Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 08:26:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549003.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_SRR1549003 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549003.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 08:26:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549003.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,184,418
Mapped reads	8,811,138 / 86.52%
Unmapped reads	1,373,280 / 13.48%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	798,764 / 7.84%
Duplication rate	8.33%
Clipped reads	424,481 / 4.17%

2.2. ACGT Content

Number/percentage of A's	104,926,320 / 29.99%
Number/percentage of C's	69,330,687 / 19.82%
Number/percentage of T's	105,366,508 / 30.11%
Number/percentage of G's	70,256,582 / 20.08%
Number/percentage of N's	3,588 / 0%
GC Percentage	39.9%

2.3. Coverage

Mean	0.113
Standard Deviation	0.9536

2.4. Mapping Quality

Mean Mapping Quality	44.51

2.5. Mismatches and indels

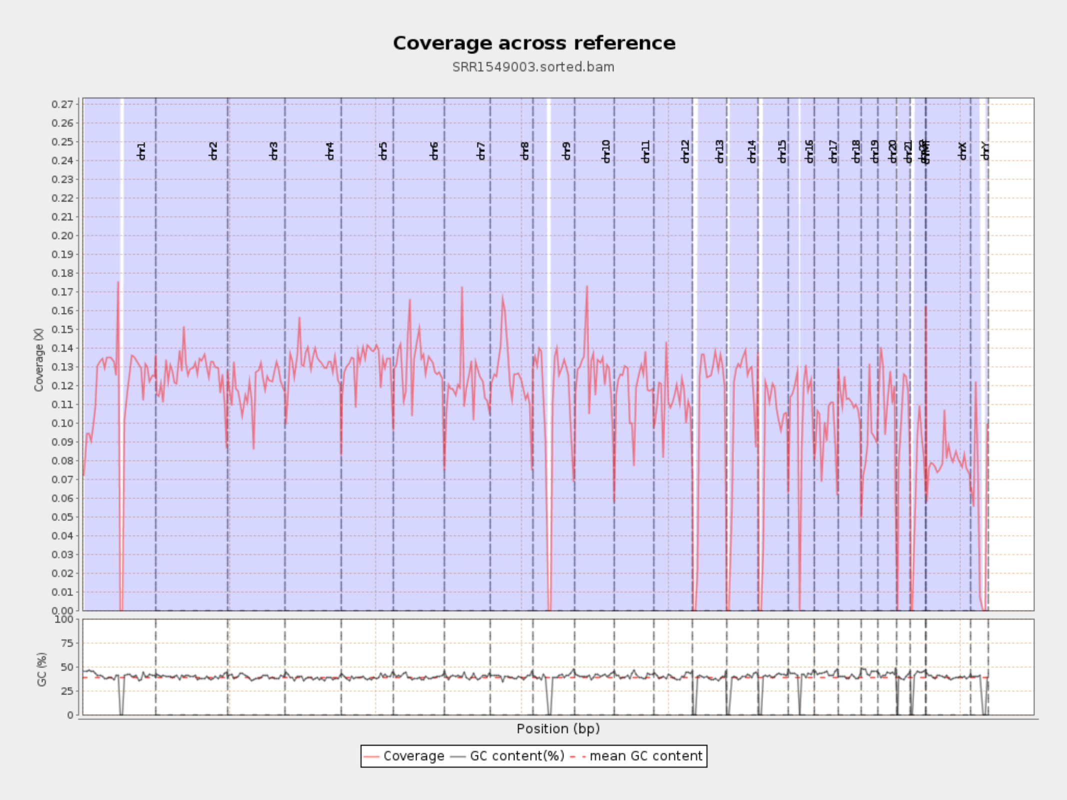
General error rate	0.29%
Mismatches	998,579
Insertions	10,484
Mapped reads with at least one insertion	0.12%
Deletions	29,738
Mapped reads with at least one deletion	0.34%
Homopolymer indels	43.93%

2.6. Chromosome stats

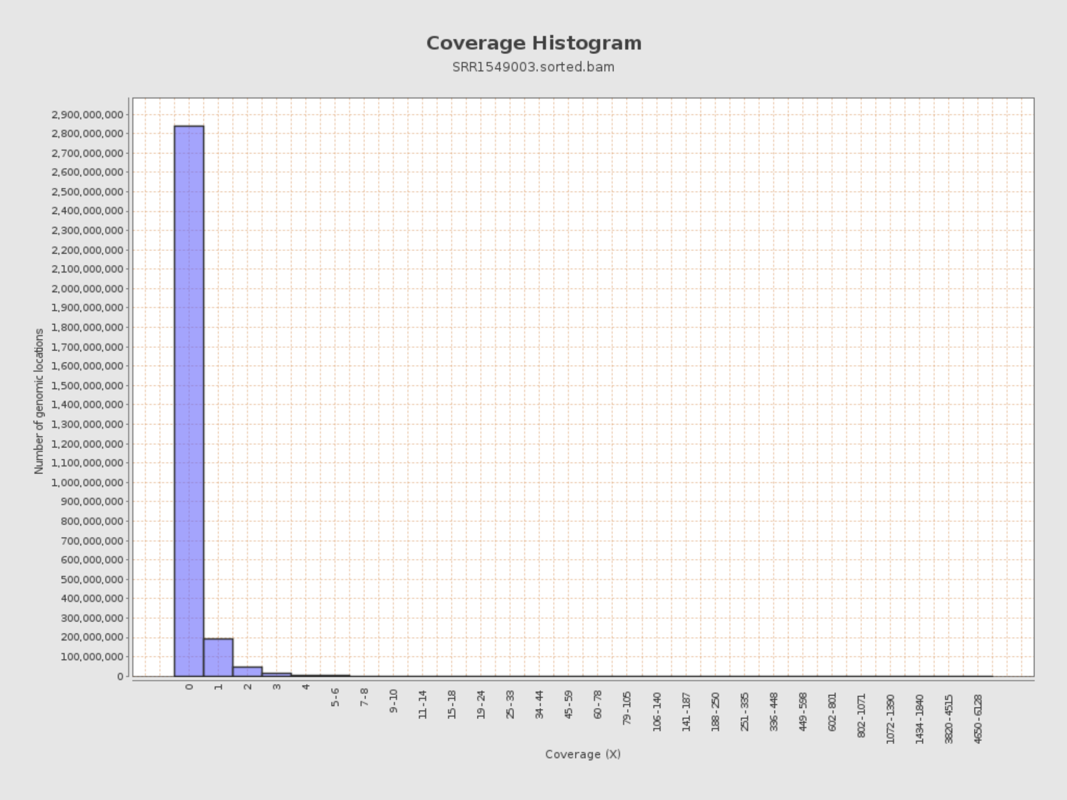
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	28704174	0.1152	1.4597
chr2	243199373	30783926	0.1266	0.6078
chr3	198022430	23688911	0.1196	0.444
chr4	191154276	25118754	0.1314	0.507
chr5	180915260	23692733	0.131	0.468
chr6	171115067	22614612	0.1322	0.5542
chr7	159138663	19035978	0.1196	0.954
chr8	146364022	18332453	0.1253	3.0221

chr9	141213431	15307339	0.1084	0.5495
chr10	135534747	17391338	0.1283	0.6868
chr11	135006516	15861567	0.1175	0.575
chr12	133851895	14957992	0.1118	0.4481
chr13	115169878	12341448	0.1072	0.4156
chr14	107349540	11145066	0.1038	0.499
chr15	102531392	9092716	0.0887	0.3772
chr16	90354753	9220538	0.102	0.4556
chr17	81195210	7791922	0.096	0.431
chr18	78077248	8789768	0.1126	1.1837
chr19	59128983	5365150	0.0907	1.0753
chr20	63025520	7287905	0.1156	0.4597
chr21	48129895	4580604	0.0952	0.4717
chr22	51304566	3356738	0.0654	0.3554
chrMT	16571	2698	0.1628	0.4485
chrX	155270560	12318557	0.0793	0.4554
chrY	59373566	3139510	0.0529	0.545

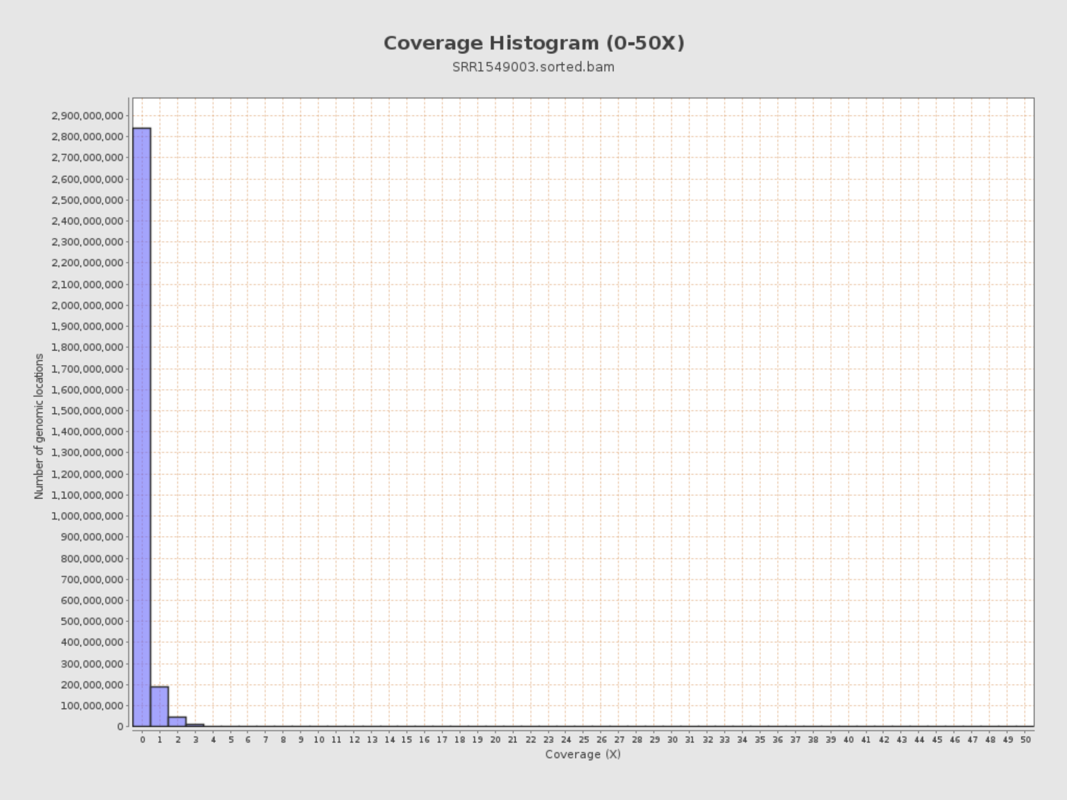
3. Results : Coverage across reference



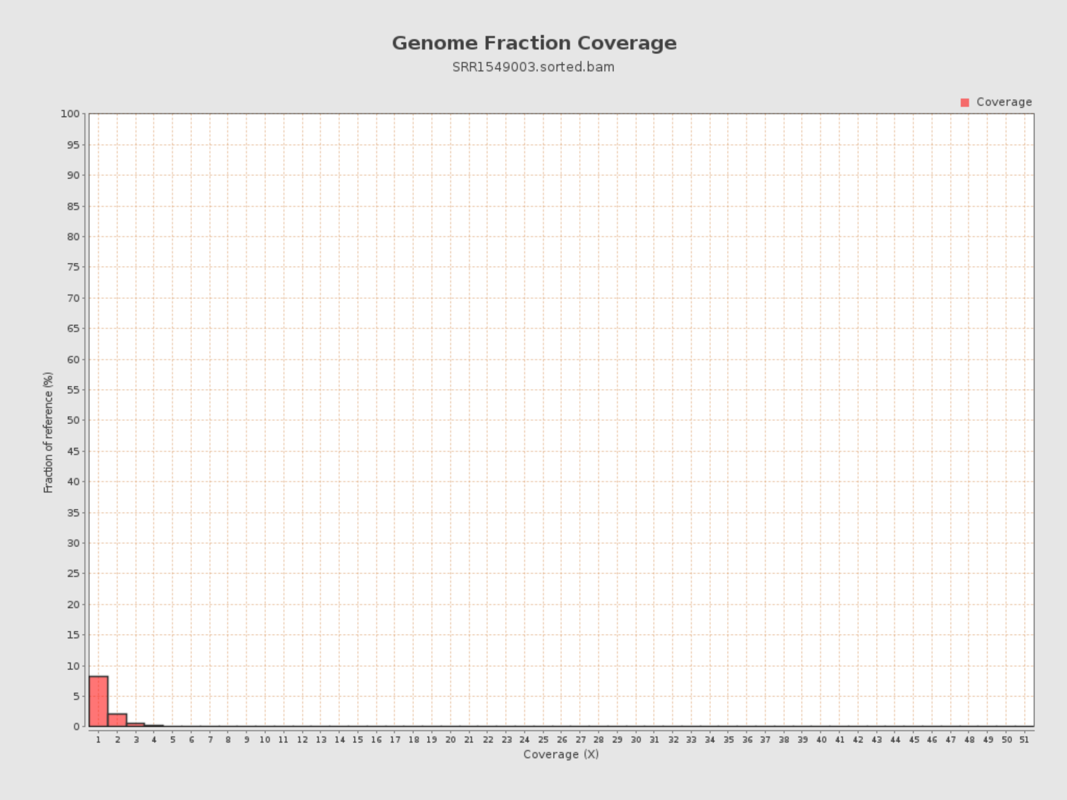
4. Results : Coverage Histogram



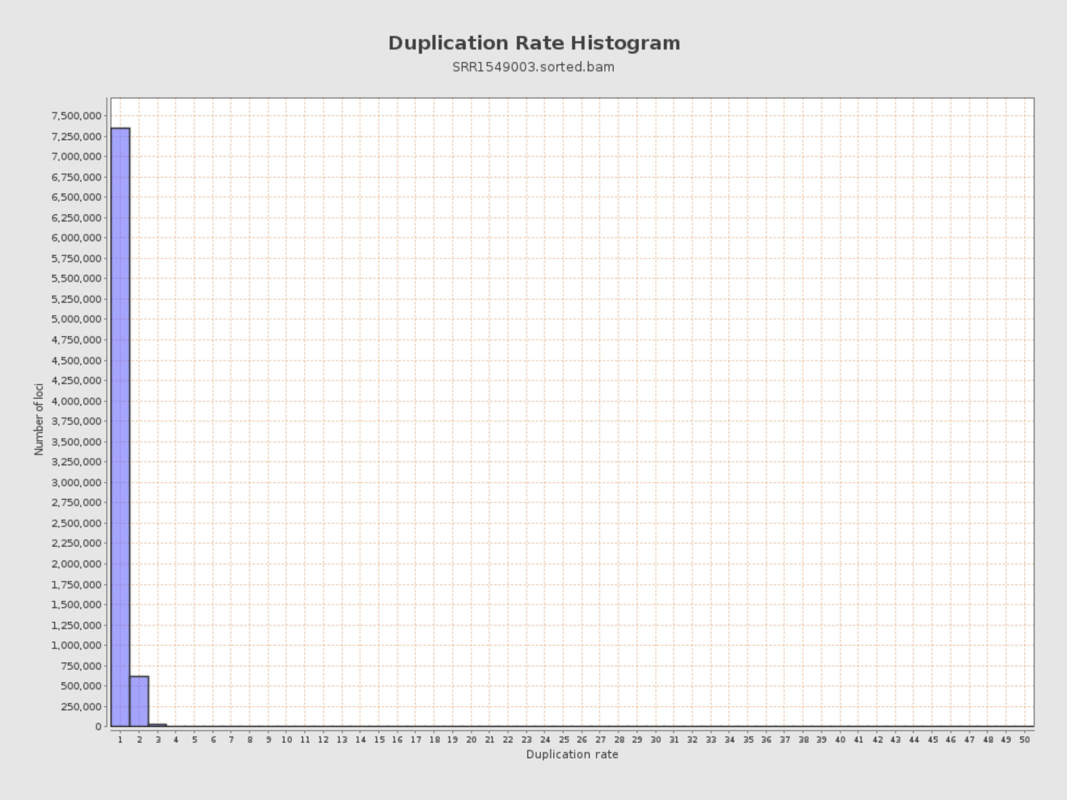
5. Results : Coverage Histogram (0-50X)



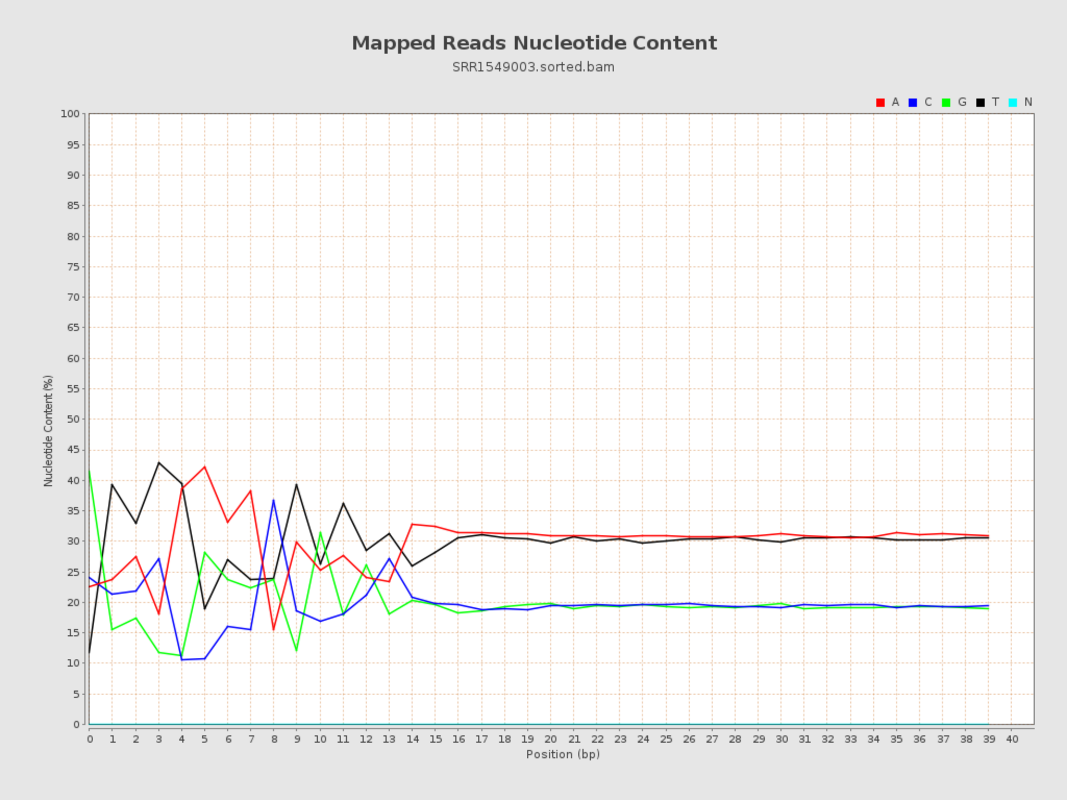
6. Results : Genome Fraction Coverage



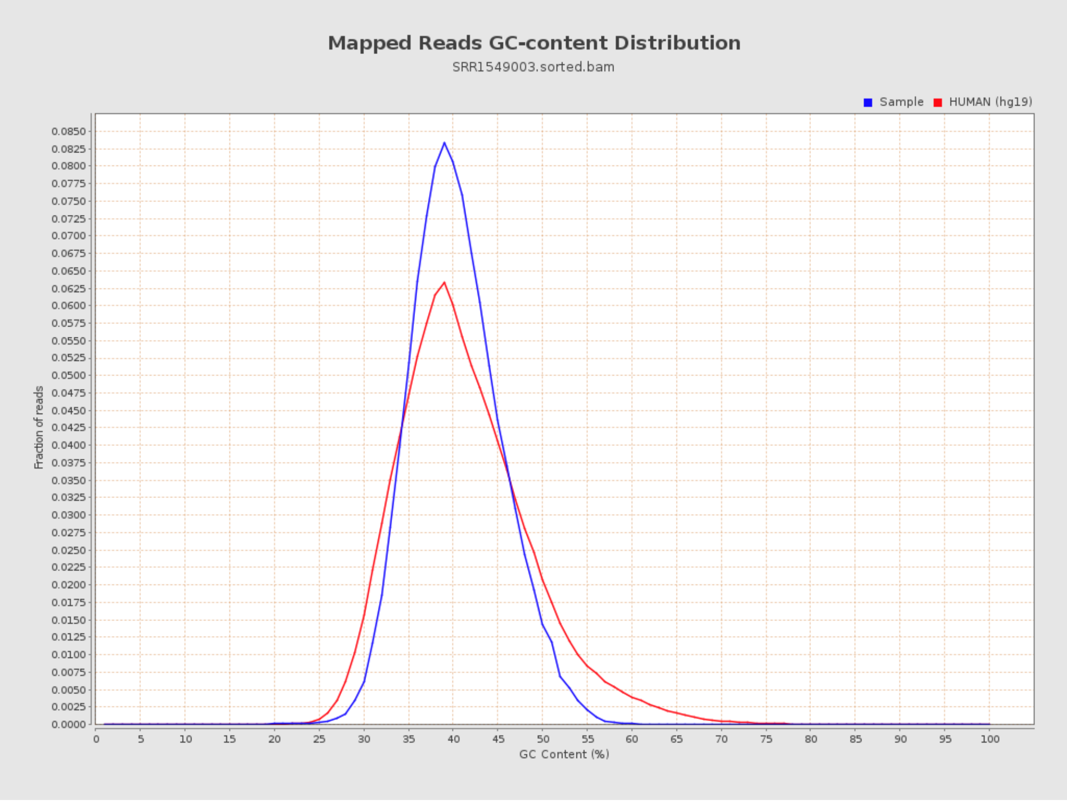
7. Results : Duplication Rate Histogram



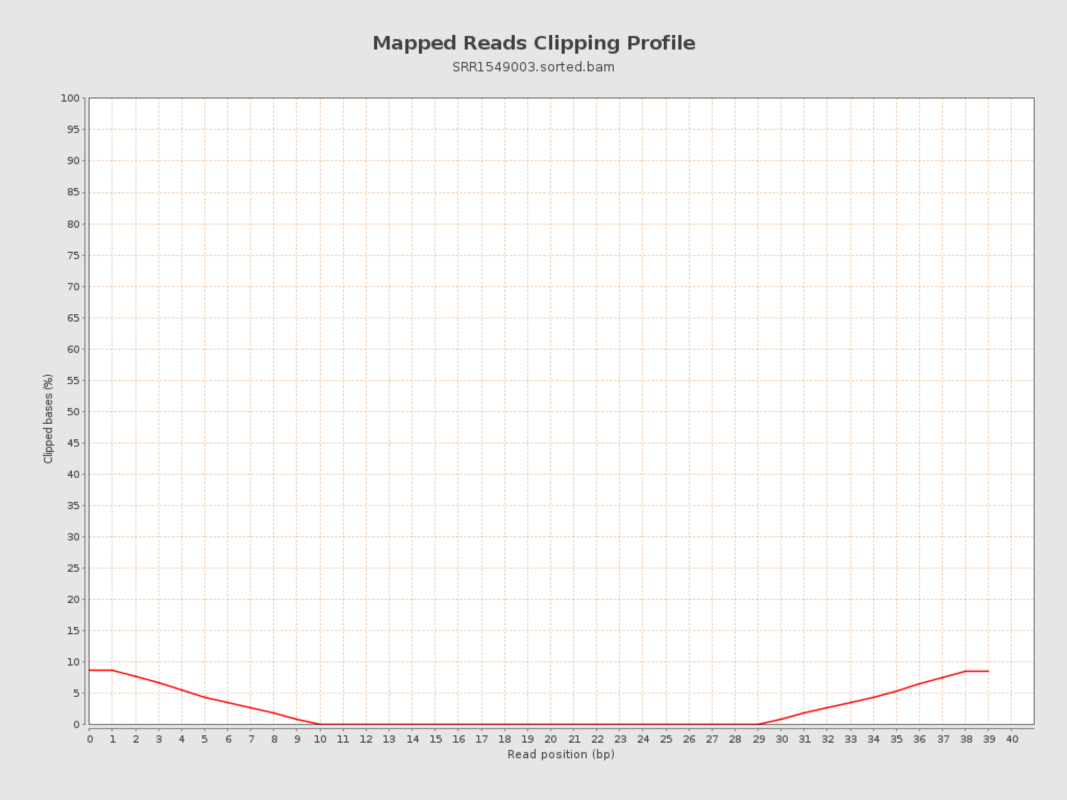
8. Results : Mapped Reads Nucleotide Content



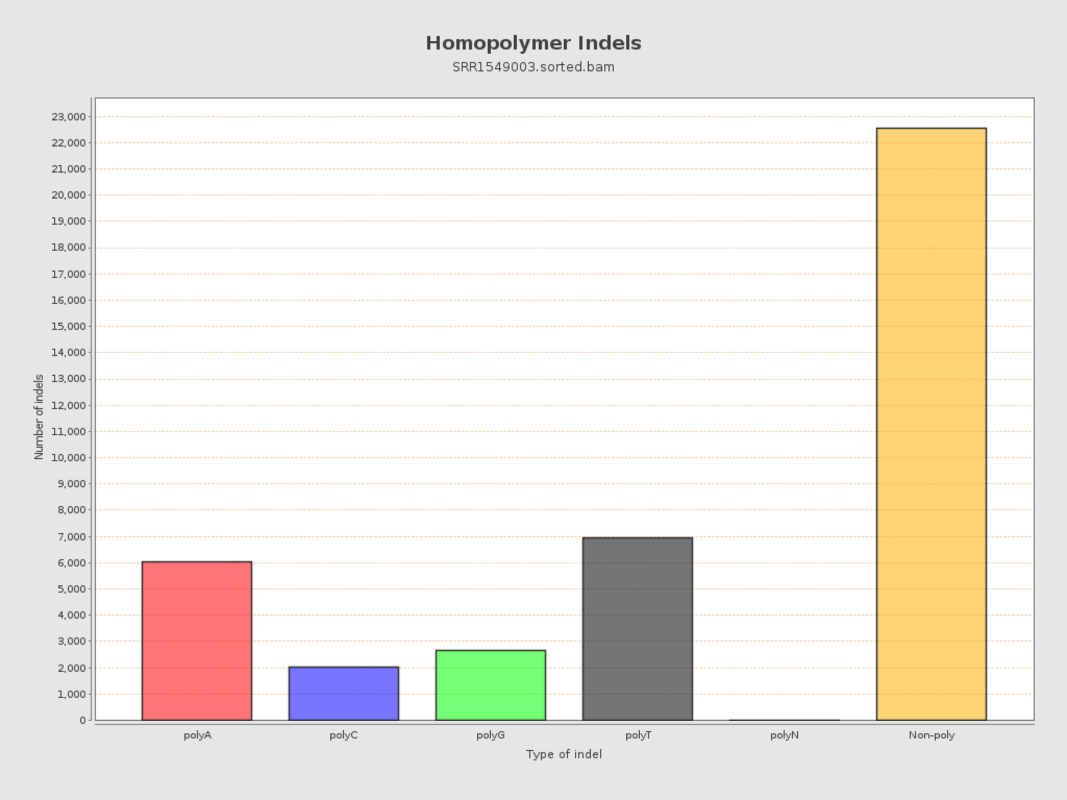
9. Results : Mapped Reads GC-content Distribution



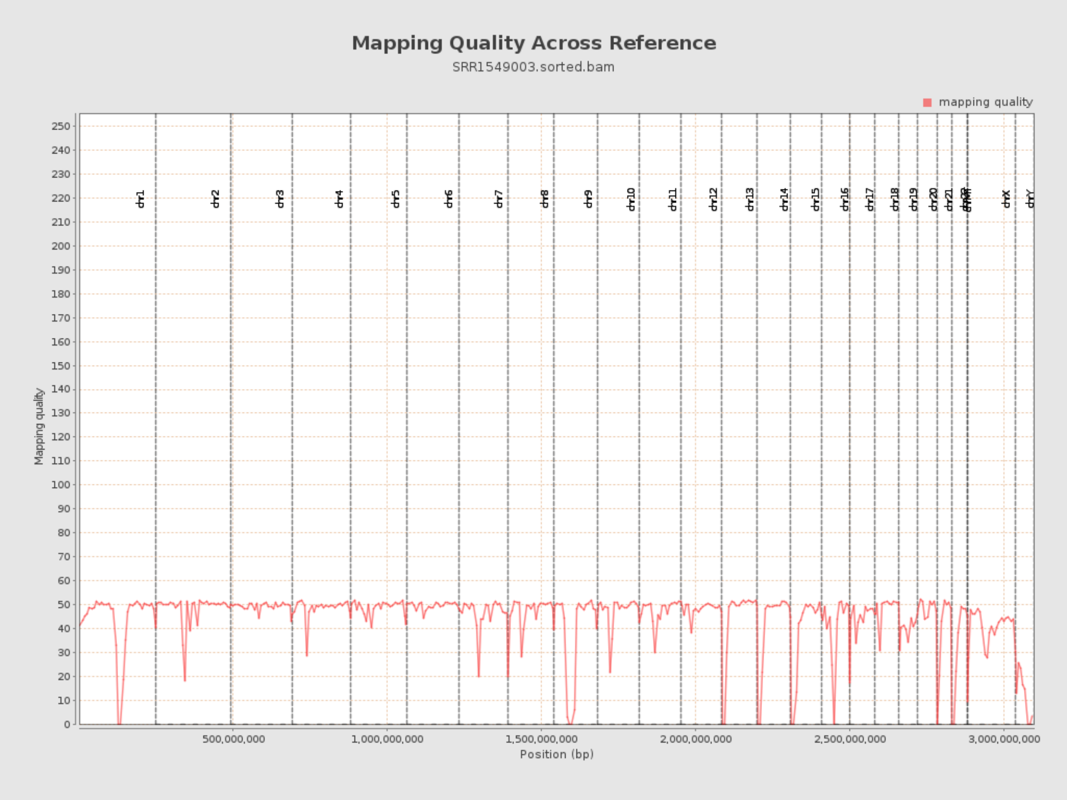
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram