Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 19:00:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549075.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_SRR1549075 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549075.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 19:00:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549075.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,084,090
Mapped reads	8,790,989 / 87.18%
Unmapped reads	1,293,101 / 12.82%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	393,473 / 3.9%
Duplication rate	2.26%
Clipped reads	627,801 / 6.23%

2.2. ACGT Content

Number/percentage of A's	105,003,568 / 30.18%
Number/percentage of C's	68,703,321 / 19.75%
Number/percentage of T's	106,621,113 / 30.64%
Number/percentage of G's	67,535,277 / 19.41%
Number/percentage of N's	86,892 / 0.02%
GC Percentage	39.15%

2.3. Coverage

Mean	0.1124
Standard Deviation	1.4096

2.4. Mapping Quality

Mean Mapping Quality	42.37

2.5. Mismatches and indels

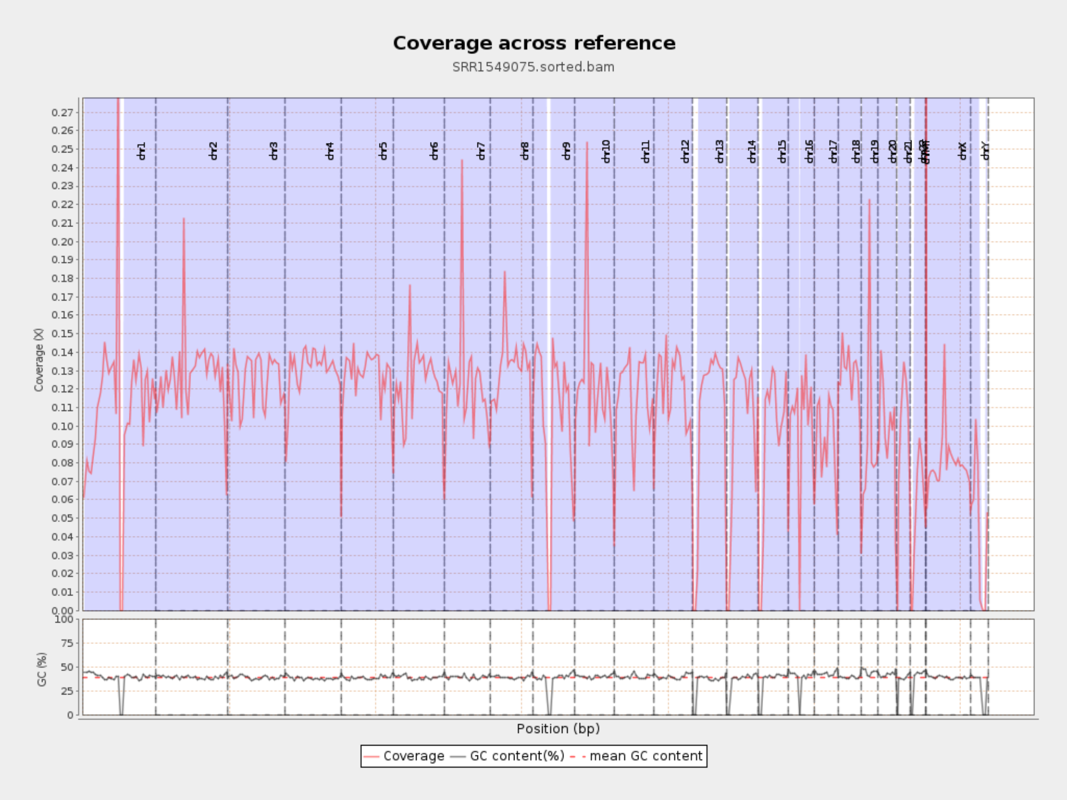
General error rate	0.44%
Mismatches	1,522,206
Insertions	10,442
Mapped reads with at least one insertion	0.12%
Deletions	27,356
Mapped reads with at least one deletion	0.31%
Homopolymer indels	44.35%

2.6. Chromosome stats

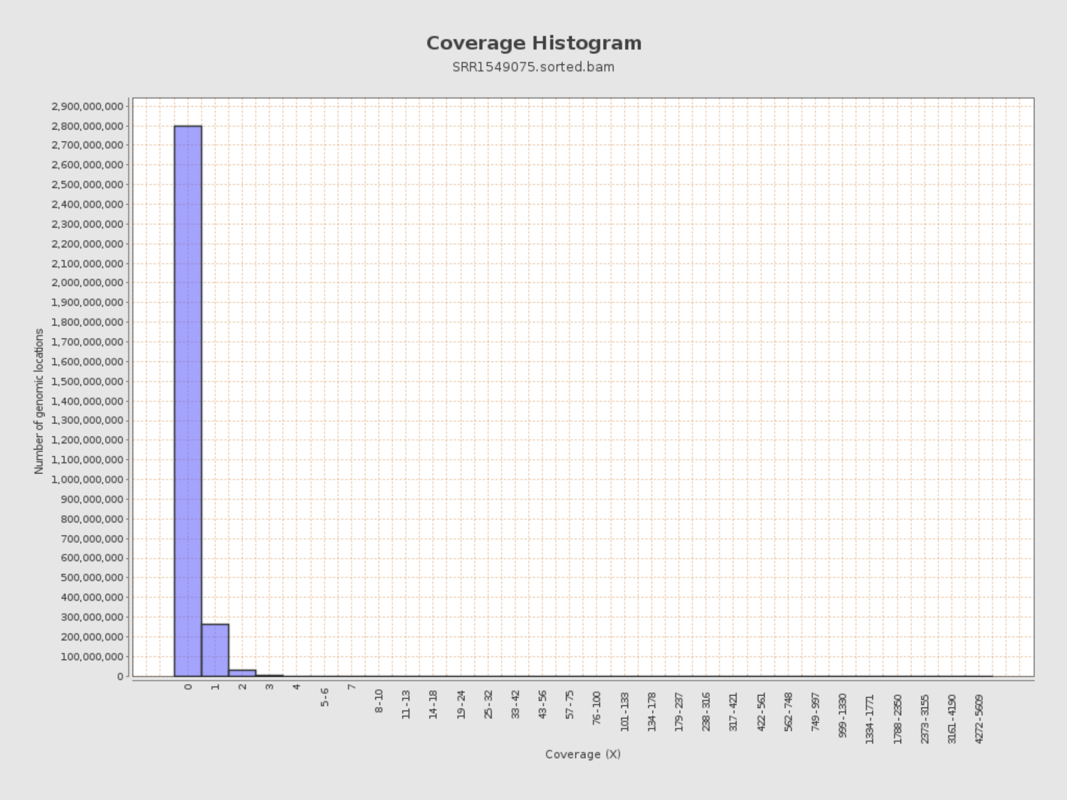
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	27752360	0.1113	3.8503
chr2	243199373	31069682	0.1278	0.9298
chr3	198022430	24837627	0.1254	0.4317
chr4	191154276	24915471	0.1303	0.4238
chr5	180915260	22970720	0.127	0.4404
chr6	171115067	21396443	0.125	0.6337
chr7	159138663	19524350	0.1227	1.3998
chr8	146364022	19082058	0.1304	0.7361

chr9	141213431	14806013	0.1048	0.952
chr10	135534747	16626432	0.1227	1.2657
chr11	135006516	15784277	0.1169	0.9288
chr12	133851895	16033965	0.1198	0.4925
chr13	115169878	12165766	0.1056	0.3511
chr14	107349540	10715581	0.0998	0.7448
chr15	102531392	9370918	0.0914	0.3426
chr16	90354753	8863084	0.0981	0.6535
chr17	81195210	7516005	0.0926	0.502
chr18	78077248	10147327	0.13	2.2108
chr19	59128983	5529686	0.0935	3.0865
chr20	63025520	6468957	0.1026	0.4226
chr21	48129895	4477929	0.093	0.4998
chr22	51304566	2809956	0.0548	0.3662
chrMT	16571	14394	0.8686	1.3399
chrX	155270560	12460743	0.0803	0.6123
chrY	59373566	2643950	0.0445	0.3325

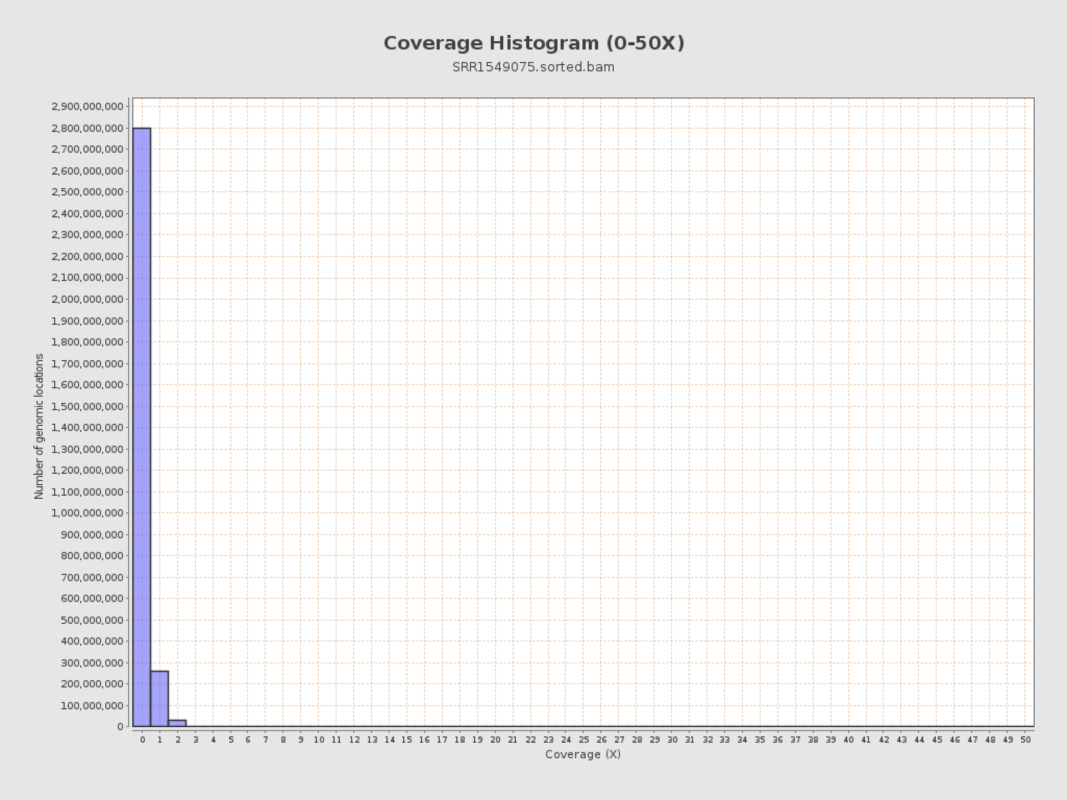
3. Results : Coverage across reference



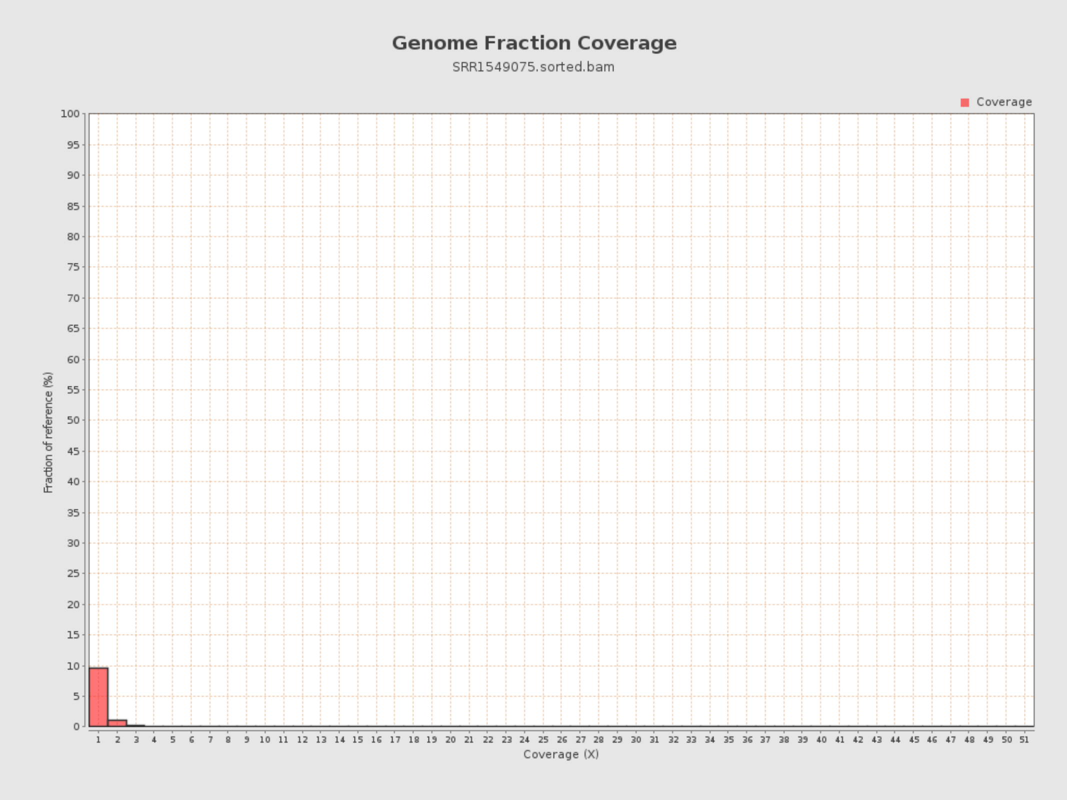
4. Results : Coverage Histogram



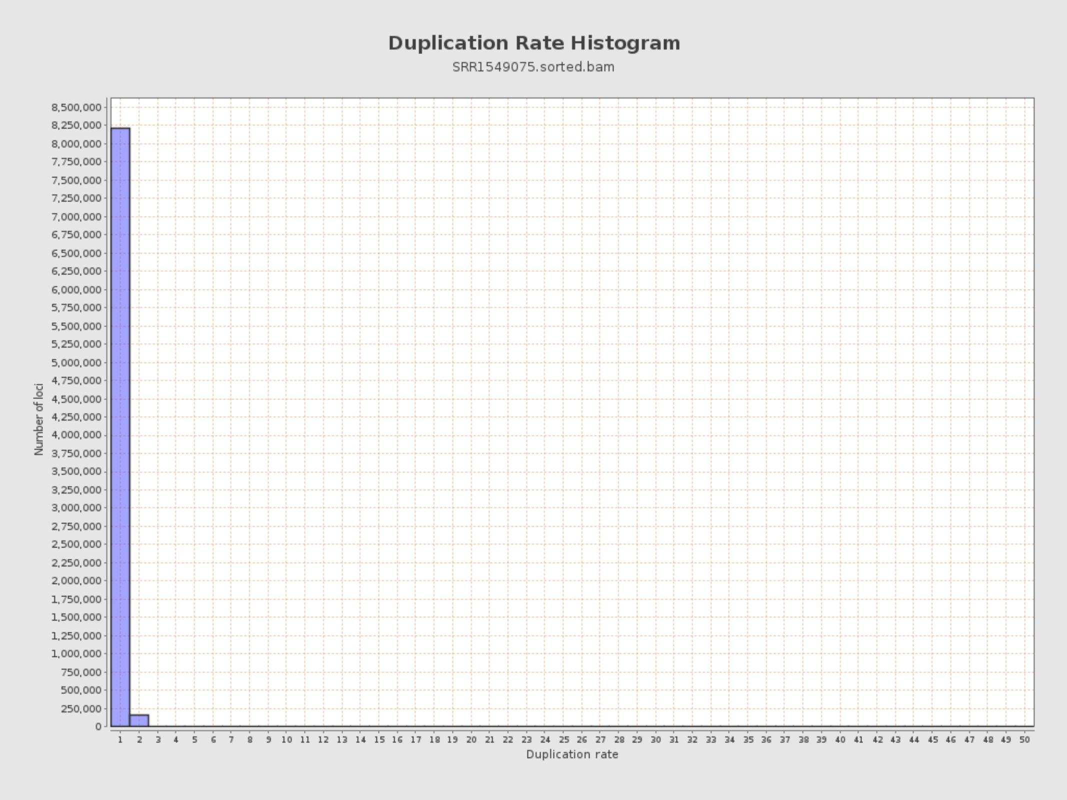
5. Results : Coverage Histogram (0-50X)



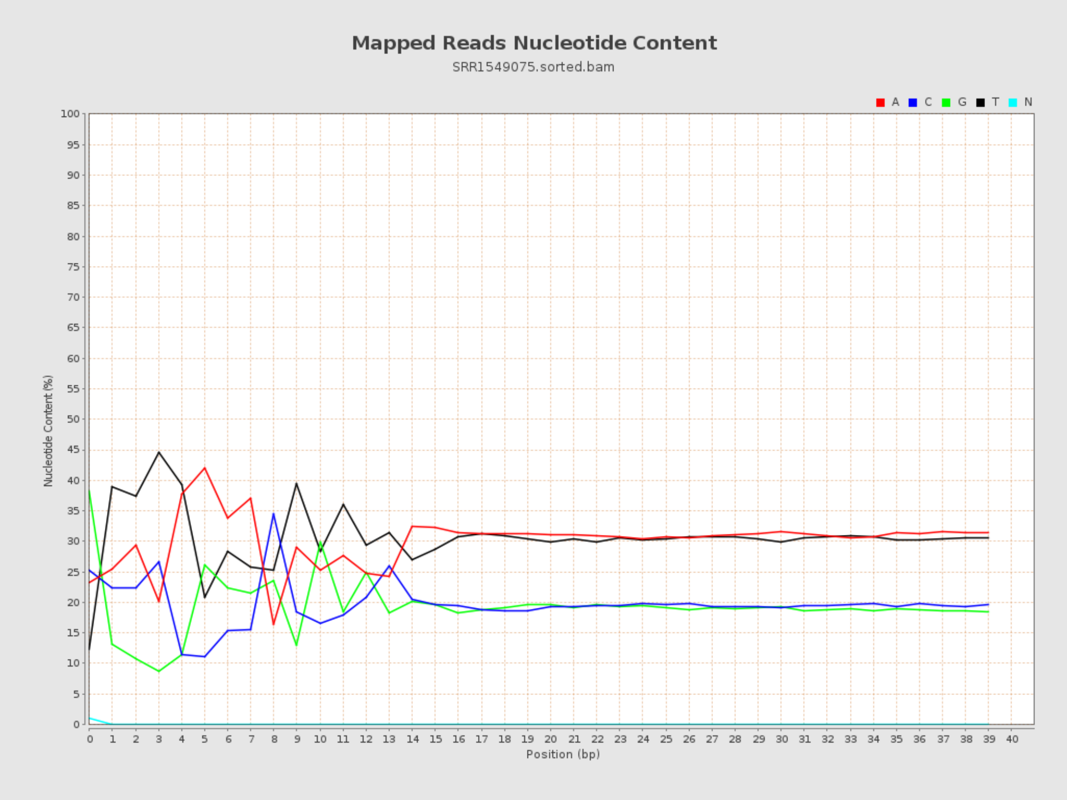
6. Results : Genome Fraction Coverage



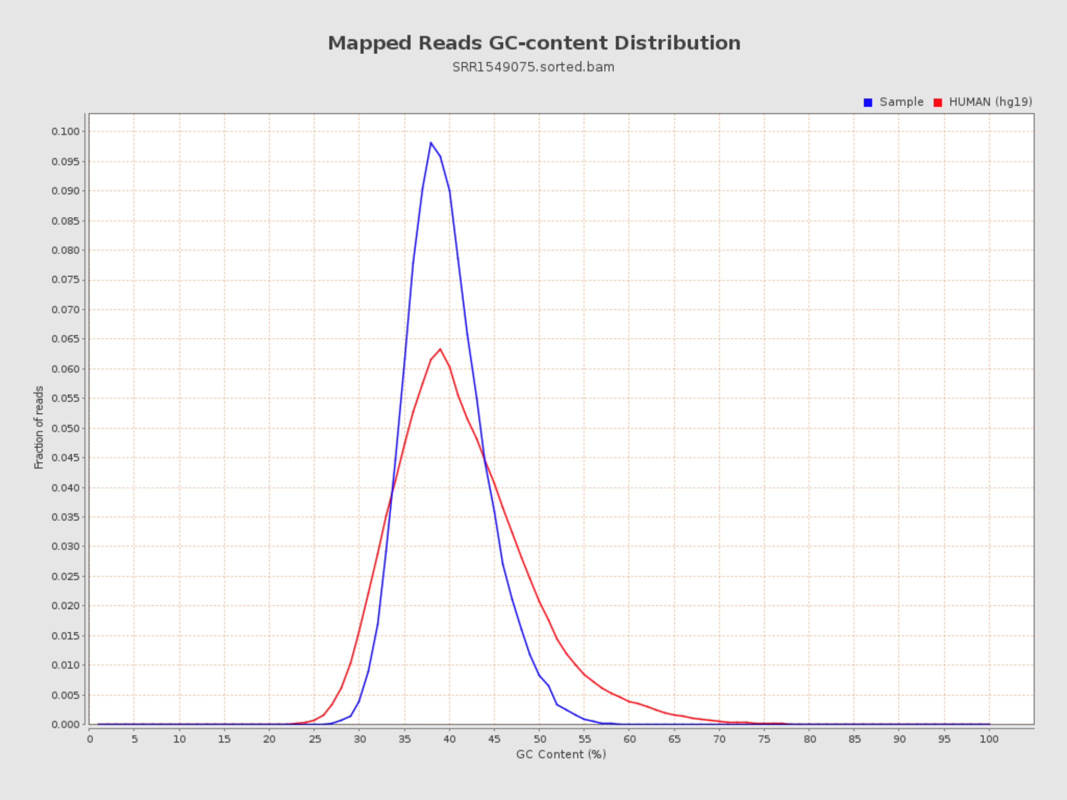
7. Results : Duplication Rate Histogram



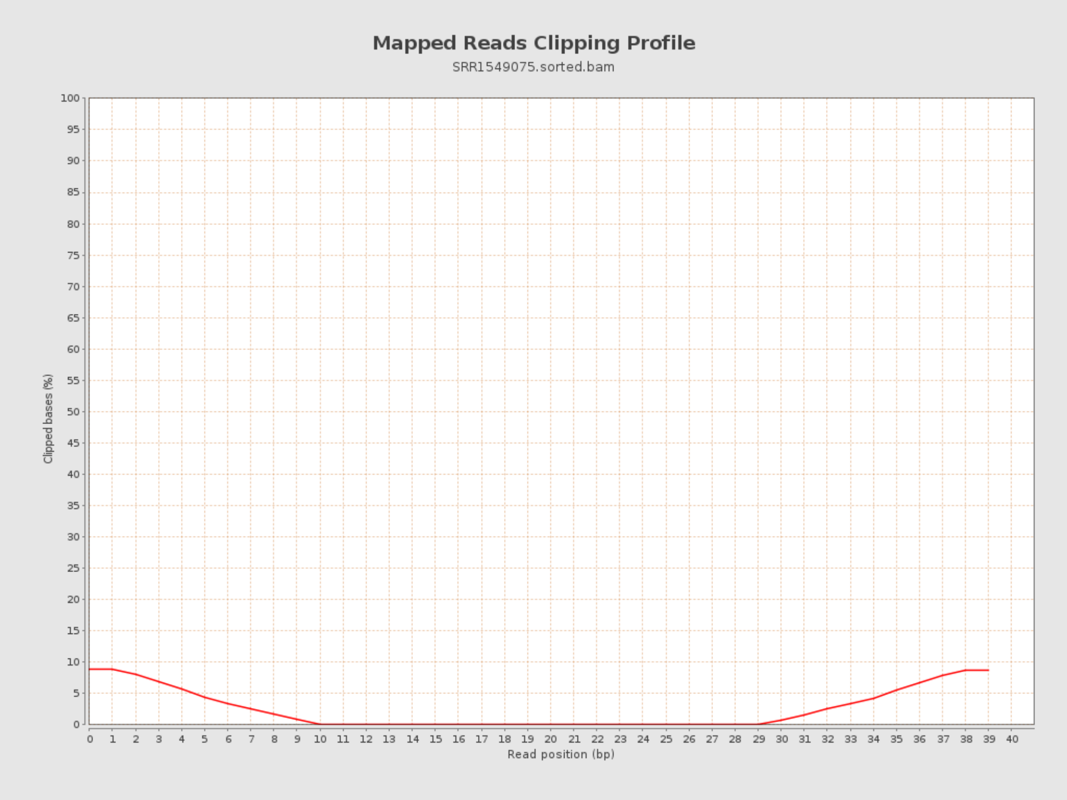
8. Results : Mapped Reads Nucleotide Content



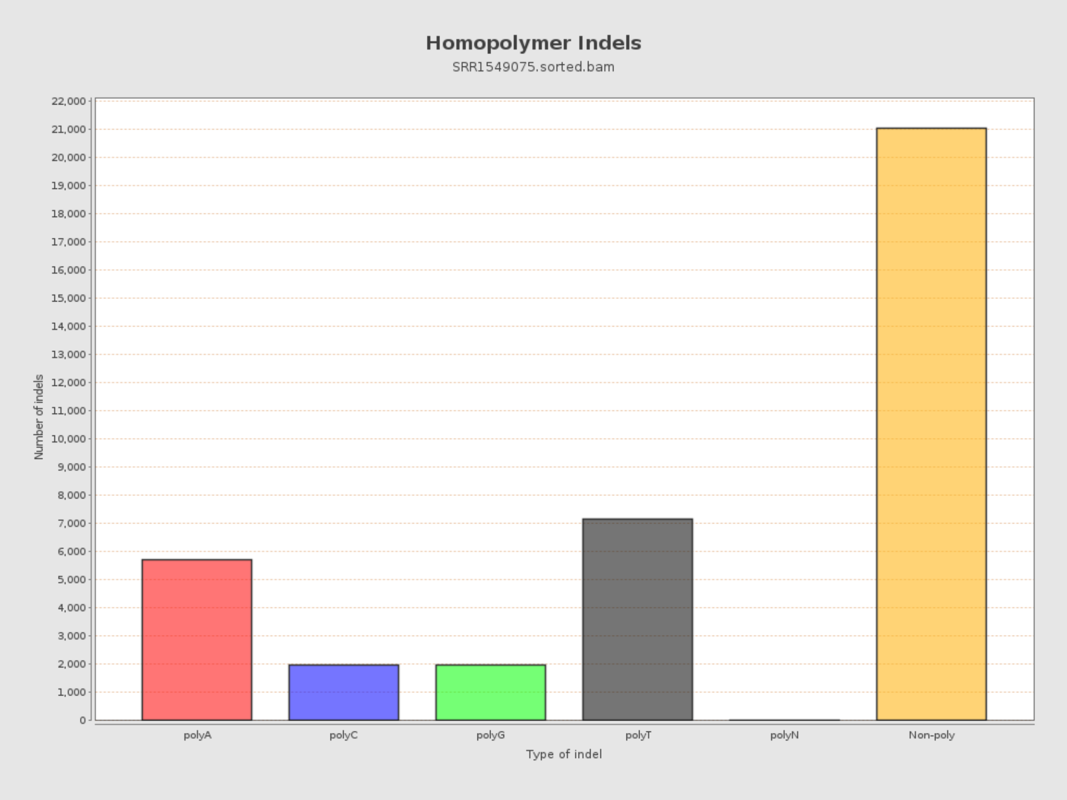
9. Results : Mapped Reads GC-content Distribution



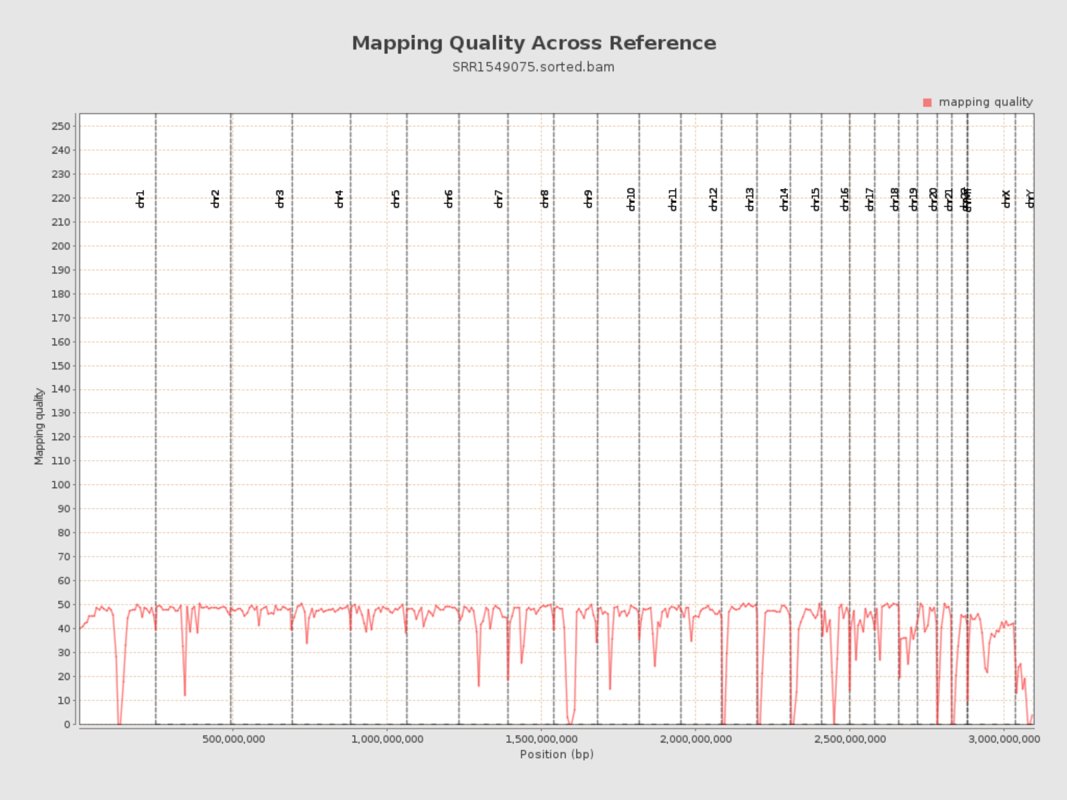
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram