Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 09:28:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549010.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_SRR1549010 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549010.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 09:28:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549010.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	9,128,073
Mapped reads	7,912,765 / 86.69%
Unmapped reads	1,215,308 / 13.31%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	613,802 / 6.72%
Duplication rate	6.99%
Clipped reads	429,609 / 4.71%

2.2. ACGT Content

Number/percentage of A's	93,695,044 / 29.84%
Number/percentage of C's	62,840,554 / 20.02%
Number/percentage of T's	93,627,088 / 29.82%
Number/percentage of G's	63,797,327 / 20.32%
Number/percentage of N's	3,026 / 0%
GC Percentage	40.34%

2.3. Coverage

Mean	0.1014
Standard Deviation	0.7811

2.4. Mapping Quality

Mean Mapping Quality	43.63

2.5. Mismatches and indels

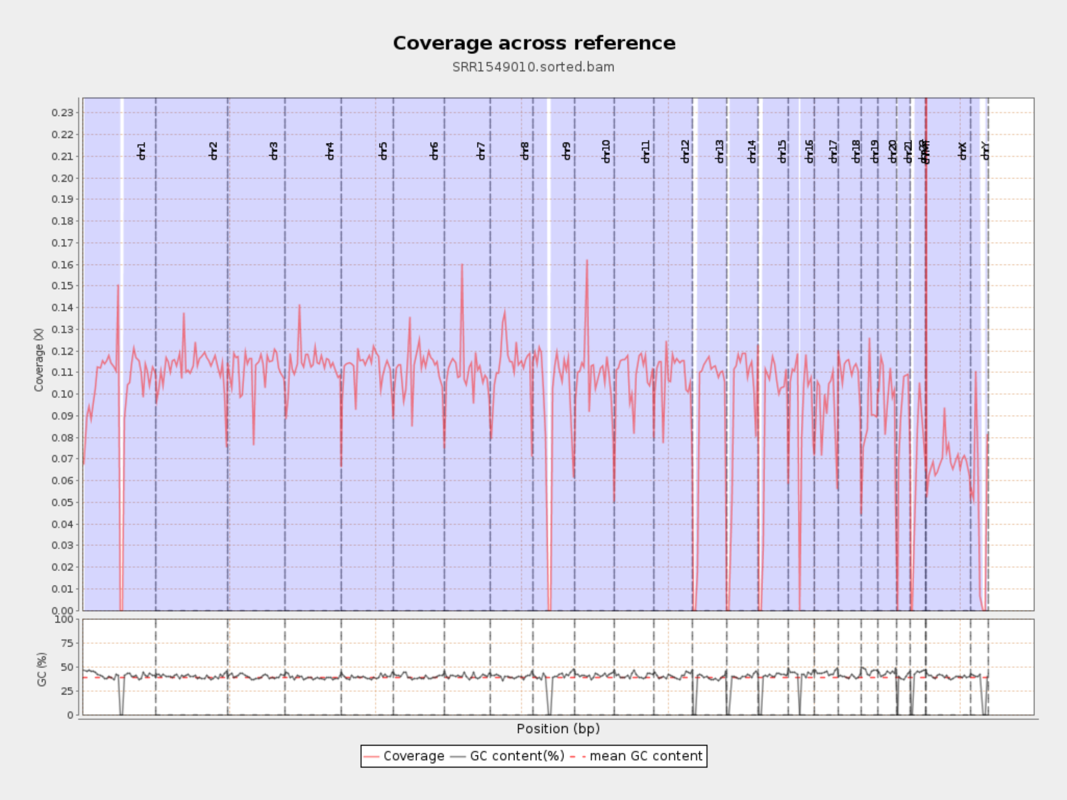
General error rate	0.31%
Mismatches	954,756
Insertions	9,872
Mapped reads with at least one insertion	0.12%
Deletions	27,344
Mapped reads with at least one deletion	0.35%
Homopolymer indels	42.13%

2.6. Chromosome stats

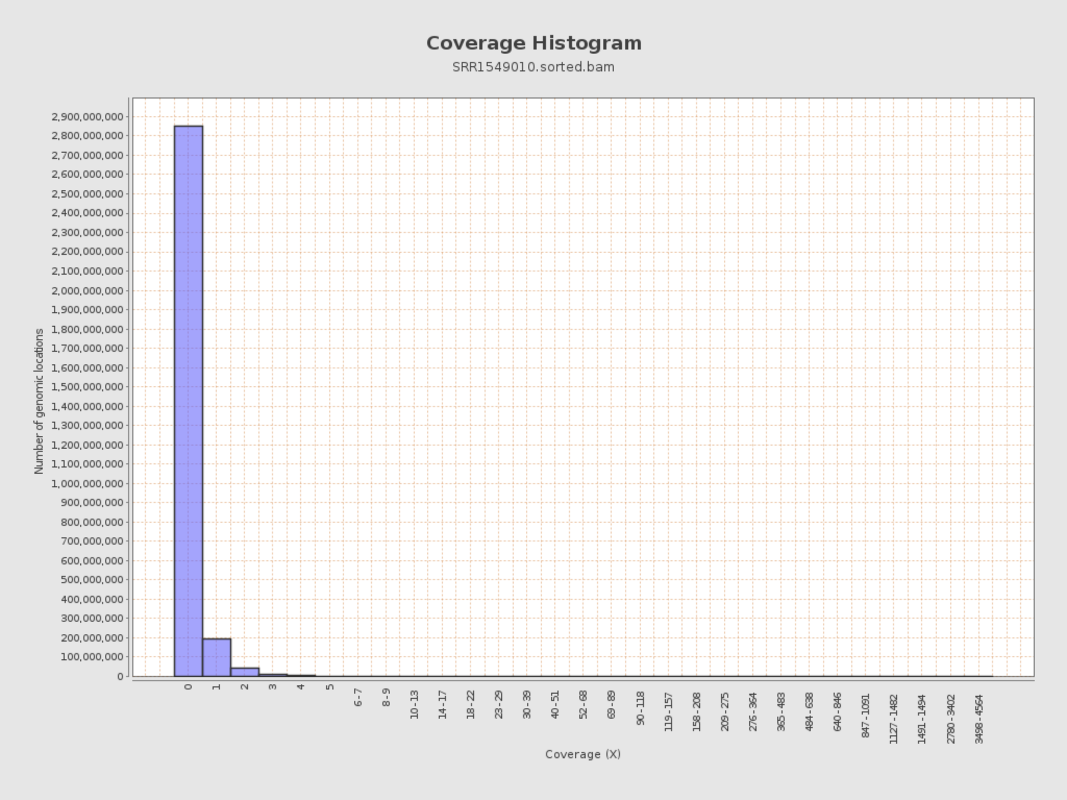
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	25273238	0.1014	1.1567
chr2	243199373	27400938	0.1127	0.5808
chr3	198022430	22093298	0.1116	0.4066
chr4	191154276	21755783	0.1138	0.4602
chr5	180915260	20205843	0.1117	0.414
chr6	171115067	19175240	0.1121	0.4861
chr7	159138663	17640151	0.1108	0.8577
chr8	146364022	16507293	0.1128	2.2716

chr9	141213431	13434806	0.0951	0.5421
chr10	135534747	14947091	0.1103	0.6311
chr11	135006516	14614078	0.1082	0.5354
chr12	133851895	14534055	0.1086	0.4197
chr13	115169878	10628788	0.0923	0.3667
chr14	107349540	9916114	0.0924	0.4692
chr15	102531392	8899039	0.0868	0.3567
chr16	90354753	8350583	0.0924	0.4244
chr17	81195210	7645321	0.0942	0.4175
chr18	78077248	8702710	0.1115	1.12
chr19	59128983	5259356	0.0889	0.9224
chr20	63025520	6300550	0.1	0.4141
chr21	48129895	4102509	0.0852	0.4421
chr22	51304566	3185638	0.0621	0.3327
chrMT	16571	13633	0.8227	1.3686
chrX	155270560	10643157	0.0685	0.4207
chrY	59373566	2769205	0.0466	0.4726

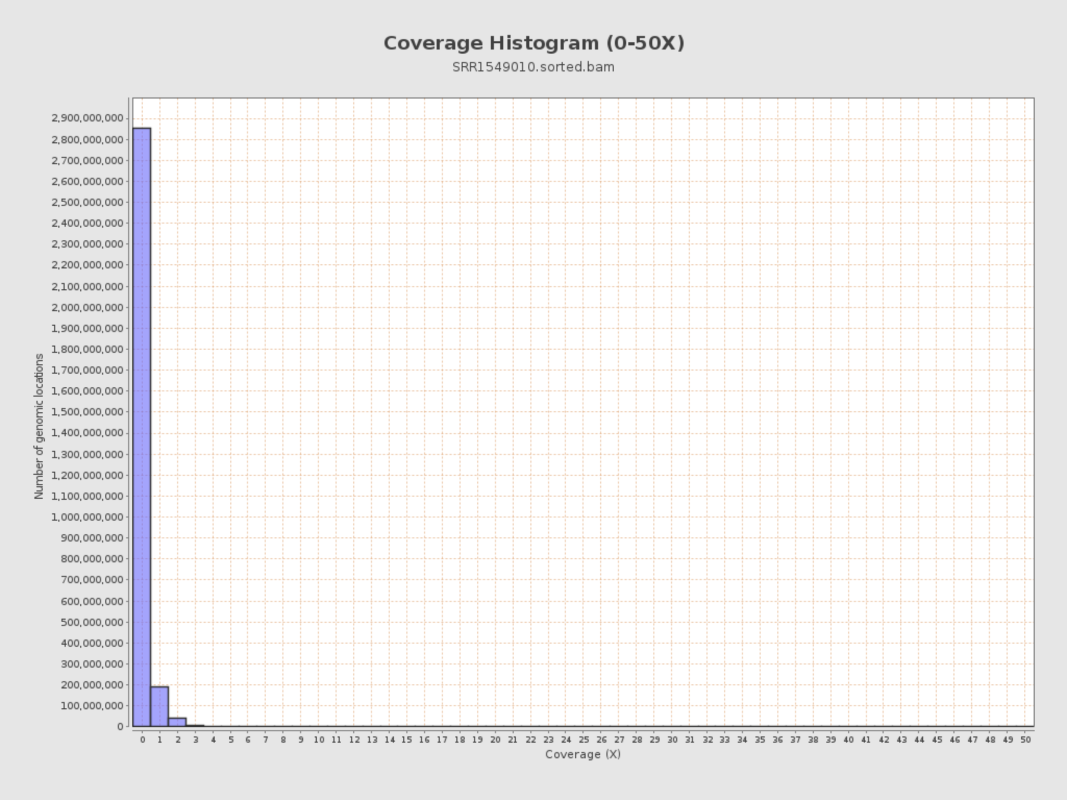
3. Results : Coverage across reference



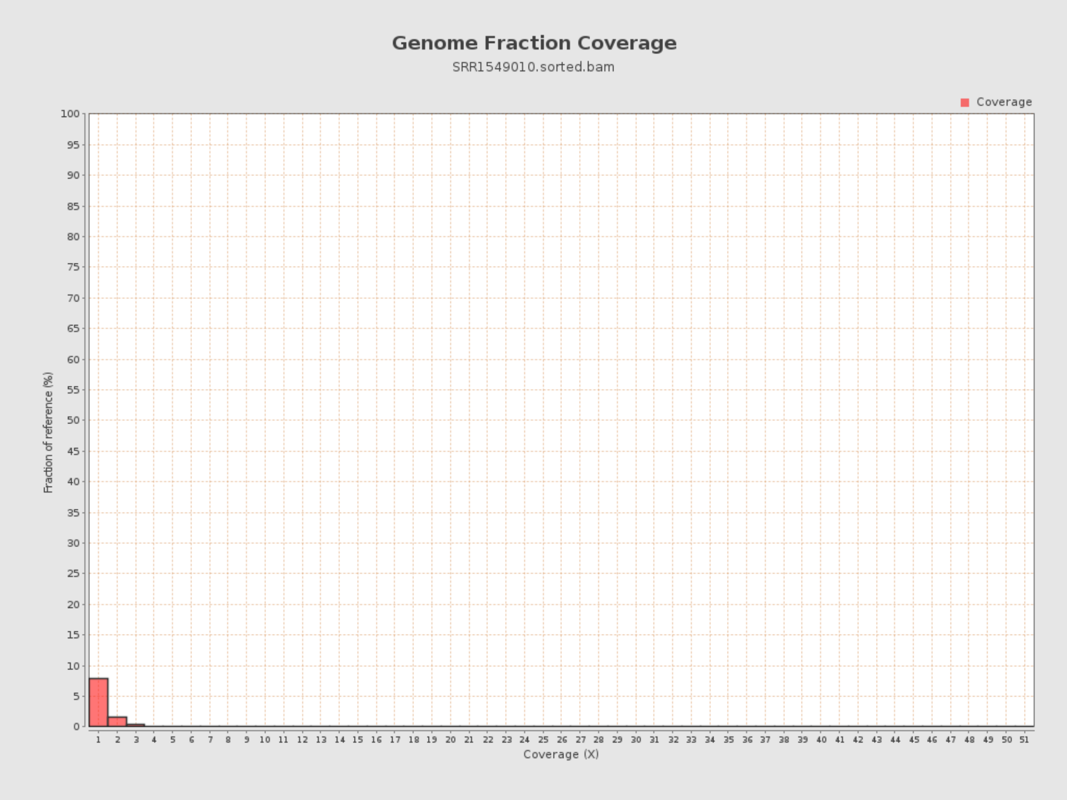
4. Results : Coverage Histogram



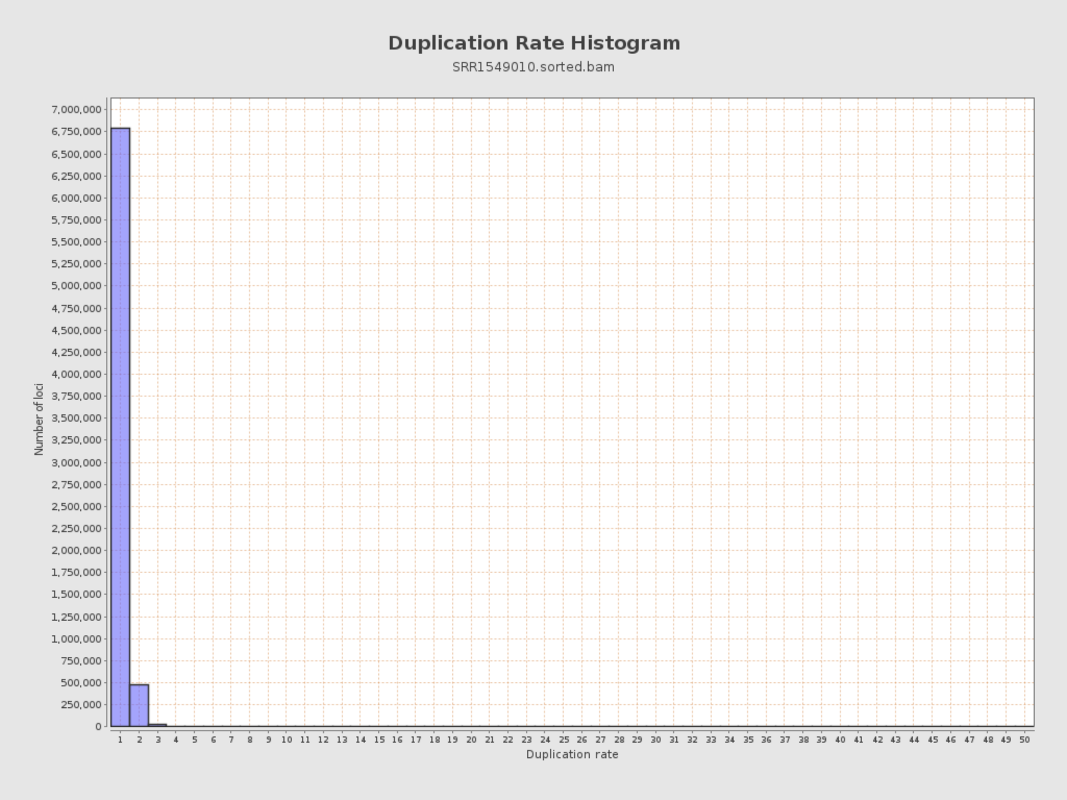
5. Results : Coverage Histogram (0-50X)



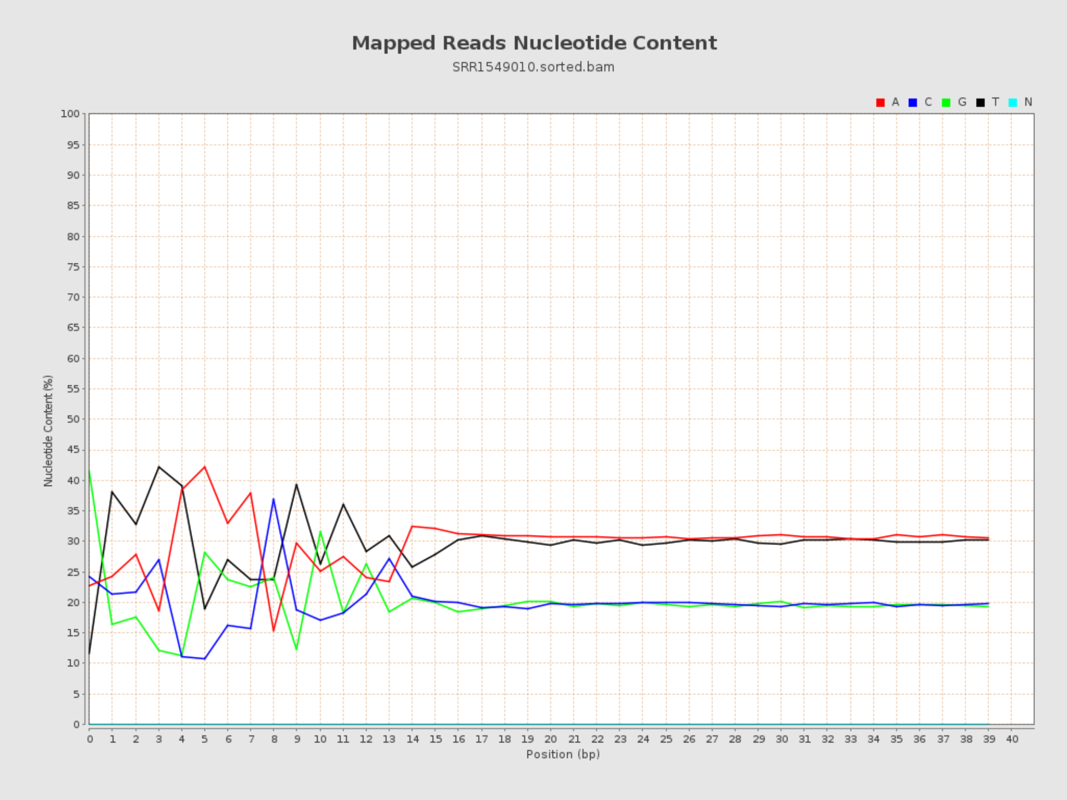
6. Results : Genome Fraction Coverage



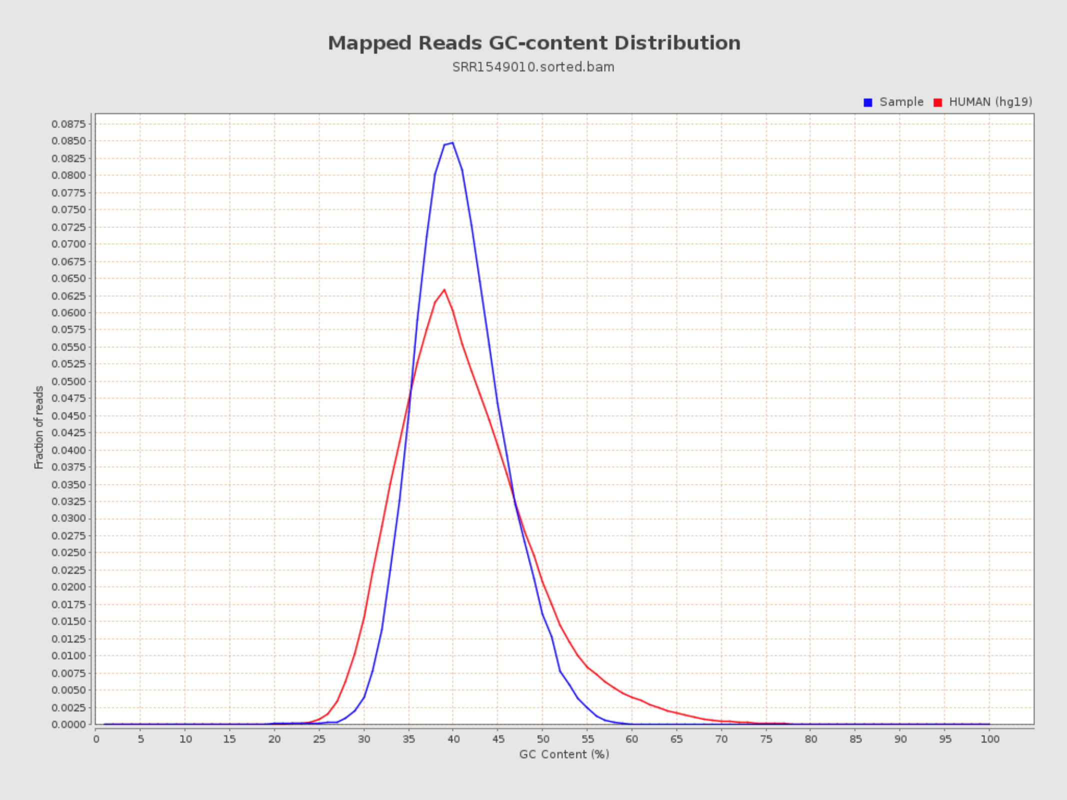
7. Results : Duplication Rate Histogram



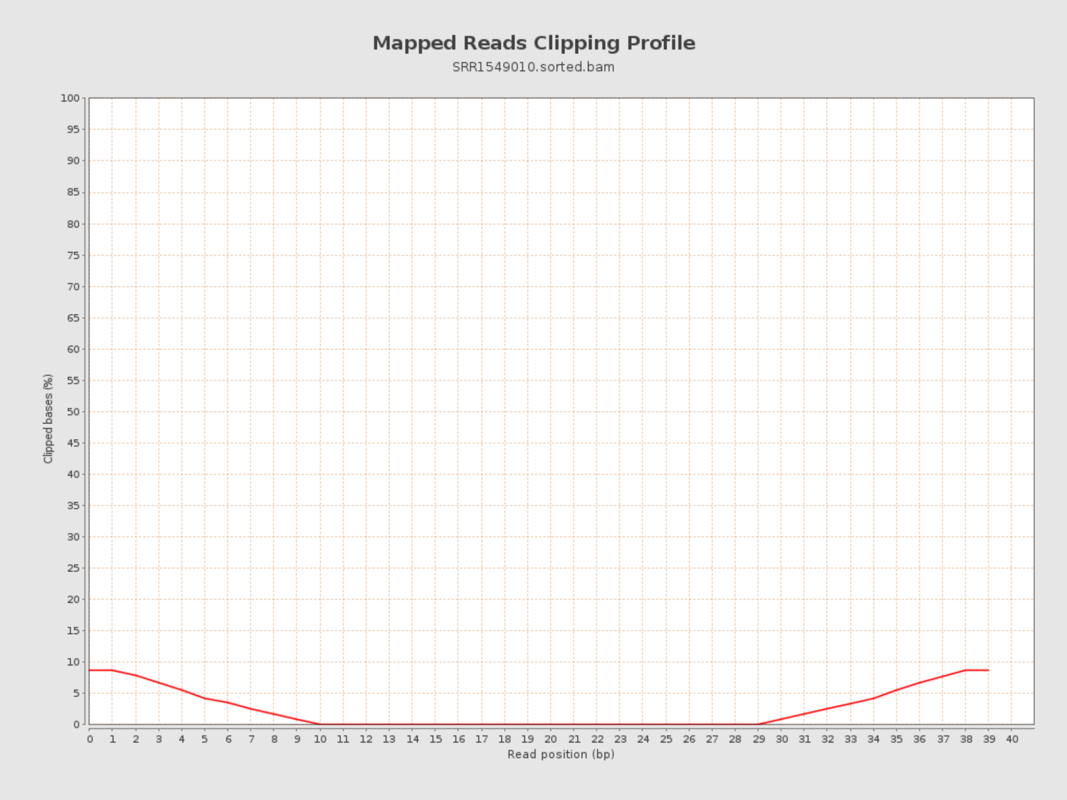
8. Results : Mapped Reads Nucleotide Content



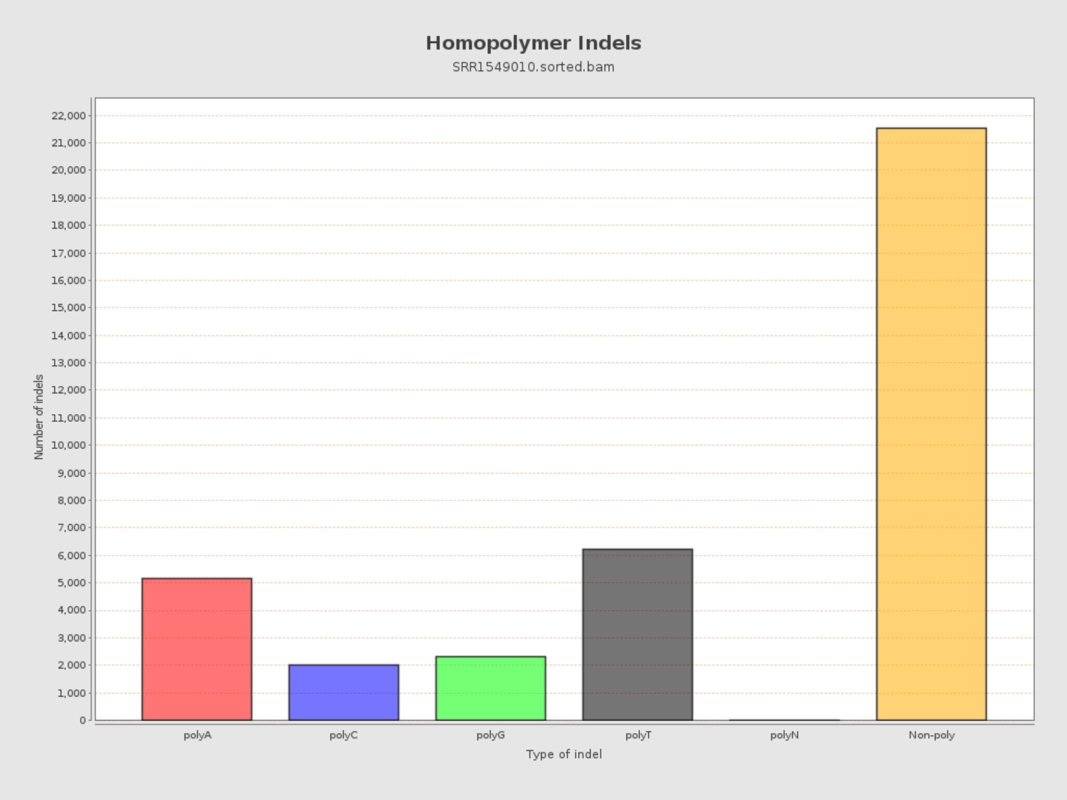
9. Results : Mapped Reads GC-content Distribution



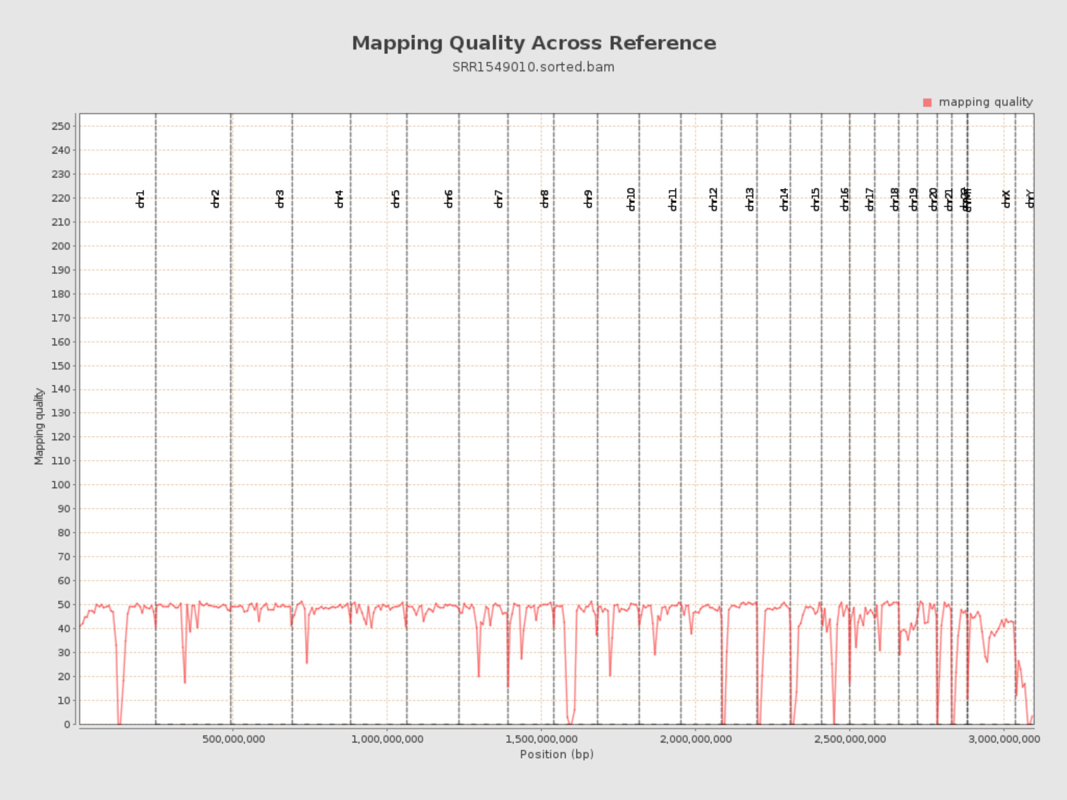
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram