Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 16:23:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549059.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_SRR1549059 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549059.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 16:23:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549059.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,490,603
Mapped reads	7,277,111 / 85.71%
Unmapped reads	1,213,492 / 14.29%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	307,722 / 3.62%
Duplication rate	2.93%
Clipped reads	287,076 / 3.38%

2.2. ACGT Content

Number/percentage of A's	85,243,286 / 29.46%
Number/percentage of C's	59,660,619 / 20.62%
Number/percentage of T's	84,979,259 / 29.37%
Number/percentage of G's	59,467,211 / 20.55%
Number/percentage of N's	5,319 / 0%
GC Percentage	41.17%

2.3. Coverage

Mean	0.0935
Standard Deviation	1.1229

2.4. Mapping Quality

Mean Mapping Quality	44.98

2.5. Mismatches and indels

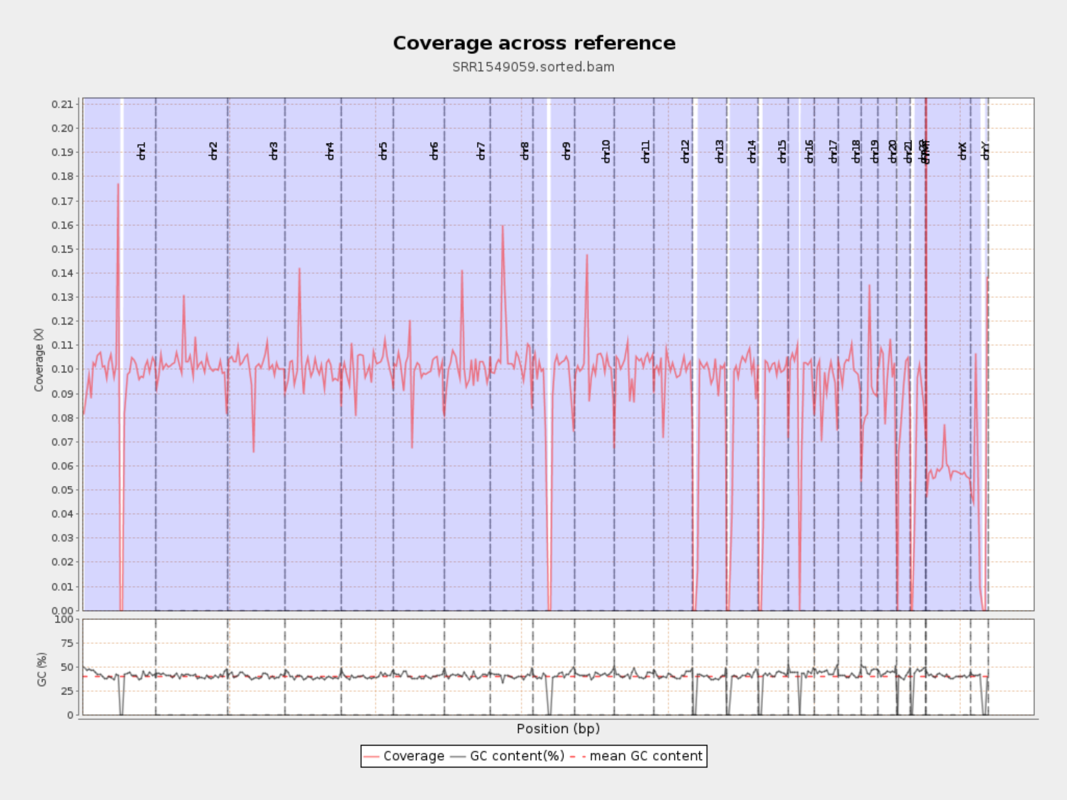
General error rate	0.31%
Mismatches	875,691
Insertions	6,713
Mapped reads with at least one insertion	0.09%
Deletions	22,074
Mapped reads with at least one deletion	0.3%
Homopolymer indels	44.78%

2.6. Chromosome stats

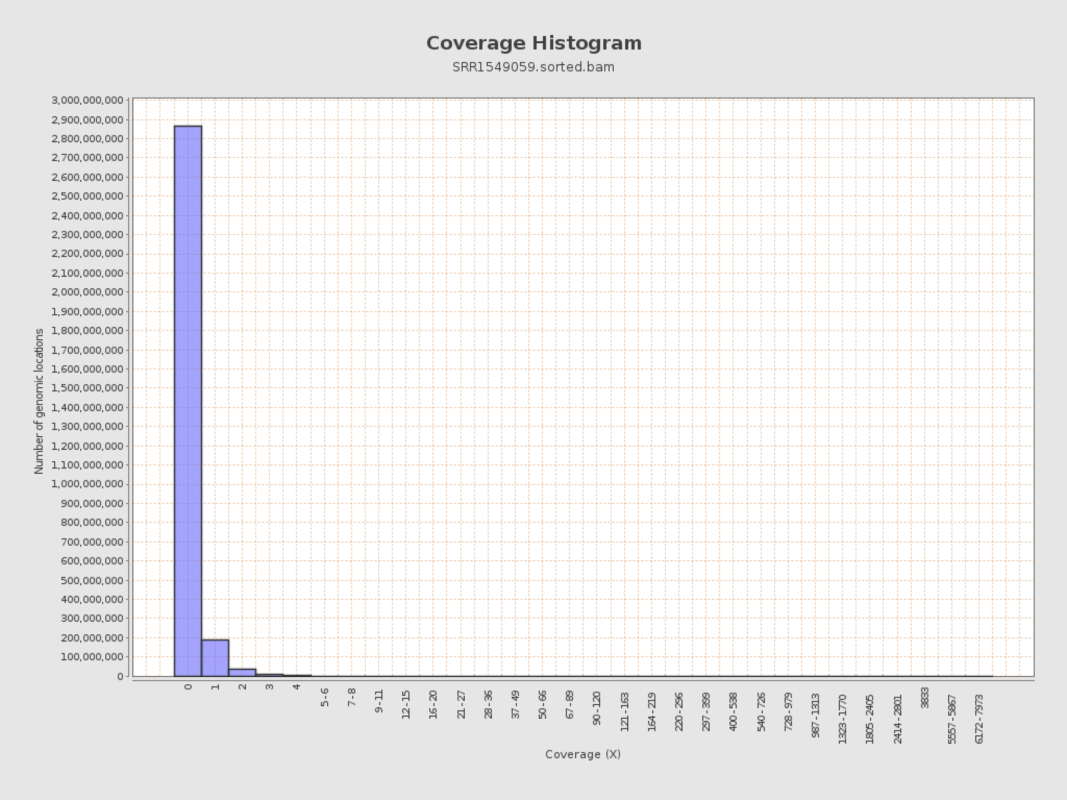
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	23780523	0.0954	1.9198
chr2	243199373	24876972	0.1023	0.5491
chr3	198022430	19980309	0.1009	0.3834
chr4	191154276	19291410	0.1009	0.4381
chr5	180915260	18267408	0.101	0.3936
chr6	171115067	17147160	0.1002	0.431
chr7	159138663	16078536	0.101	0.7711
chr8	146364022	15593855	0.1065	3.8887

chr9	141213431	12279168	0.087	0.4889
chr10	135534747	13928095	0.1028	0.6333
chr11	135006516	13650005	0.1011	0.5442
chr12	133851895	13293821	0.0993	0.394
chr13	115169878	9541386	0.0828	0.34
chr14	107349540	9030468	0.0841	0.3894
chr15	102531392	8411054	0.082	0.3382
chr16	90354753	8041350	0.089	0.4059
chr17	81195210	7604956	0.0937	0.4019
chr18	78077248	7860985	0.1007	1.0145
chr19	59128983	5365061	0.0907	1.3312
chr20	63025520	6199204	0.0984	0.3969
chr21	48129895	3846144	0.0799	0.4242
chr22	51304566	3297579	0.0643	0.3283
chrMT	16571	7733	0.4667	0.9428
chrX	155270560	8967758	0.0578	0.3672
chrY	59373566	3042572	0.0512	0.6934

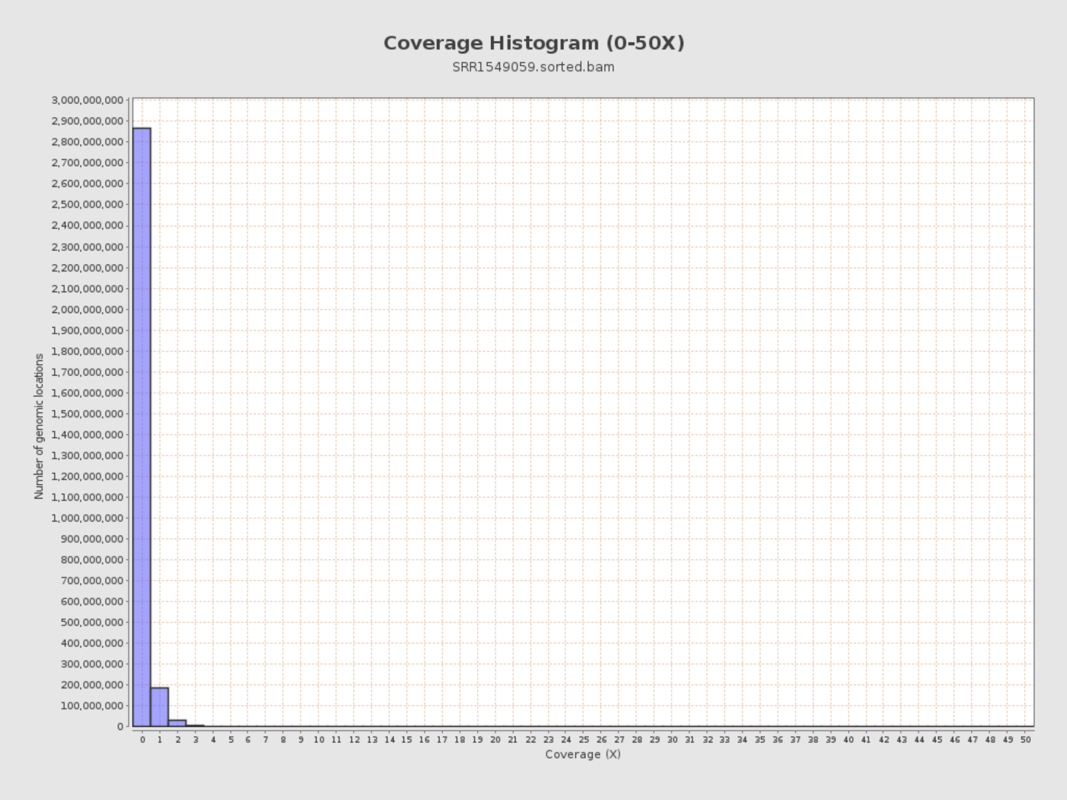
3. Results : Coverage across reference



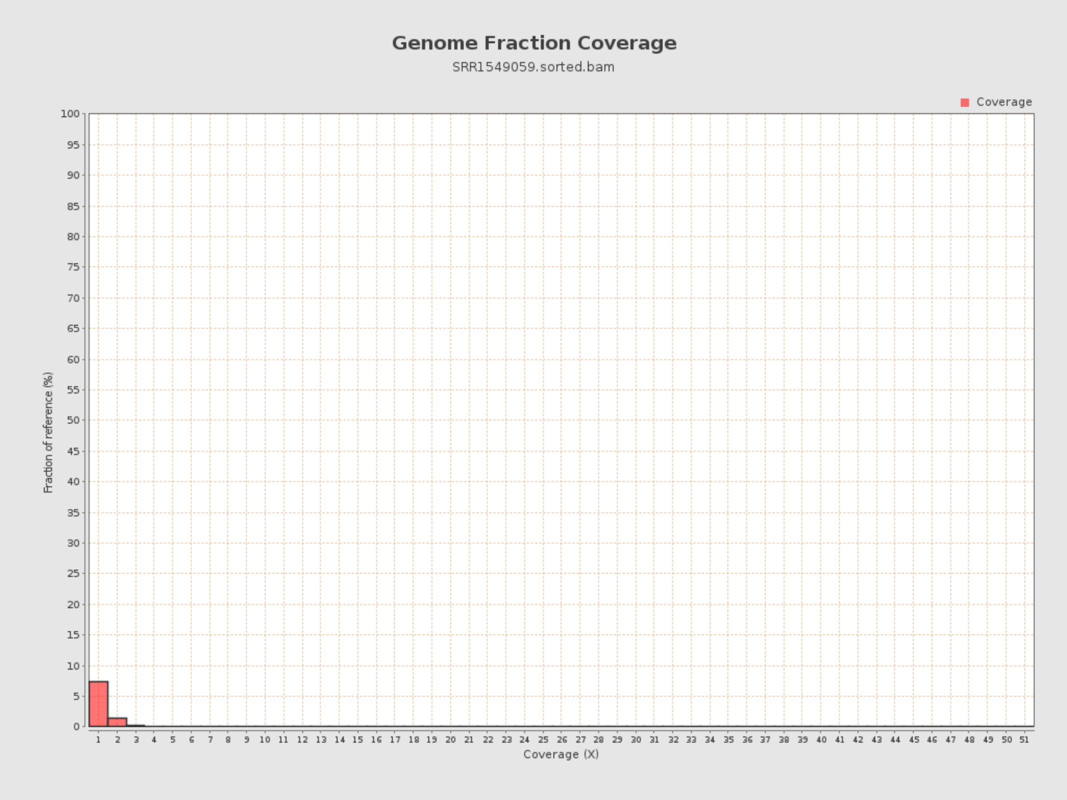
4. Results : Coverage Histogram



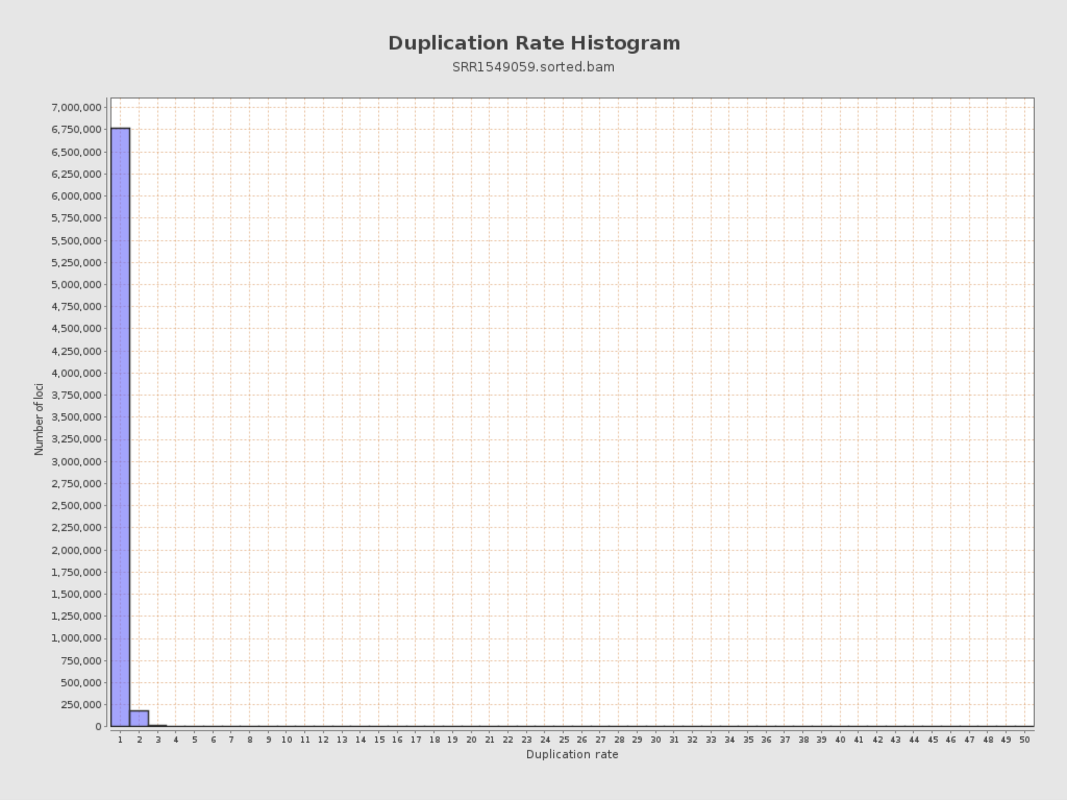
5. Results : Coverage Histogram (0-50X)



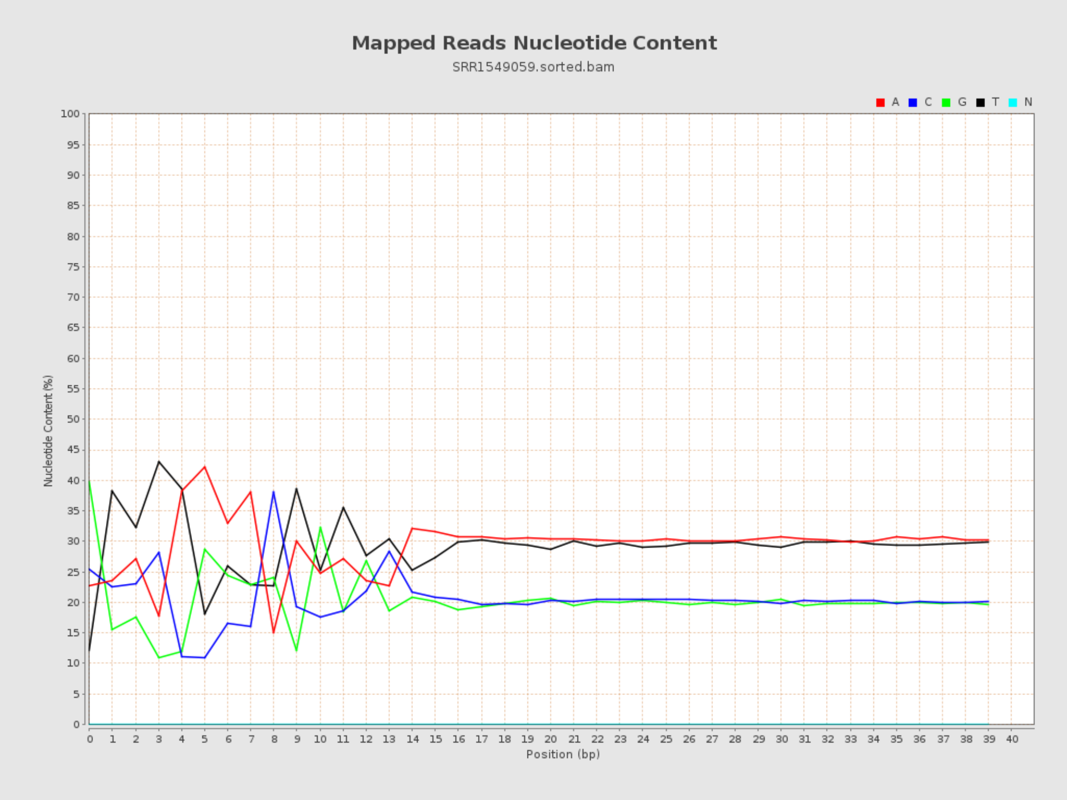
6. Results : Genome Fraction Coverage



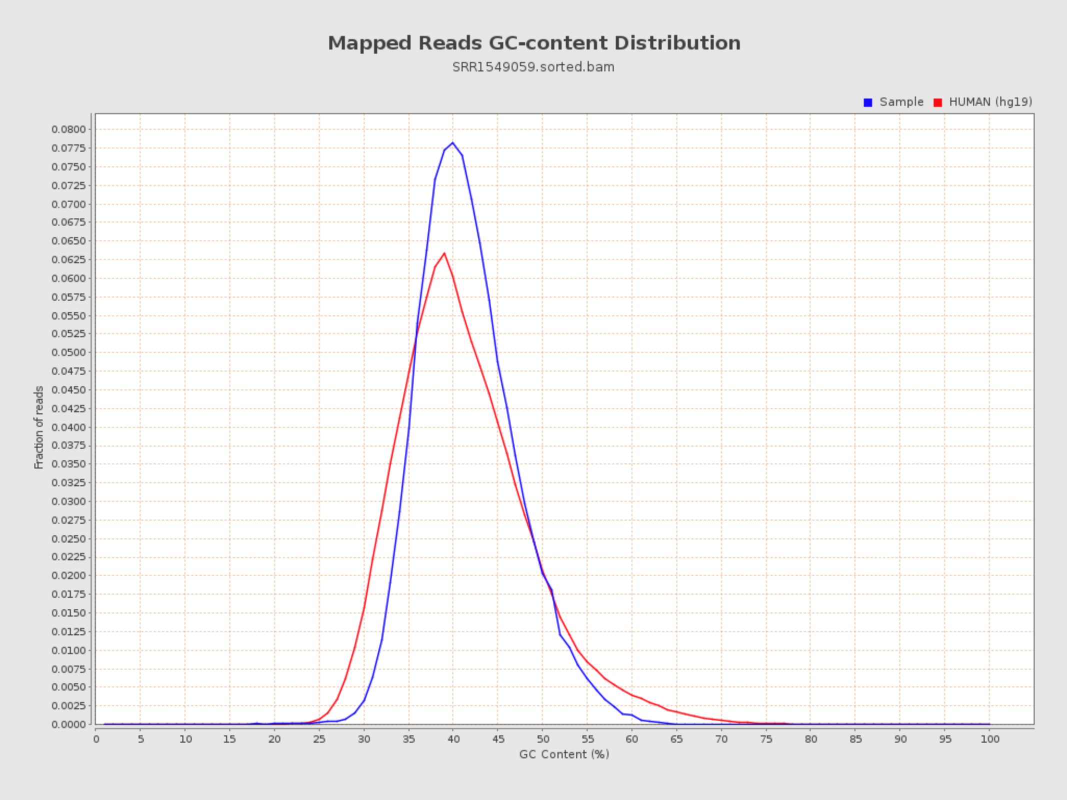
7. Results : Duplication Rate Histogram



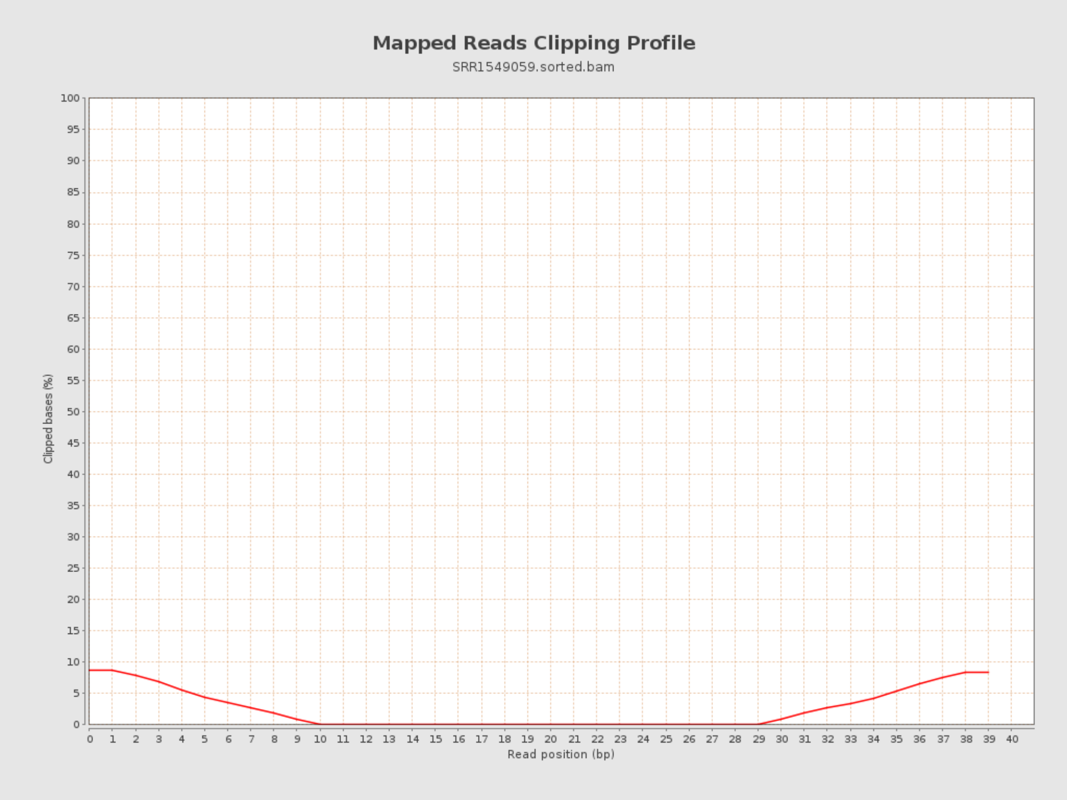
8. Results : Mapped Reads Nucleotide Content



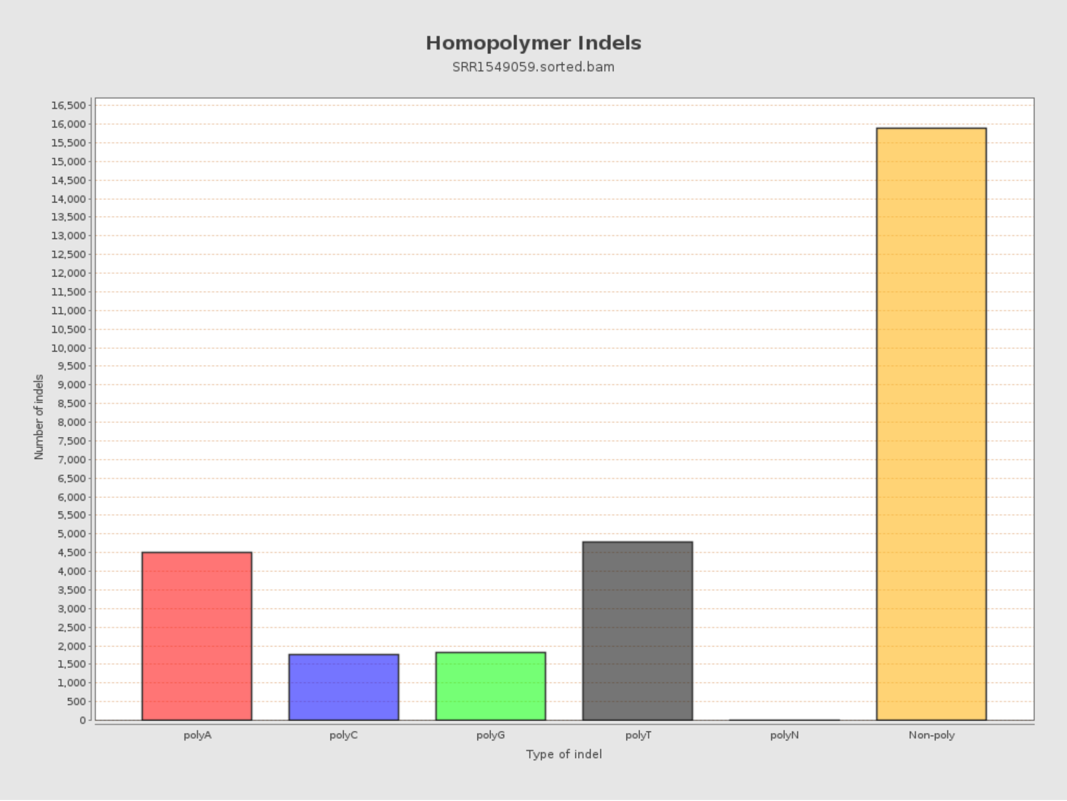
9. Results : Mapped Reads GC-content Distribution



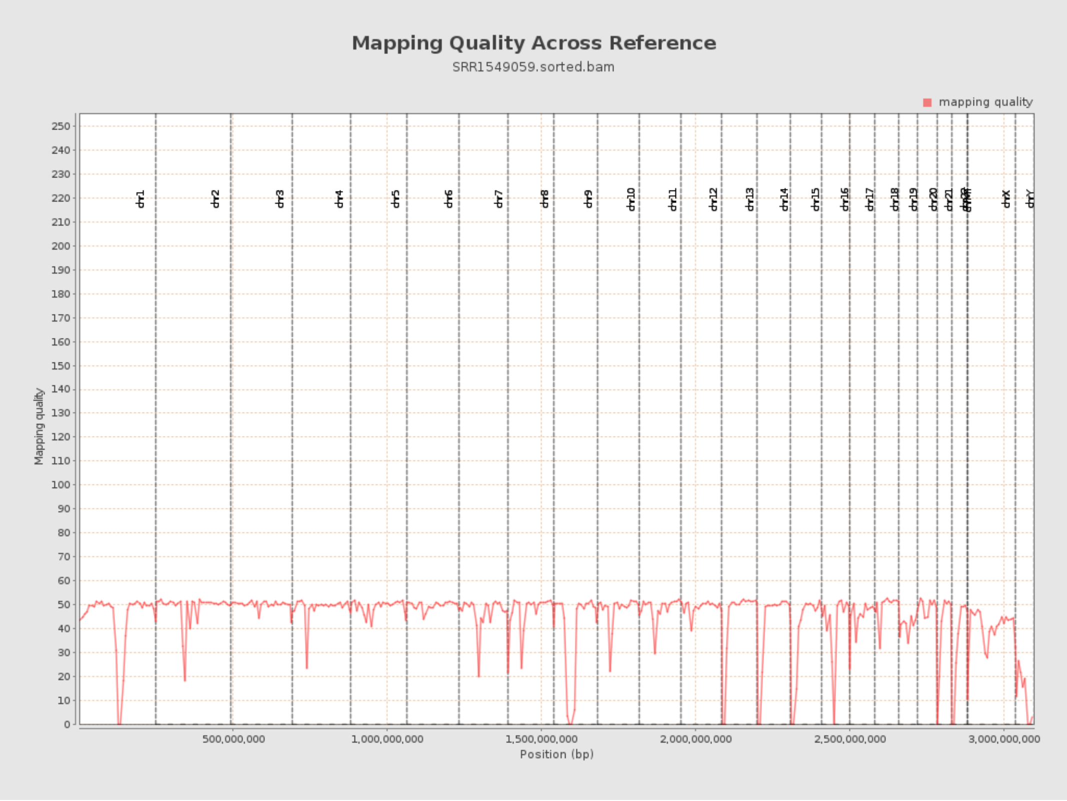
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram