Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 20:04:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549079.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_SRR1549079 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549079.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 20:04:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549079.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,444,203
Mapped reads	6,570,910 / 88.27%
Unmapped reads	873,293 / 11.73%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	199,960 / 2.69%
Duplication rate	1.96%
Clipped reads	297,738 / 4%

2.2. ACGT Content

Number/percentage of A's	78,553,907 / 30.09%
Number/percentage of C's	52,265,096 / 20.02%
Number/percentage of T's	79,457,631 / 30.44%
Number/percentage of G's	50,720,049 / 19.43%
Number/percentage of N's	64,647 / 0.02%
GC Percentage	39.45%

2.3. Coverage

Mean	0.0843
Standard Deviation	0.7063

2.4. Mapping Quality

Mean Mapping Quality	44.43

2.5. Mismatches and indels

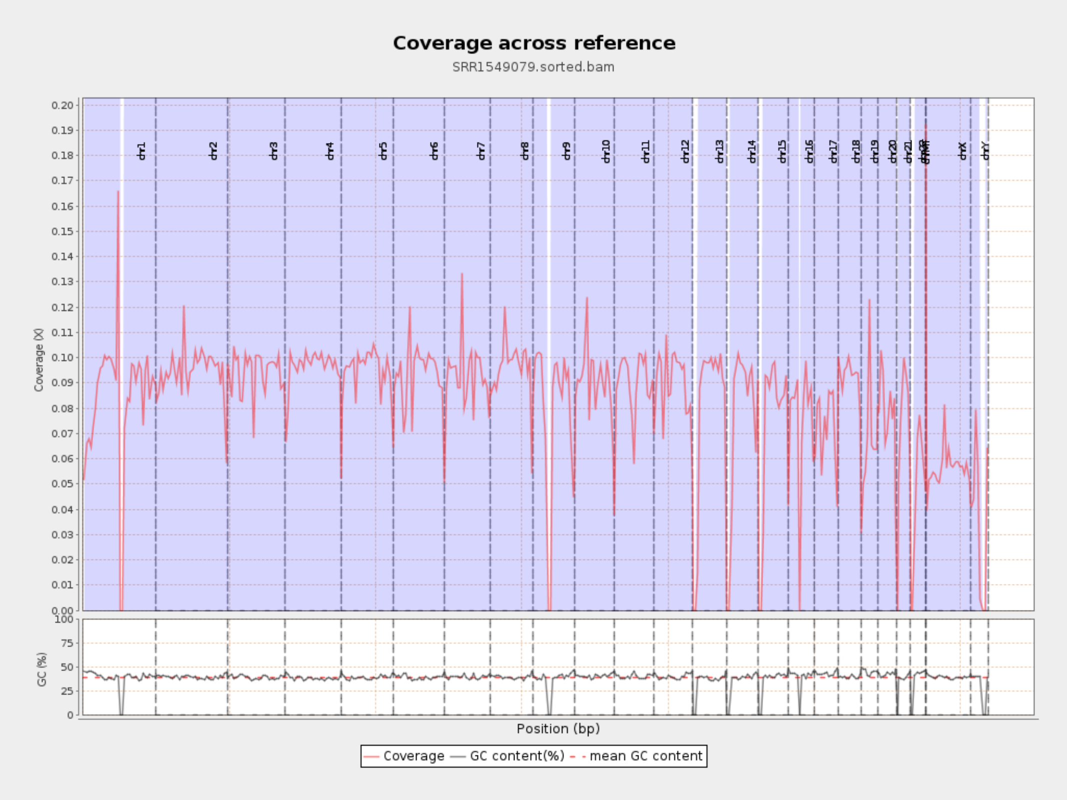
General error rate	0.39%
Mismatches	1,019,453
Insertions	6,102
Mapped reads with at least one insertion	0.09%
Deletions	20,702
Mapped reads with at least one deletion	0.32%
Homopolymer indels	45.86%

2.6. Chromosome stats

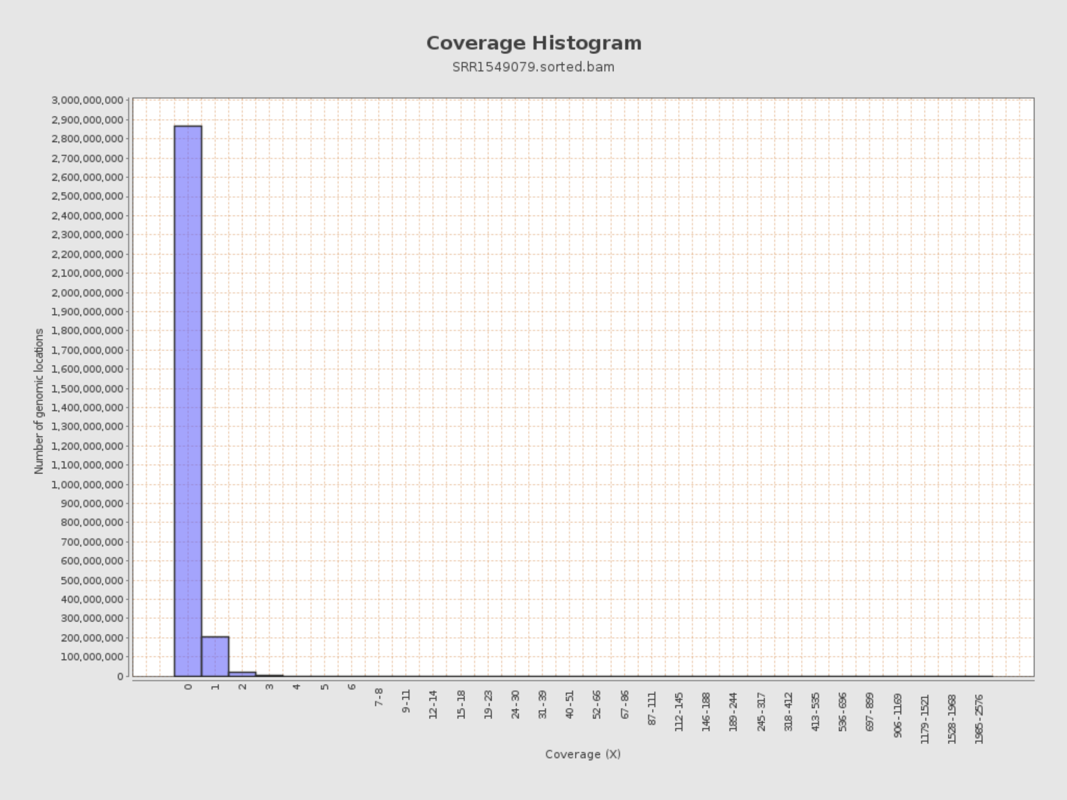
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	20966796	0.0841	1.753
chr2	243199373	23044973	0.0948	0.4953
chr3	198022430	18688704	0.0944	0.344
chr4	191154276	18464589	0.0966	0.3529
chr5	180915260	17151221	0.0948	0.3509
chr6	171115067	16134485	0.0943	0.4321
chr7	159138663	14716236	0.0925	0.7078
chr8	146364022	14052753	0.096	0.9981

chr9	141213431	11099103	0.0786	0.4691
chr10	135534747	12343309	0.0911	0.5266
chr11	135006516	12090077	0.0896	0.5086
chr12	133851895	12092630	0.0903	0.3523
chr13	115169878	9108668	0.0791	0.3046
chr14	107349540	8127191	0.0757	0.3585
chr15	102531392	7402485	0.0722	0.2934
chr16	90354753	6587916	0.0729	0.3585
chr17	81195210	5927139	0.073	0.34
chr18	78077248	7287804	0.0933	0.9832
chr19	59128983	4041647	0.0684	1.3017
chr20	63025520	5051840	0.0802	0.3261
chr21	48129895	3436221	0.0714	0.3468
chr22	51304566	2385056	0.0465	0.2787
chrMT	16571	3189	0.1924	0.4998
chrX	155270560	8736609	0.0563	0.3386
chrY	59373566	2146894	0.0362	0.3414

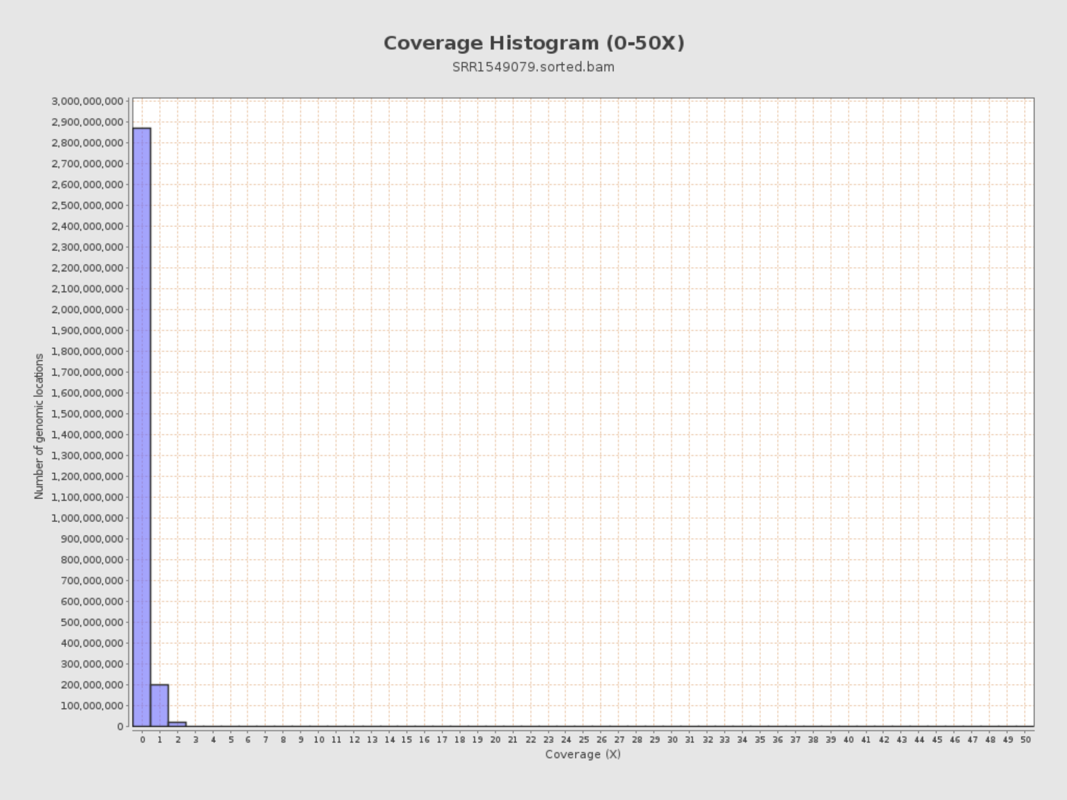
3. Results : Coverage across reference



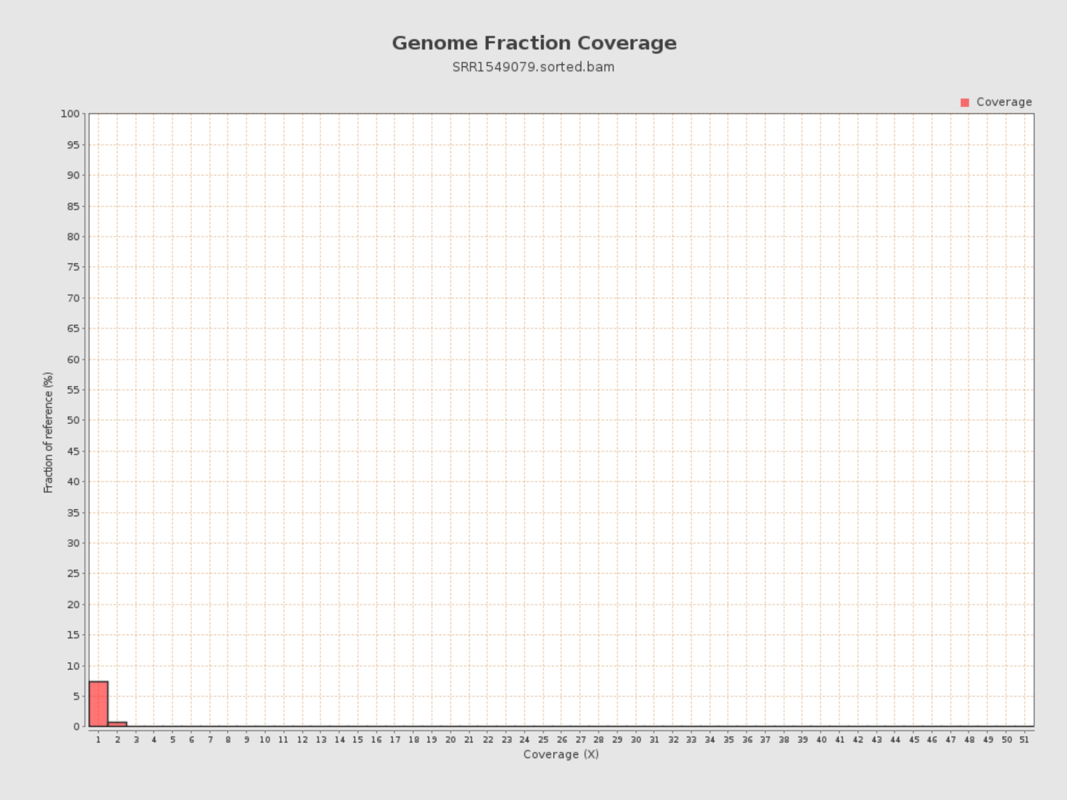
4. Results : Coverage Histogram



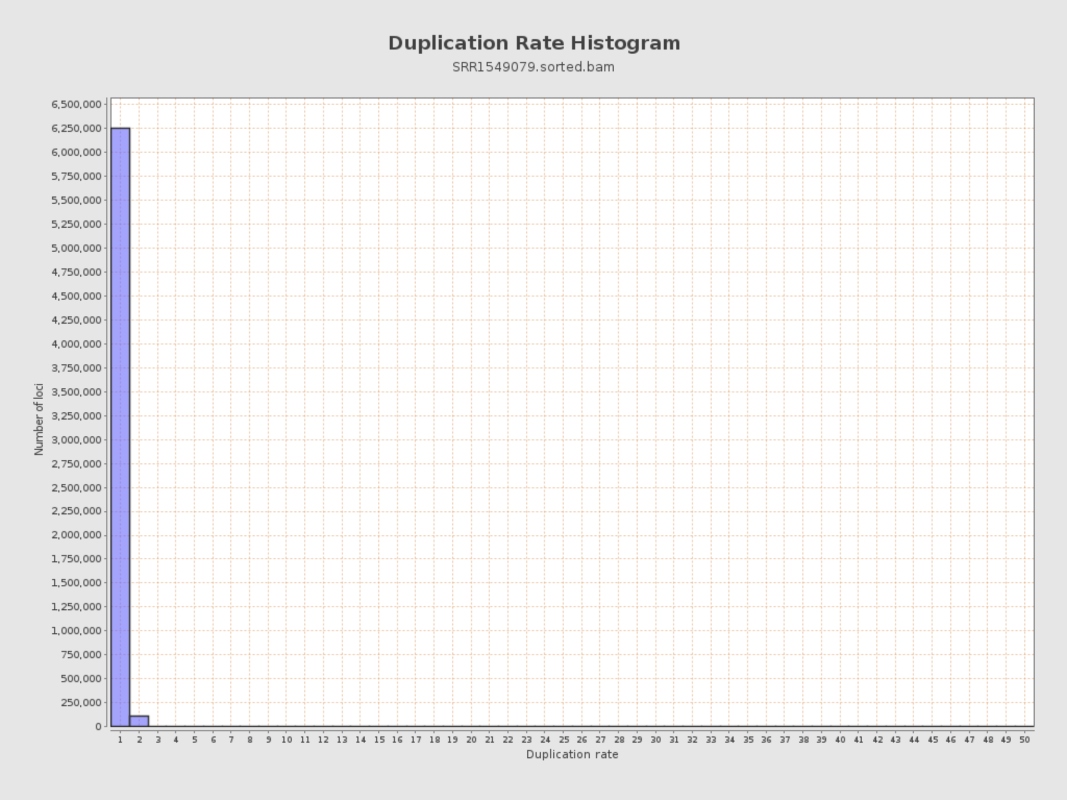
5. Results : Coverage Histogram (0-50X)



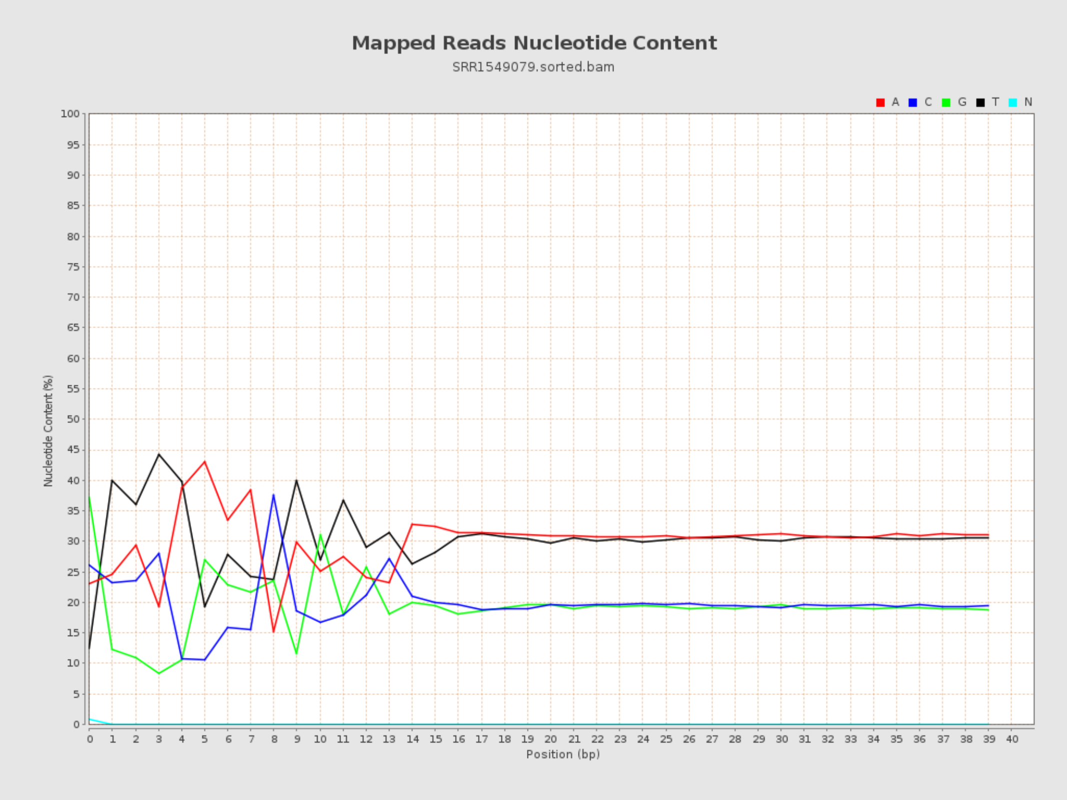
6. Results : Genome Fraction Coverage



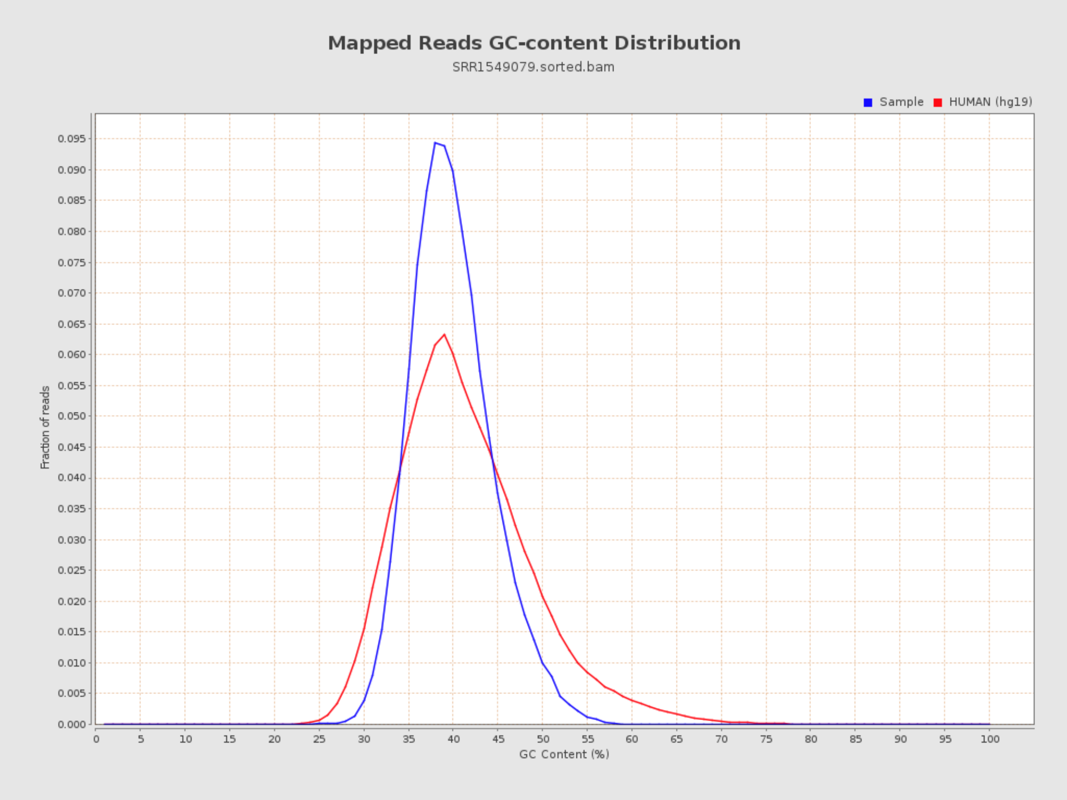
7. Results : Duplication Rate Histogram



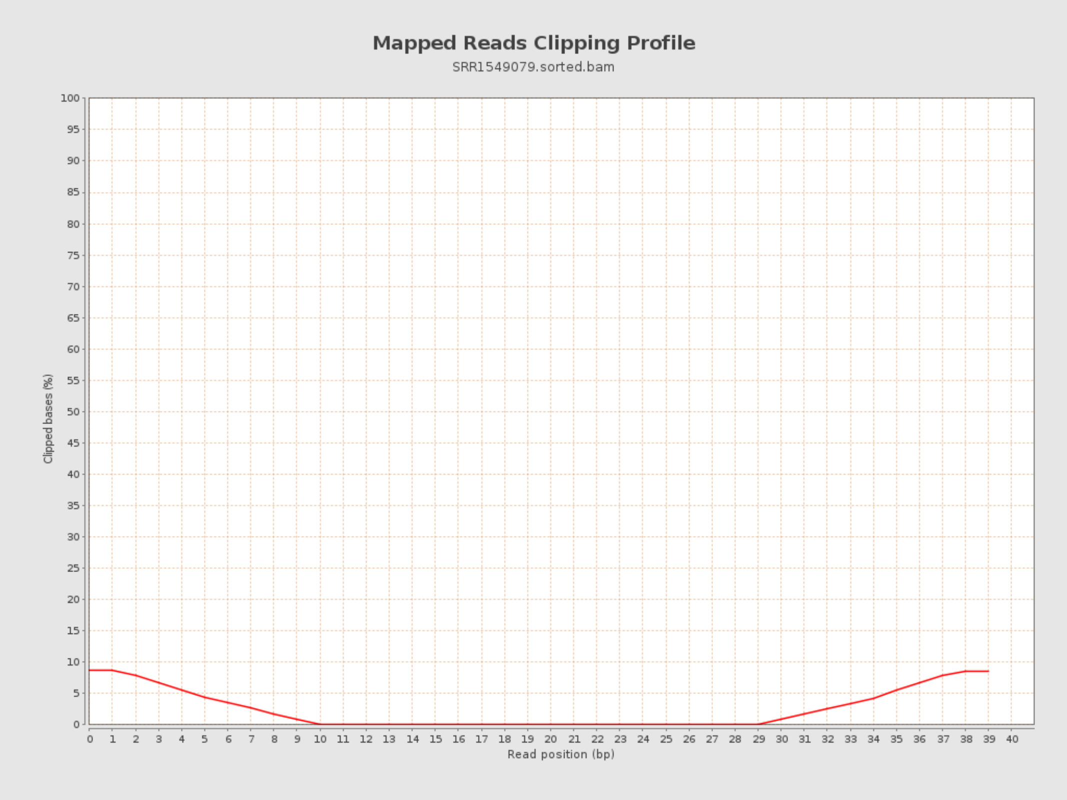
8. Results : Mapped Reads Nucleotide Content



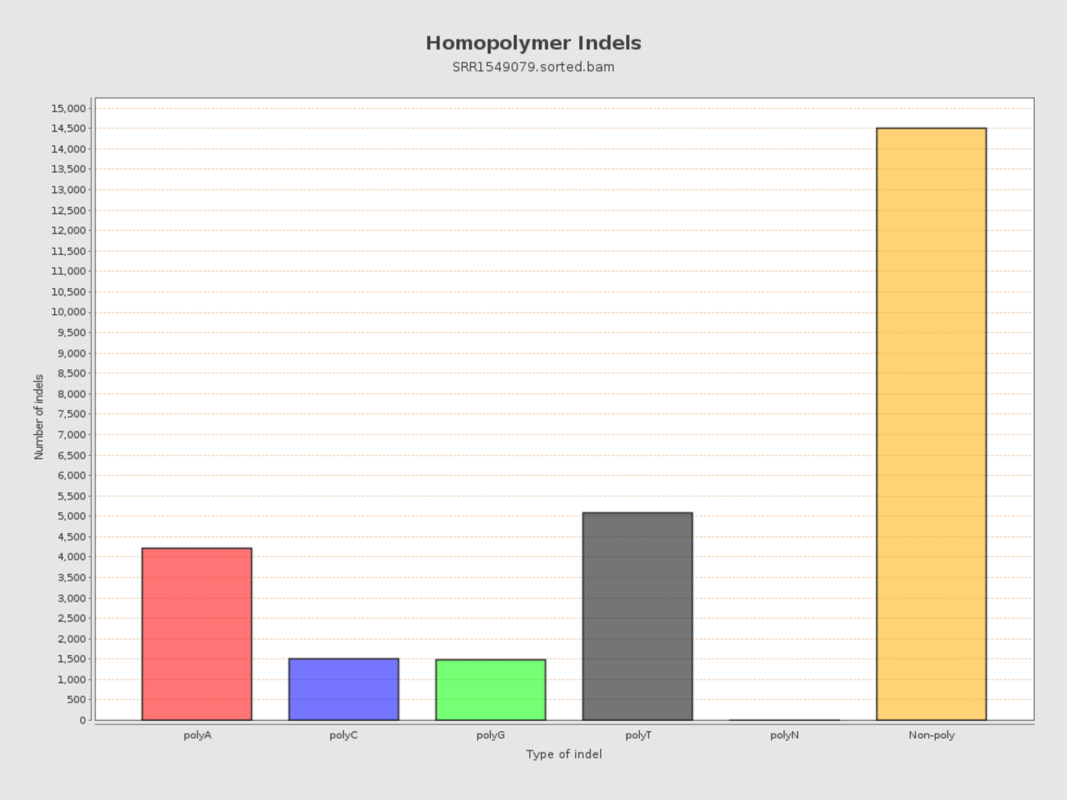
9. Results : Mapped Reads GC-content Distribution



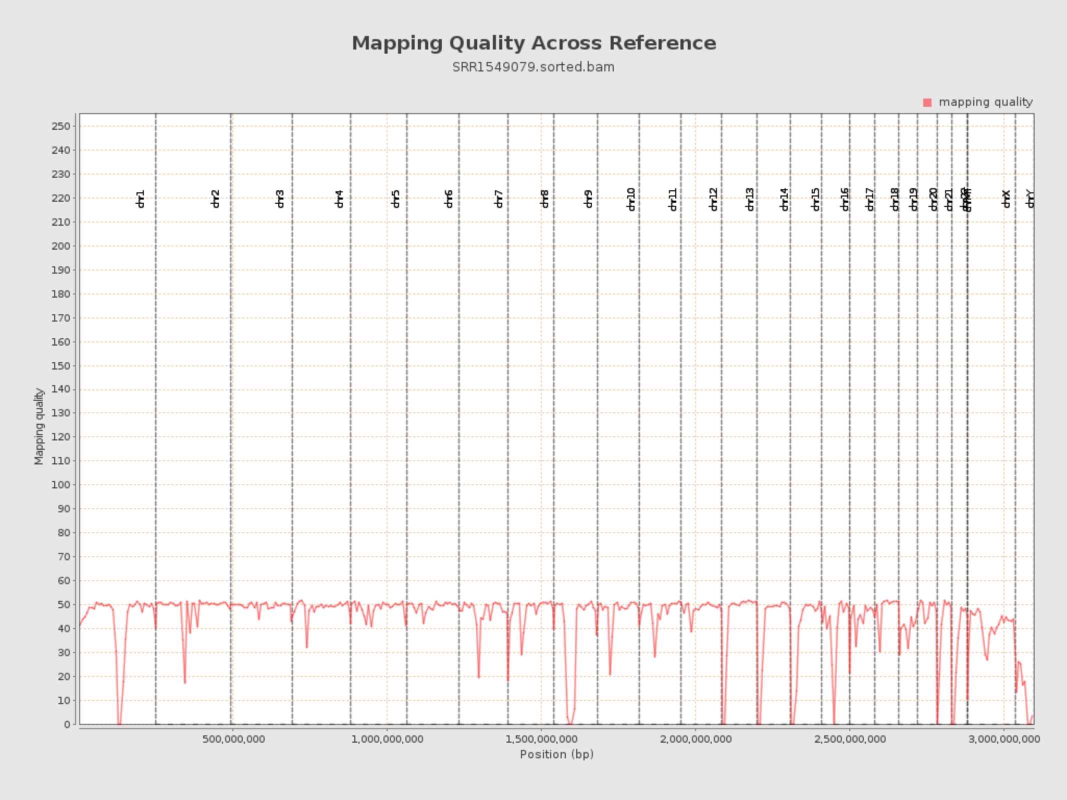
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram