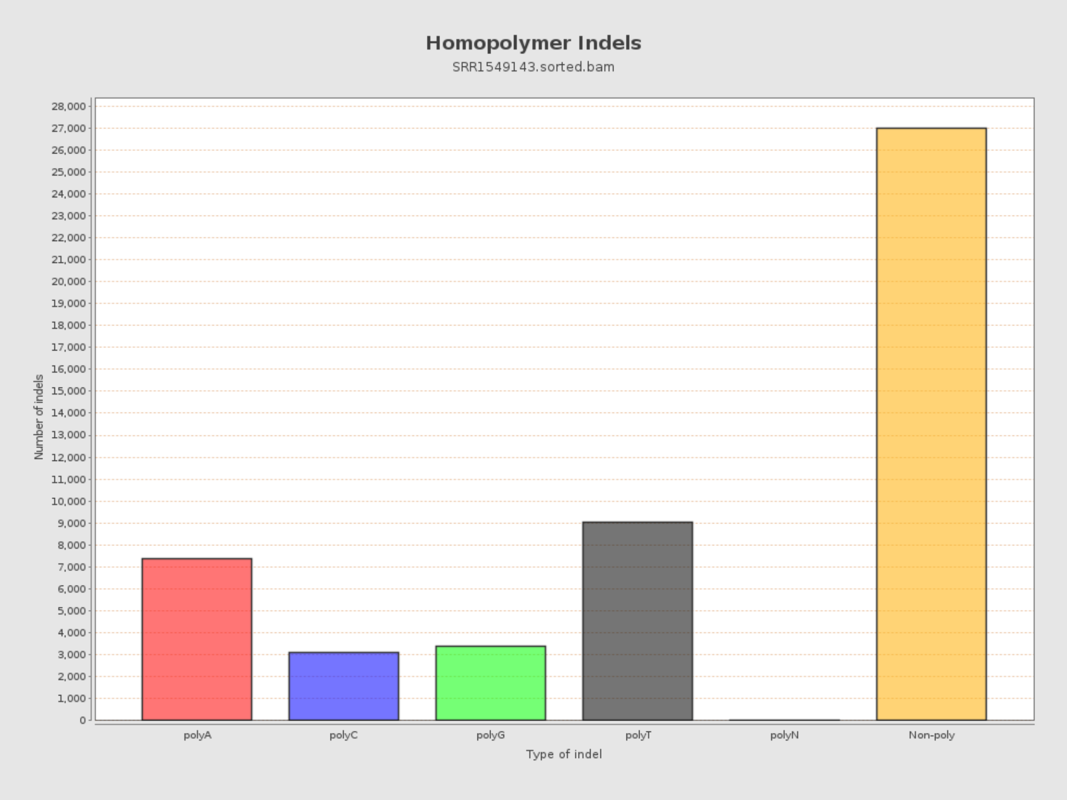
9. Results : Mapped Reads GC-content Distribution



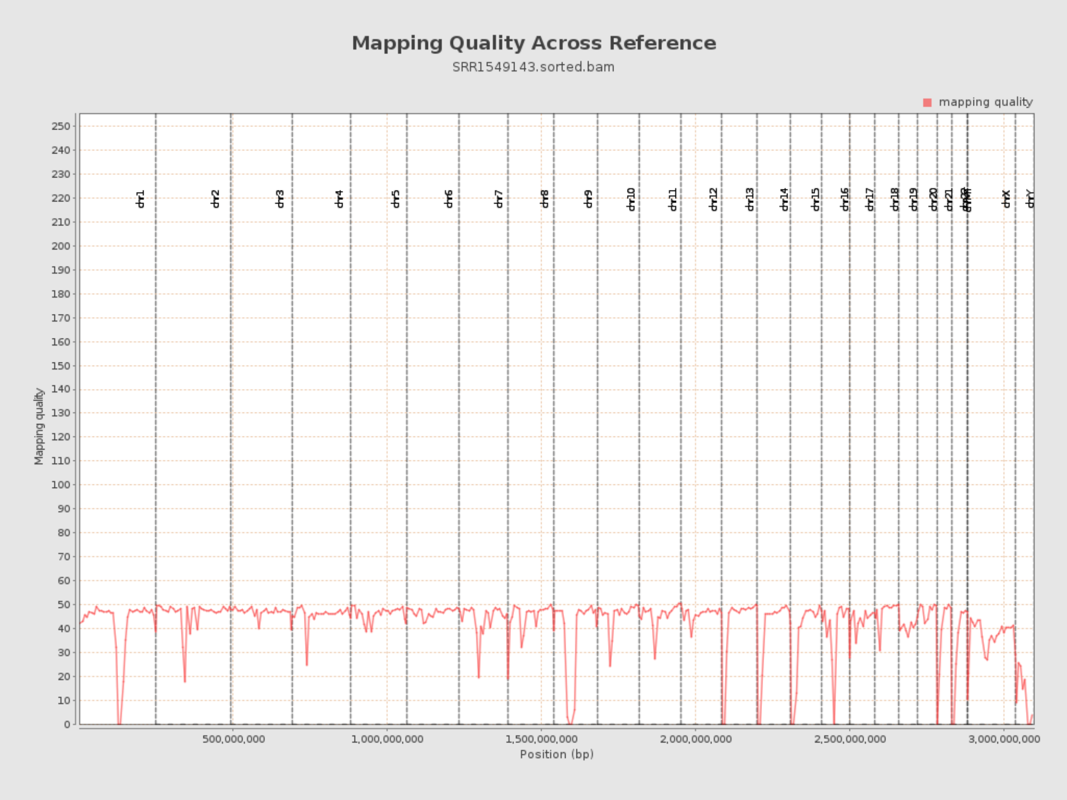
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram