Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 19:53:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549078.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_SRR1549078 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549078.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 19:53:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549078.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	9,411,267
Mapped reads	8,240,910 / 87.56%
Unmapped reads	1,170,357 / 12.44%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	307,771 / 3.27%
Duplication rate	2.25%
Clipped reads	437,694 / 4.65%

2.2. ACGT Content

Number/percentage of A's	98,717,675 / 30.18%
Number/percentage of C's	64,592,396 / 19.75%
Number/percentage of T's	100,219,680 / 30.64%
Number/percentage of G's	63,441,682 / 19.4%
Number/percentage of N's	82,793 / 0.03%
GC Percentage	39.15%

2.3. Coverage

Mean	0.1057
Standard Deviation	0.9753

2.4. Mapping Quality

Mean Mapping Quality	43.47

2.5. Mismatches and indels

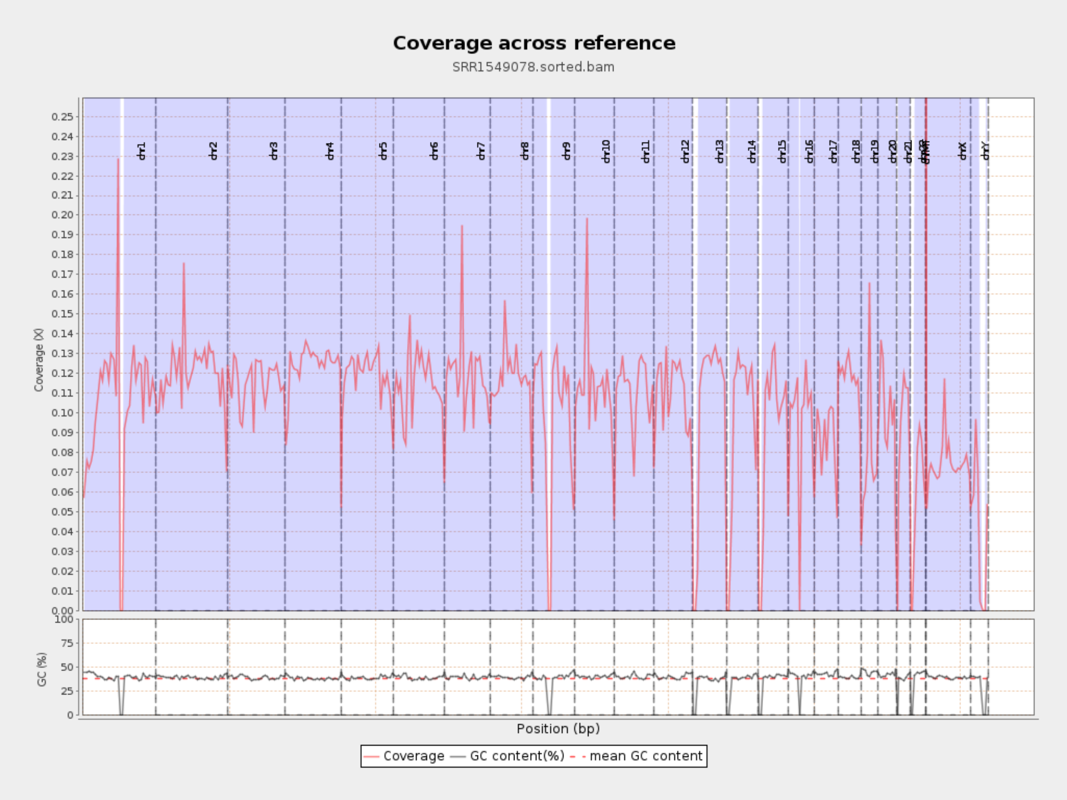
General error rate	0.41%
Mismatches	1,328,433
Insertions	8,323
Mapped reads with at least one insertion	0.1%
Deletions	24,486
Mapped reads with at least one deletion	0.3%
Homopolymer indels	46.09%

2.6. Chromosome stats

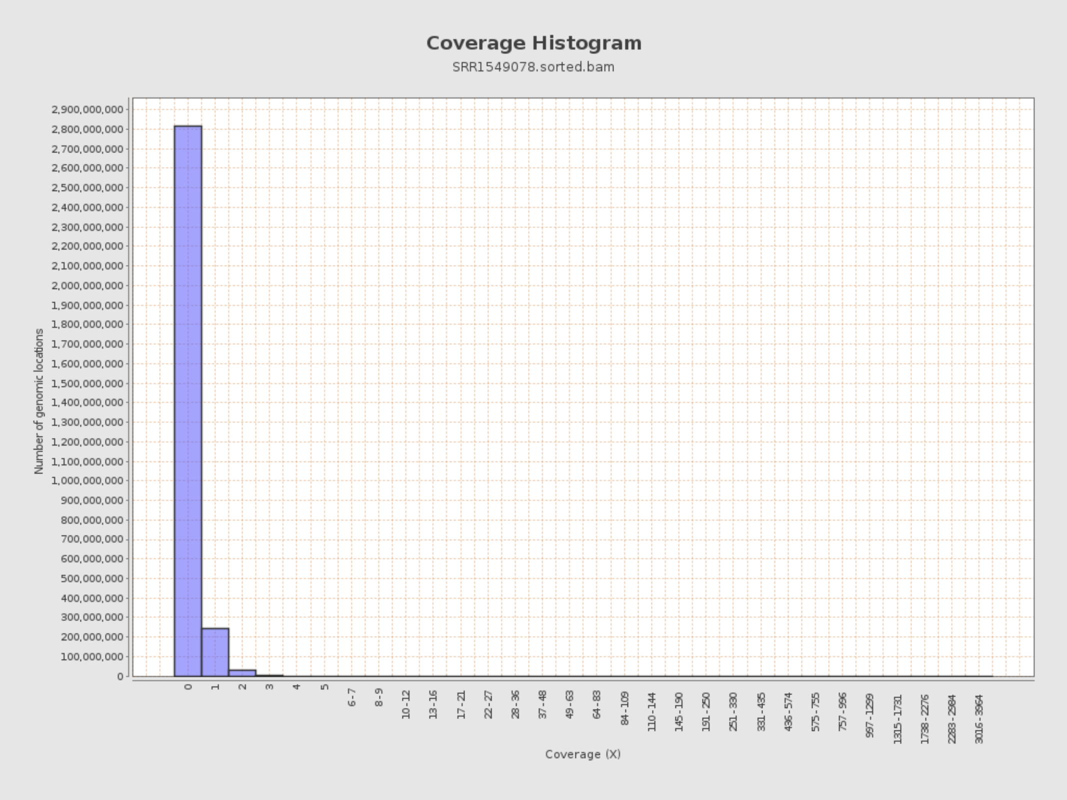
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	26182367	0.105	2.5391
chr2	243199373	29344098	0.1207	0.7036
chr3	198022430	22939367	0.1158	0.3996
chr4	191154276	23826958	0.1246	0.4047
chr5	180915260	21453401	0.1186	0.4094
chr6	171115067	19735203	0.1153	0.5288
chr7	159138663	18841633	0.1184	1.0488
chr8	146364022	17119971	0.117	0.6228

chr9	141213431	13941938	0.0987	0.6737
chr10	135534747	15420783	0.1138	0.9084
chr11	135006516	14970362	0.1109	0.7057
chr12	133851895	14764039	0.1103	0.4267
chr13	115169878	11862905	0.103	0.3519
chr14	107349540	10271993	0.0957	0.4703
chr15	102531392	9337930	0.0911	0.3391
chr16	90354753	8360906	0.0925	0.5032
chr17	81195210	7061483	0.087	0.4054
chr18	78077248	9290056	0.119	1.5712
chr19	59128983	4701952	0.0795	1.982
chr20	63025520	6470134	0.1027	0.3913
chr21	48129895	4234155	0.088	0.4374
chr22	51304566	2909827	0.0567	0.3359
chrMT	16571	12972	0.7828	1.2352
chrX	155270560	11546076	0.0744	0.4675
chrY	59373566	2484015	0.0418	0.3204

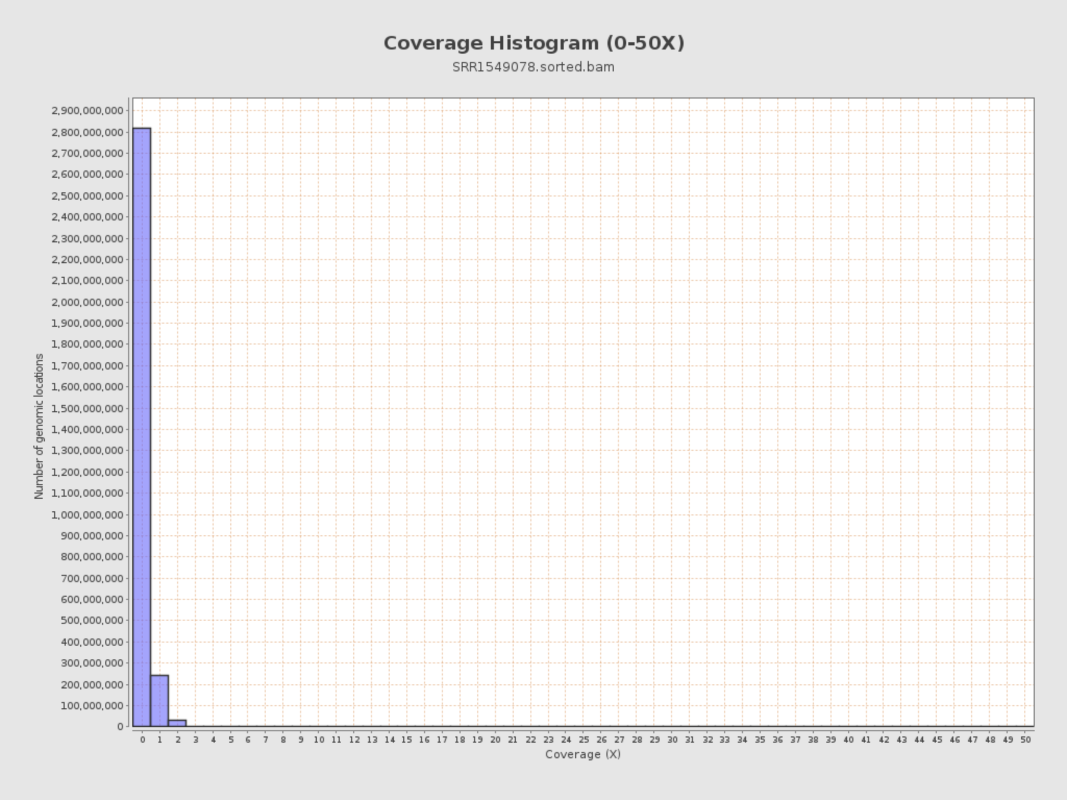
3. Results : Coverage across reference



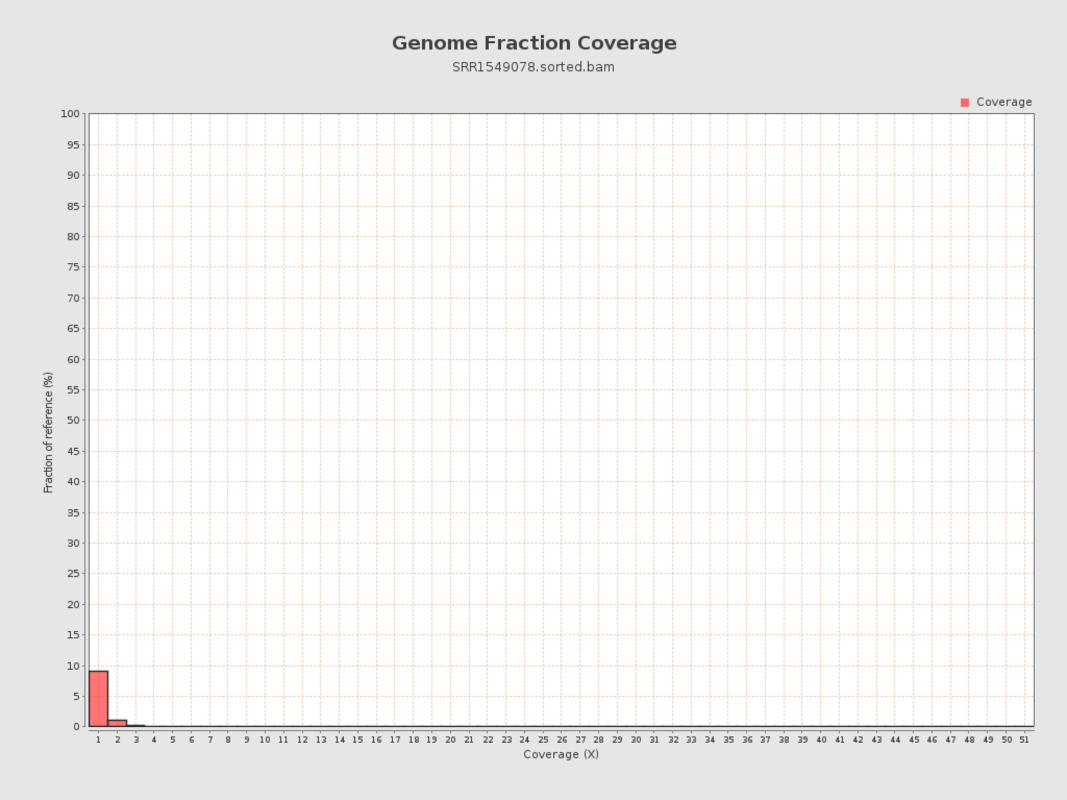
4. Results : Coverage Histogram



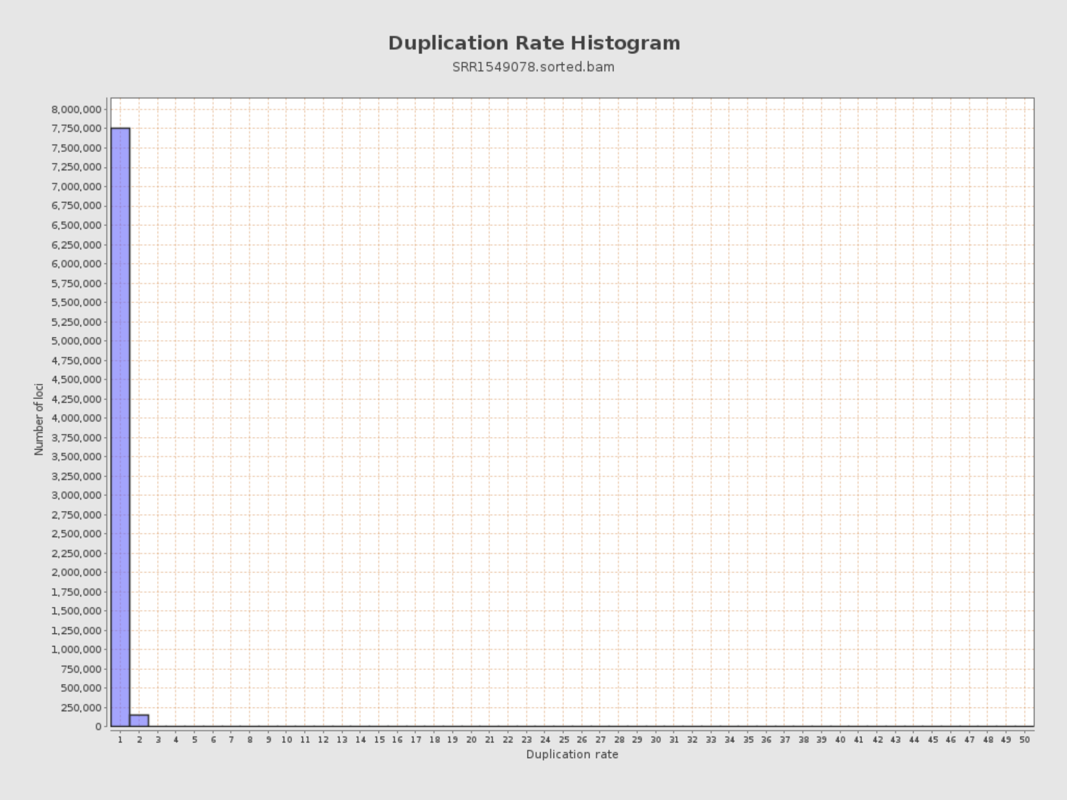
5. Results : Coverage Histogram (0-50X)



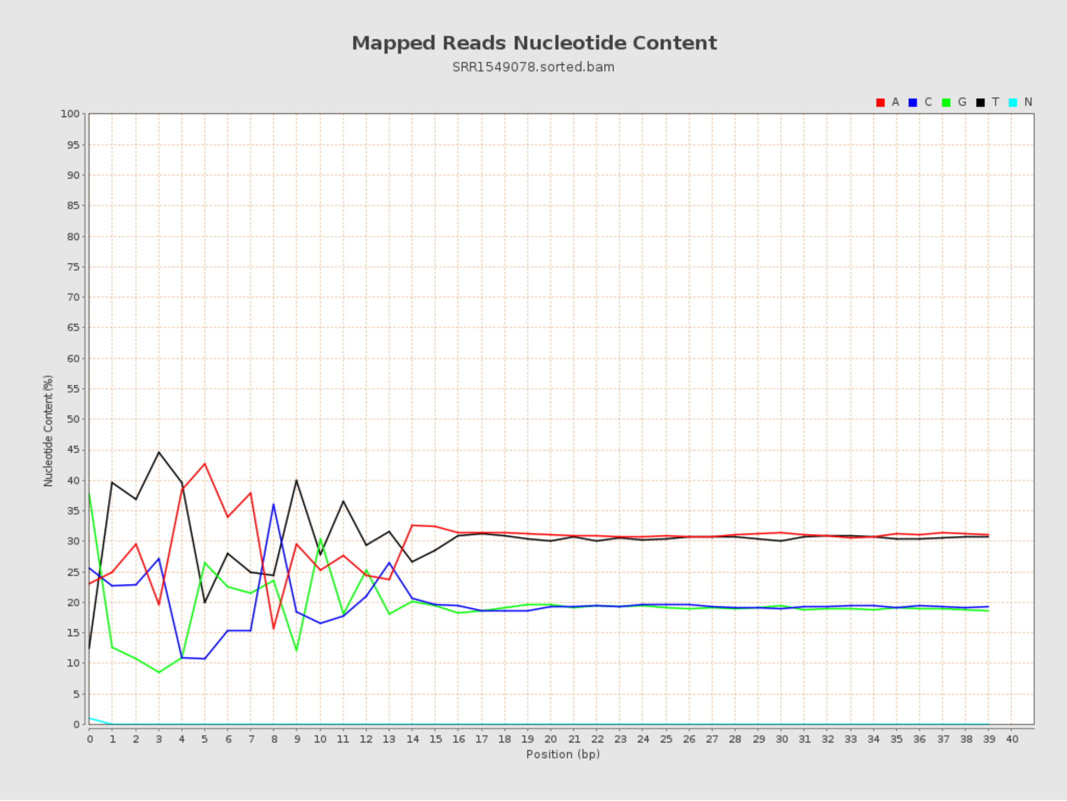
6. Results : Genome Fraction Coverage



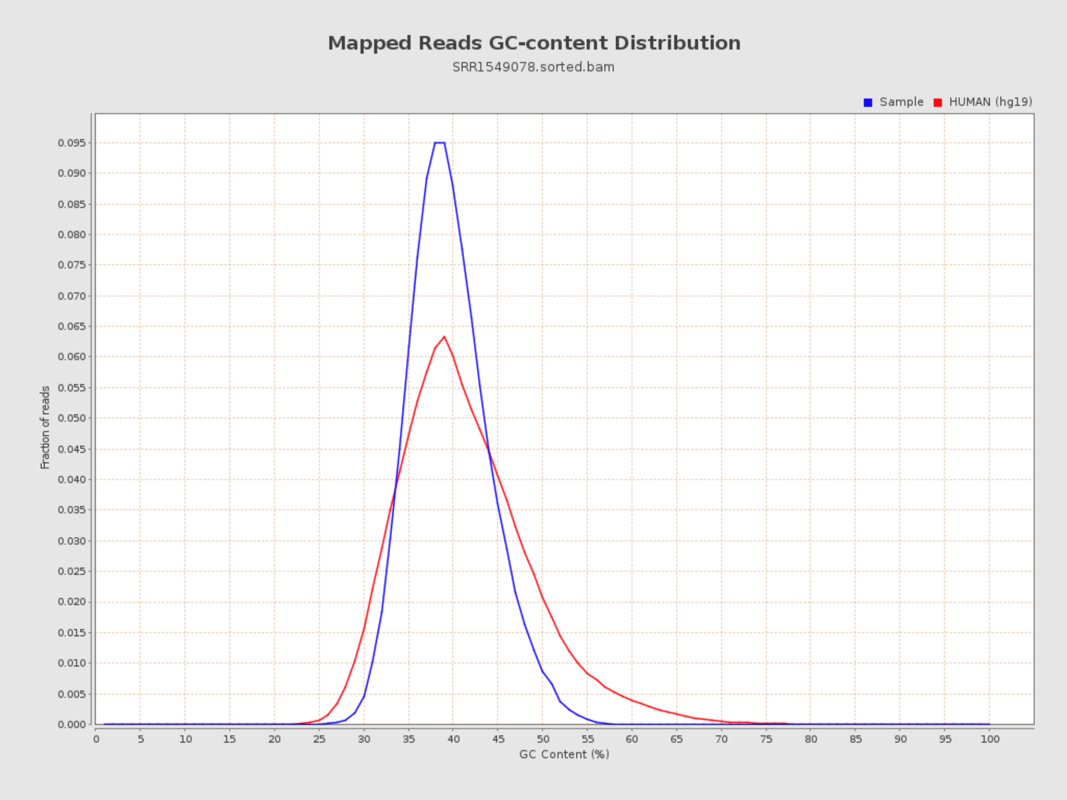
7. Results : Duplication Rate Histogram



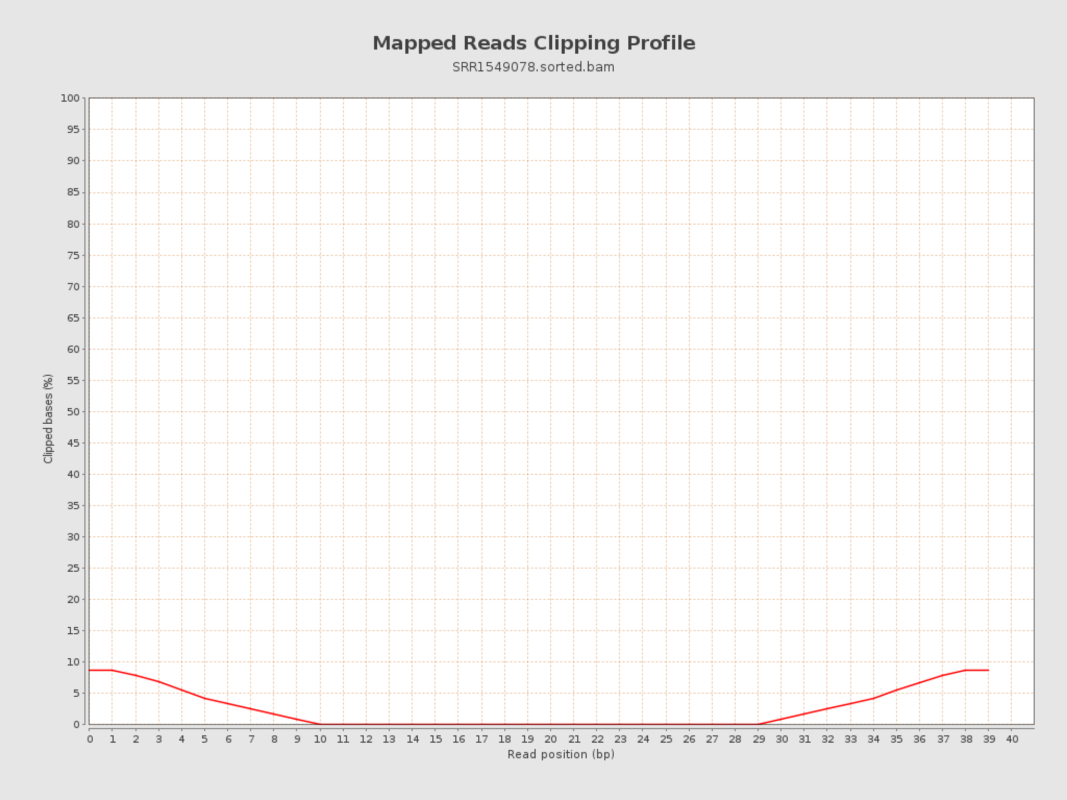
8. Results : Mapped Reads Nucleotide Content



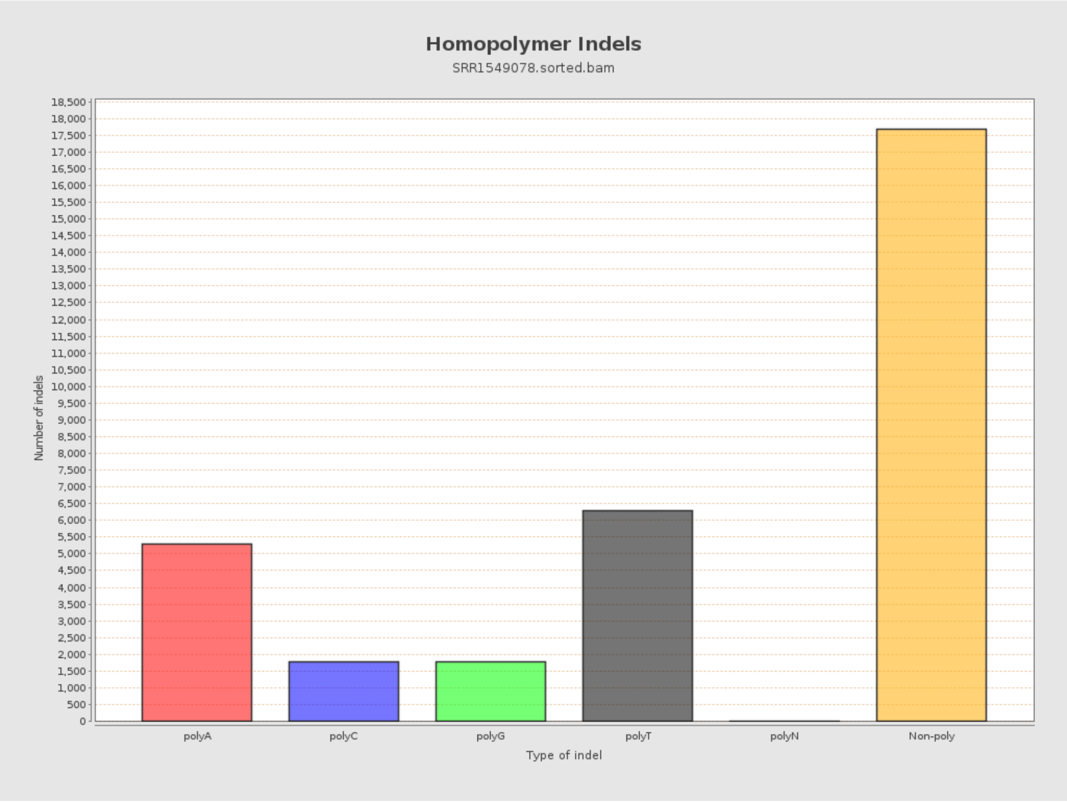
9. Results : Mapped Reads GC-content Distribution



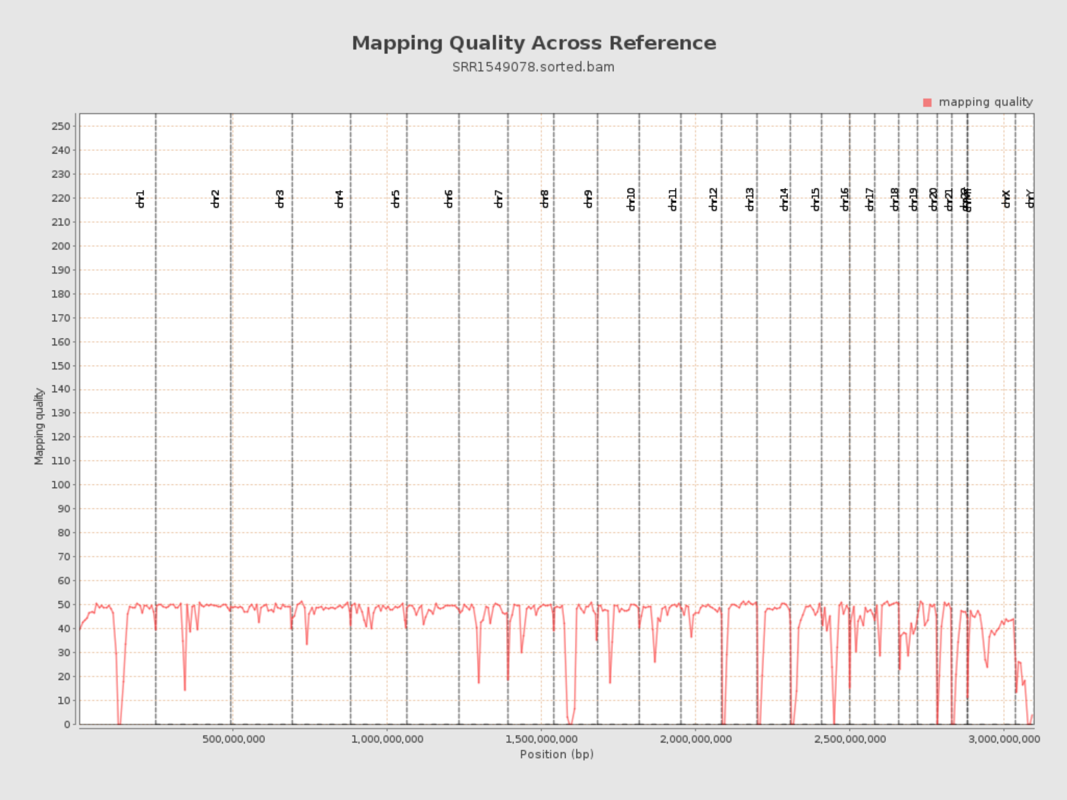
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram