Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 14:55:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549054.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_SRR1549054 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549054.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 14:55:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549054.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,912,838
Mapped reads	3,396,363 / 86.8%
Unmapped reads	516,475 / 13.2%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	117,700 / 3.01%
Duplication rate	2.15%
Clipped reads	283,808 / 7.25%

2.2. ACGT Content

Number/percentage of A's	37,725,252 / 28.1%
Number/percentage of C's	28,966,497 / 21.58%
Number/percentage of T's	38,567,710 / 28.73%
Number/percentage of G's	28,977,059 / 21.59%
Number/percentage of N's	1,065 / 0%
GC Percentage	43.16%

2.3. Coverage

Mean	0.0434
Standard Deviation	0.4467

2.4. Mapping Quality

Mean Mapping Quality	37.22

2.5. Mismatches and indels

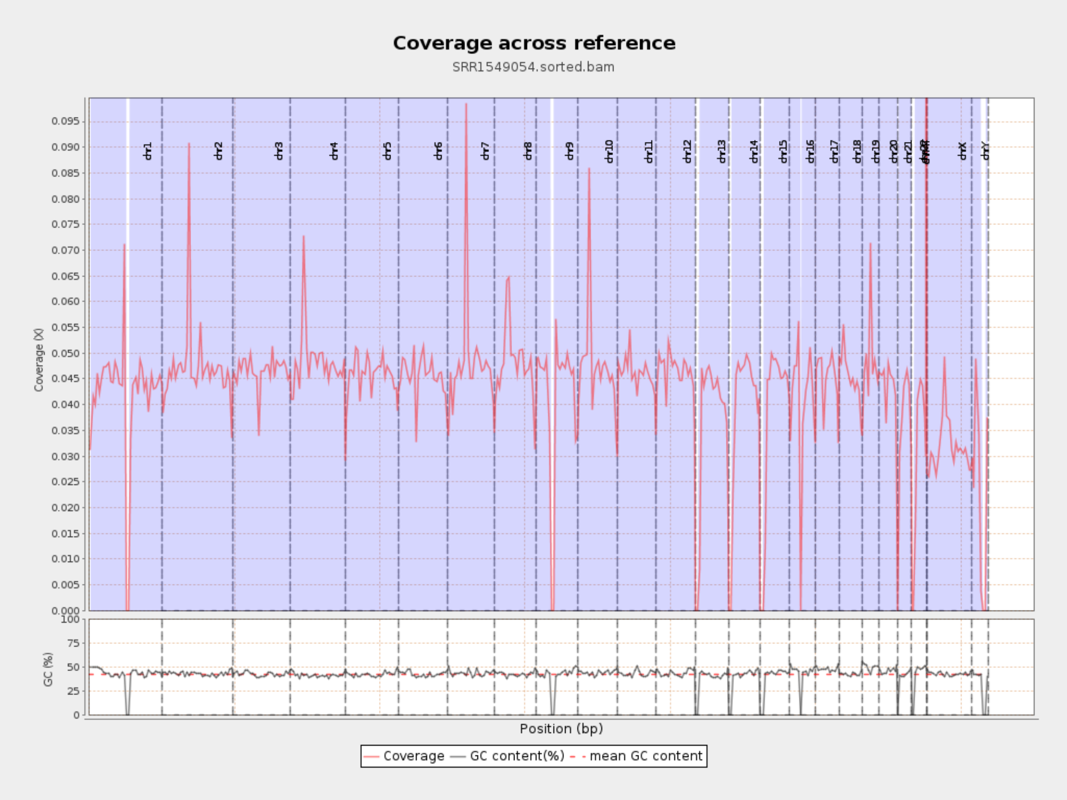
General error rate	0.3%
Mismatches	401,679
Insertions	4,377
Mapped reads with at least one insertion	0.13%
Deletions	9,892
Mapped reads with at least one deletion	0.29%
Homopolymer indels	39.41%

2.6. Chromosome stats

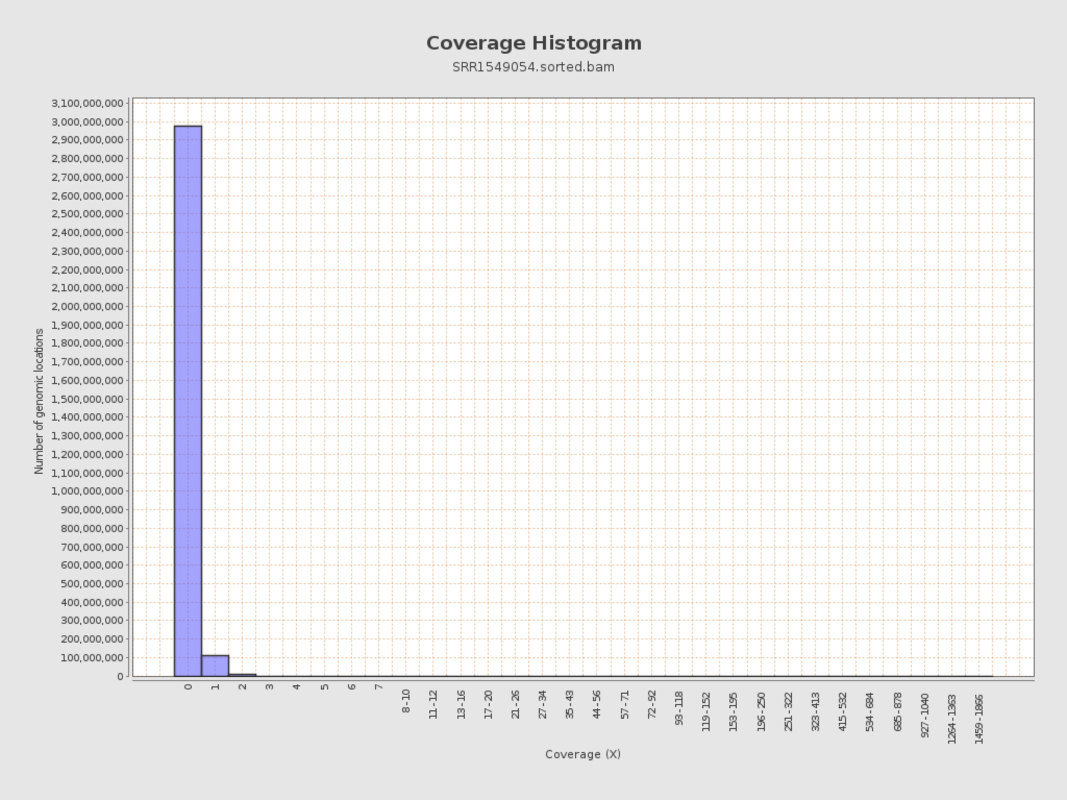
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10452086	0.0419	0.7393
chr2	243199373	11522971	0.0474	0.4279
chr3	198022430	9222734	0.0466	0.2359
chr4	191154276	9244206	0.0484	0.2676
chr5	180915260	8318157	0.046	0.2398
chr6	171115067	7806734	0.0456	0.2453
chr7	159138663	7754479	0.0487	0.6193
chr8	146364022	7023244	0.048	0.9532

chr9	141213431	5834004	0.0413	0.4145
chr10	135534747	6509016	0.048	0.3883
chr11	135006516	6206480	0.046	0.3166
chr12	133851895	6252579	0.0467	0.2487
chr13	115169878	4139454	0.0359	0.2038
chr14	107349540	4120620	0.0384	0.2712
chr15	102531392	3832064	0.0374	0.2115
chr16	90354753	3662040	0.0405	0.2586
chr17	81195210	3664693	0.0451	0.2426
chr18	78077248	3582688	0.0459	0.7444
chr19	59128983	2891527	0.0489	0.7619
chr20	63025520	2740340	0.0435	0.2434
chr21	48129895	1719097	0.0357	0.2706
chr22	51304566	1478964	0.0288	0.2498
chrMT	16571	9144	0.5518	0.9546
chrX	155270560	4960921	0.032	0.2675
chrY	59373566	1302135	0.0219	0.2466

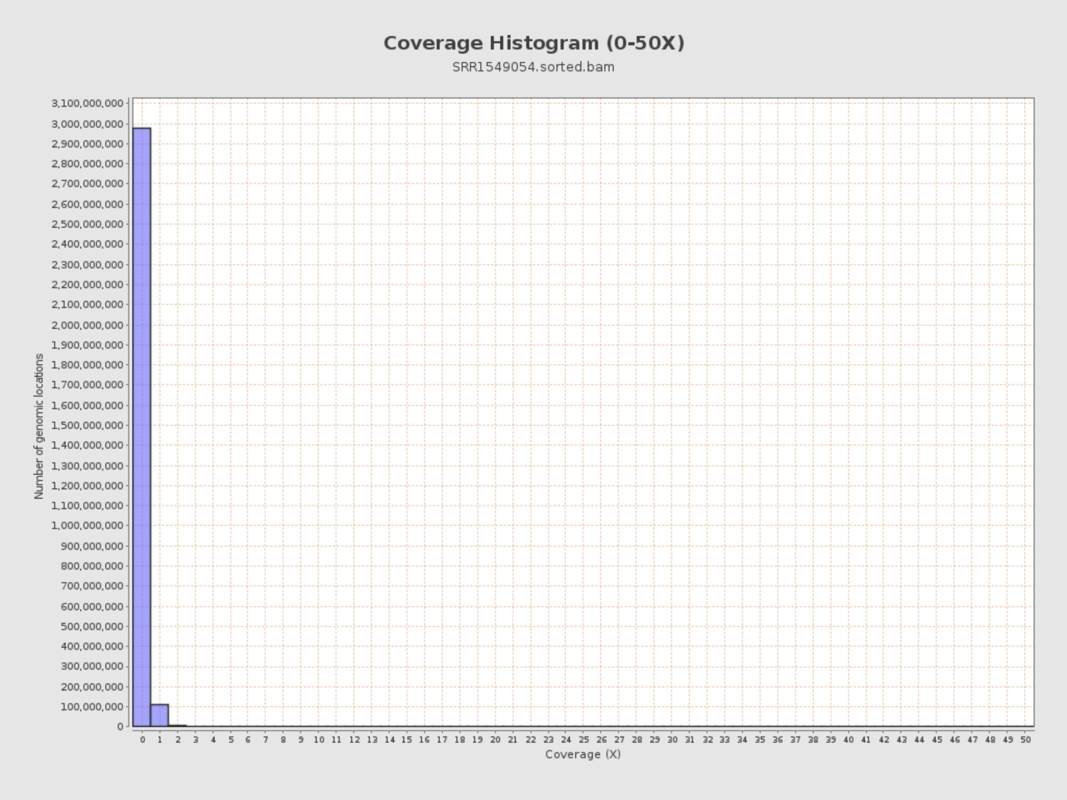
3. Results : Coverage across reference



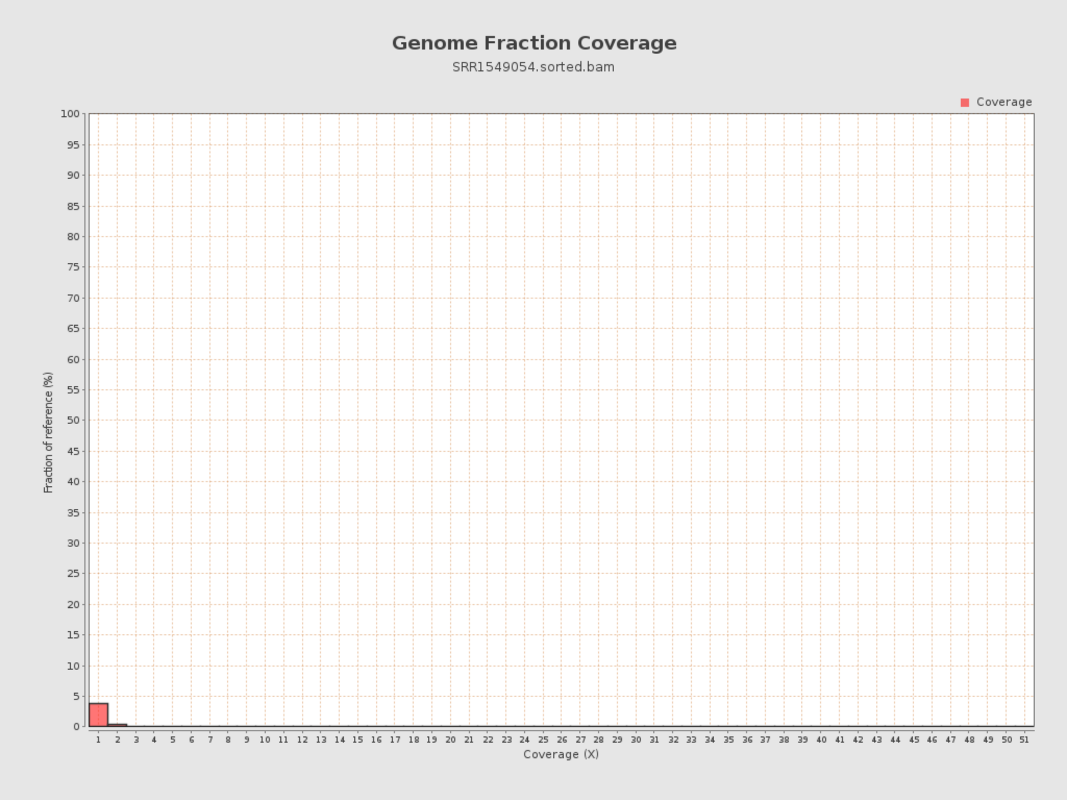
4. Results : Coverage Histogram



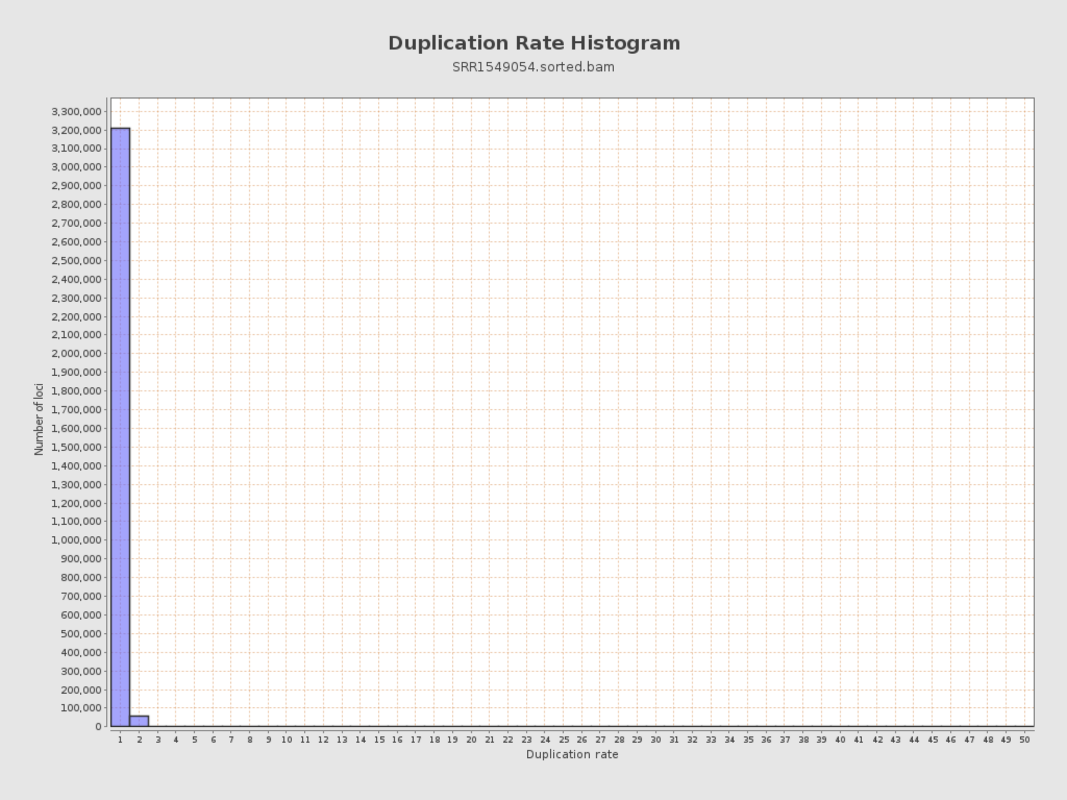
5. Results : Coverage Histogram (0-50X)



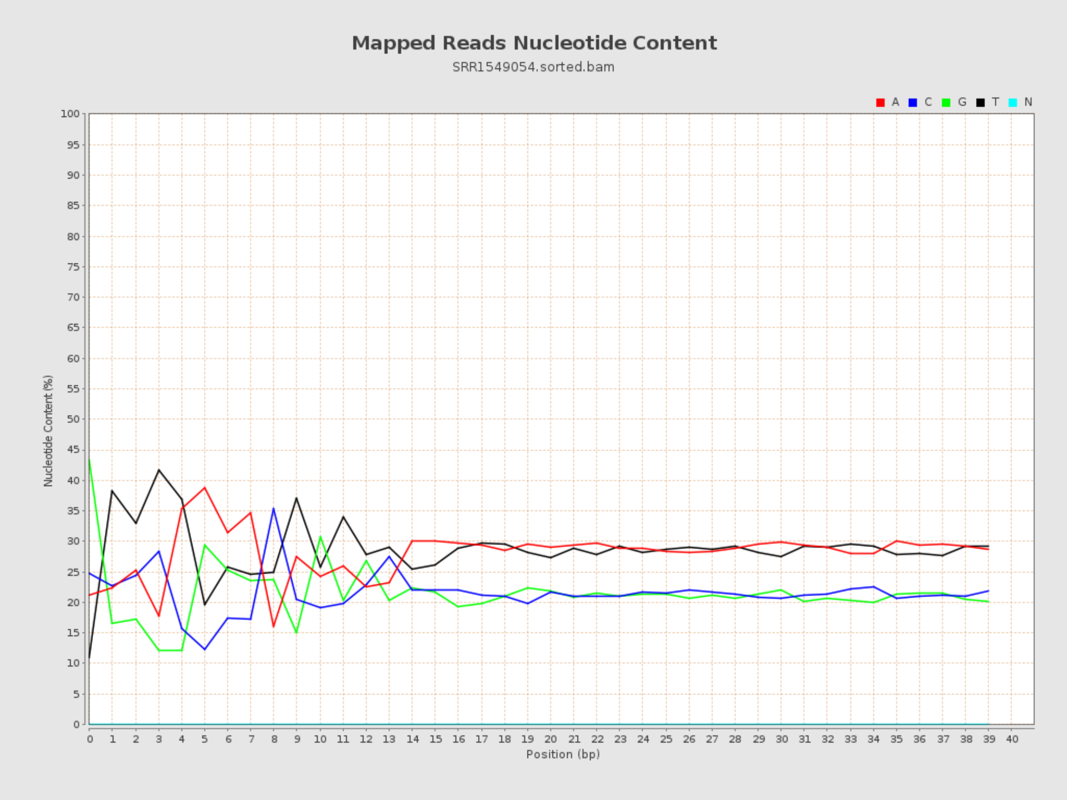
6. Results : Genome Fraction Coverage



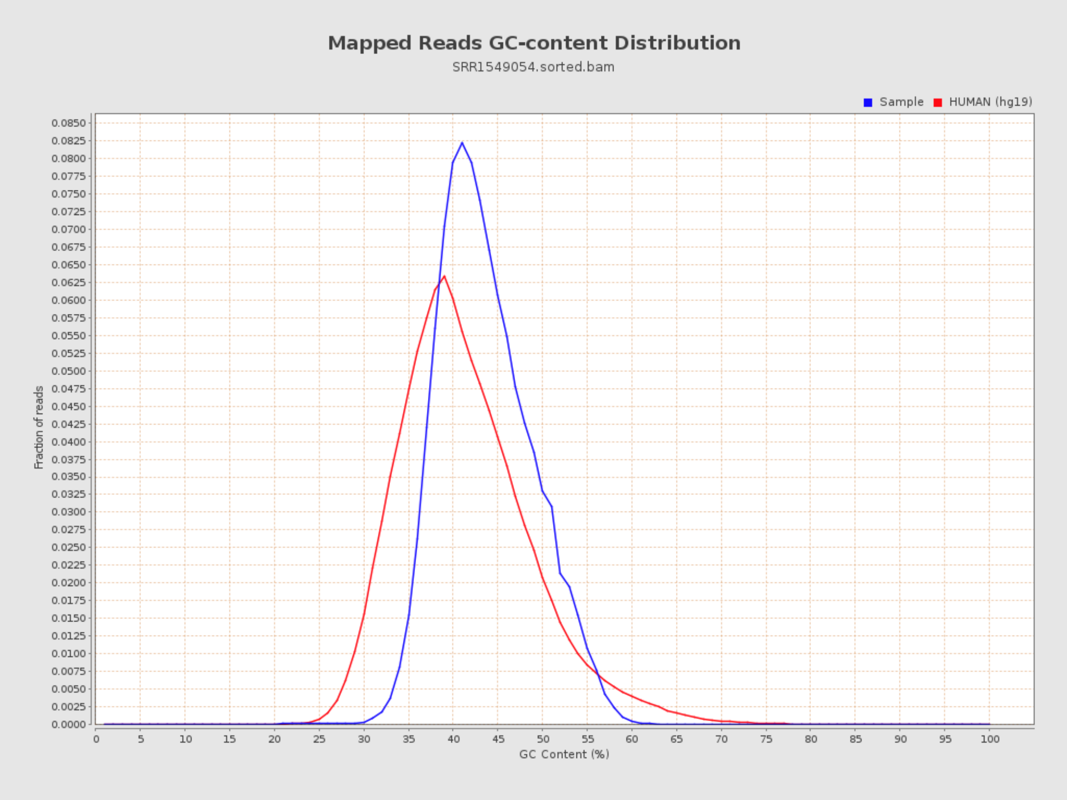
7. Results : Duplication Rate Histogram



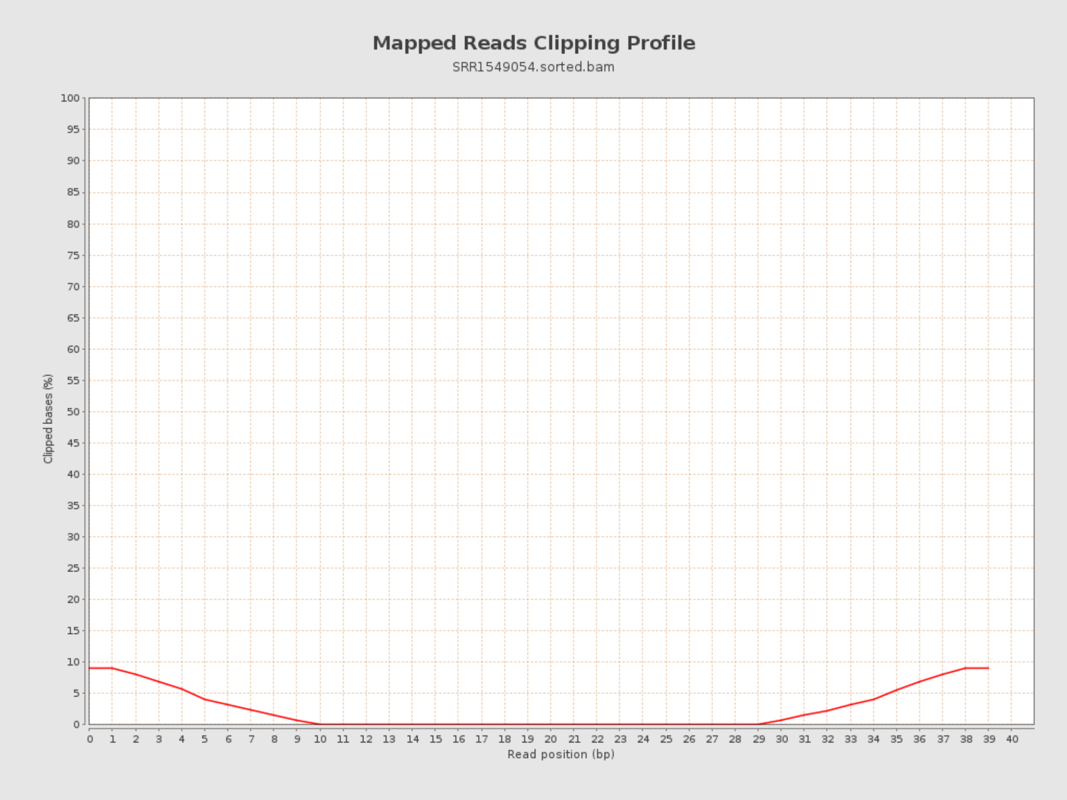
8. Results : Mapped Reads Nucleotide Content



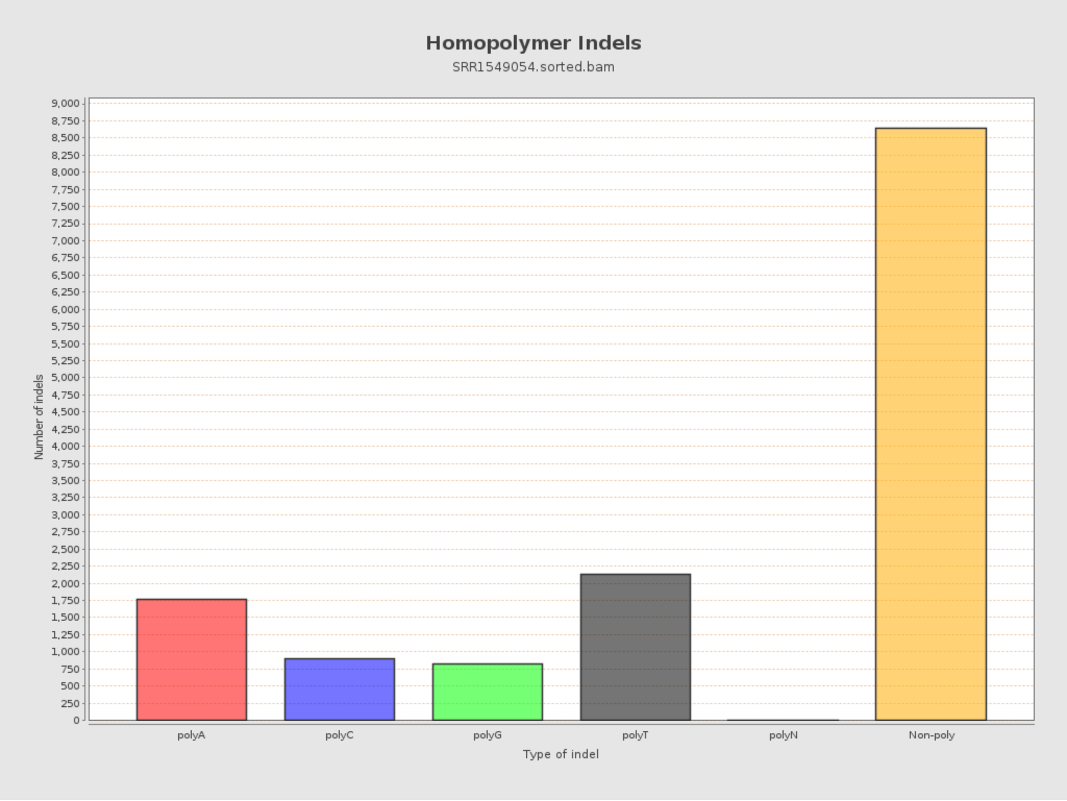
9. Results : Mapped Reads GC-content Distribution



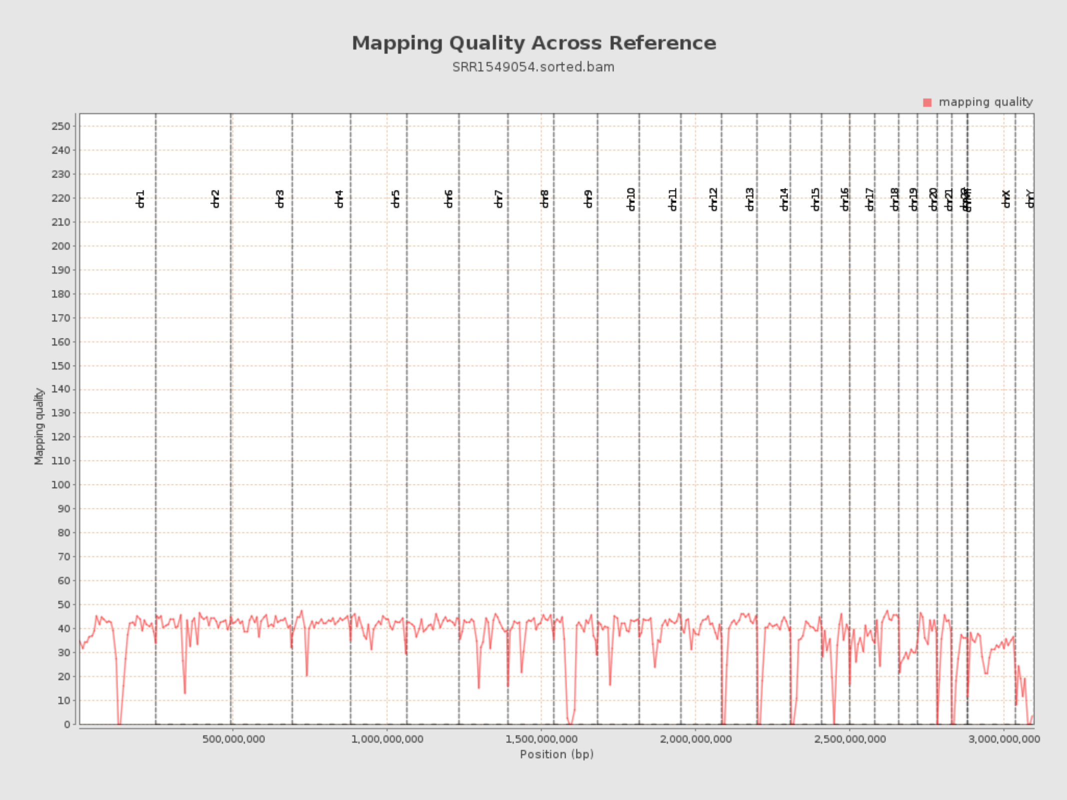
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram