Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 09:49:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818942.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_SRR1818942 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818942.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 09:49:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818942.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,951,596
Mapped reads	1,921,098 / 98.44%
Unmapped reads	30,498 / 1.56%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	24,547 / 1.26%
Read min/max/mean length	30 / 101 / 101.48
Duplicated reads (estimated)	722,516 / 37.02%
Duplication rate	32.26%
Clipped reads	1,934,797 / 99.14%

2.2. ACGT Content

Number/percentage of A's	51,849,478 / 29.16%
Number/percentage of C's	38,153,981 / 21.46%
Number/percentage of T's	50,149,243 / 28.2%
Number/percentage of G's	37,651,400 / 21.17%
Number/percentage of N's	8,109 / 0%
GC Percentage	42.63%

2.3. Coverage

Mean	0.0575

Standard Deviation	0.6471

2.4. Mapping Quality

Mean Mapping Quality	49.22

2.5. Mismatches and indels

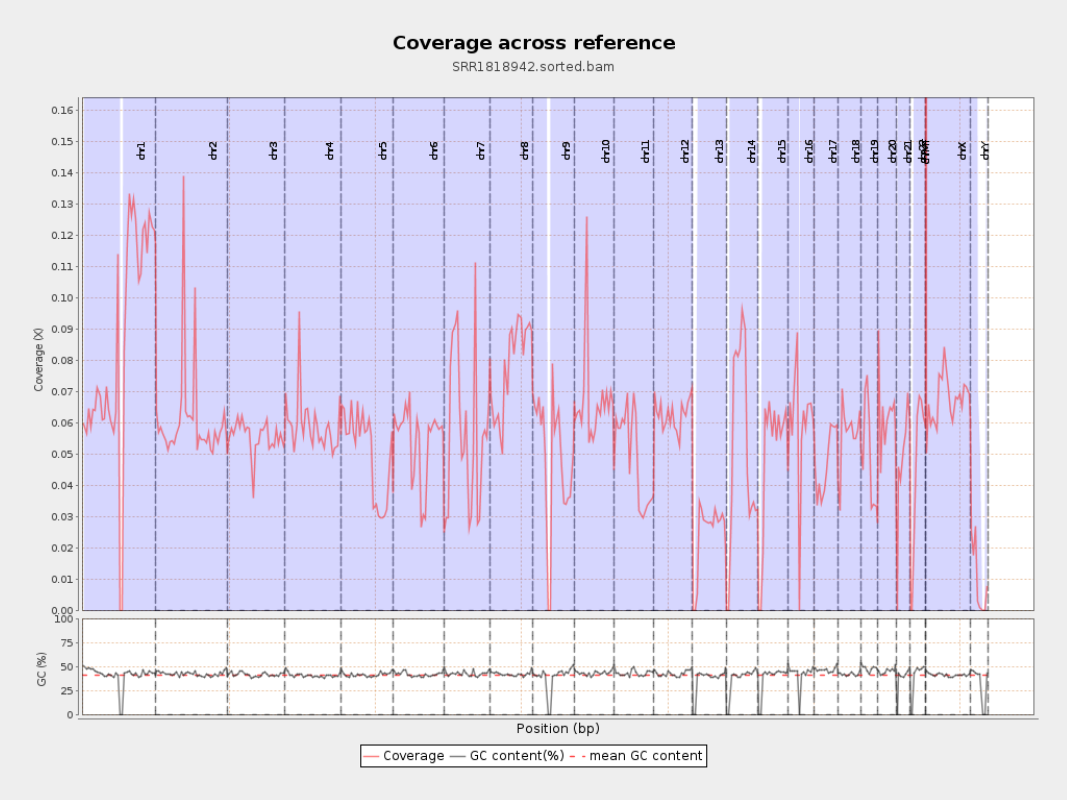
General error rate	0.68%
Mismatches	1,161,981
Insertions	23,127
Mapped reads with at least one insertion	1.17%
Deletions	52,116
Mapped reads with at least one deletion	2.66%
Homopolymer indels	42.8%

2.6. Chromosome stats

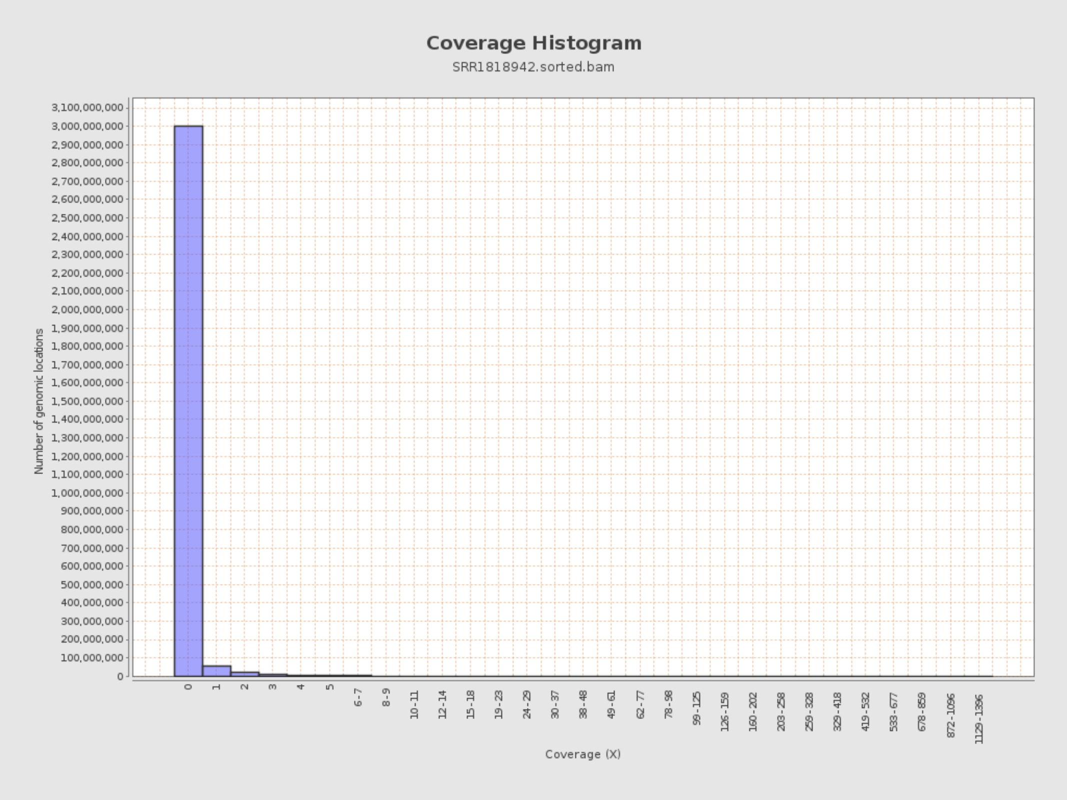
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	21265237	0.0853	1.2269
chr2	243199373	14859742	0.0611	0.8553
chr3	198022430	10982412	0.0555	0.3957
chr4	191154276	11380095	0.0595	0.4594
chr5	180915260	9125189	0.0504	0.3875
chr6	171115067	9300431	0.0544	0.4207
chr7	159138663	9010802	0.0566	0.5278

chr8	146364022	11448714	0.0782	0.5653
chr9	141213431	6848704	0.0485	0.6819
chr10	135534747	9046834	0.0667	0.825
chr11	135006516	6585868	0.0488	0.465
chr12	133851895	8411389	0.0628	0.4313
chr13	115169878	2849549	0.0247	0.2562
chr14	107349540	5629722	0.0524	0.4208
chr15	102531392	5013250	0.0489	0.3726
chr16	90354753	5298910	0.0586	0.6605
chr17	81195210	3845644	0.0474	0.4119
chr18	78077248	4396385	0.0563	0.9282
chr19	59128983	2929496	0.0495	1.048
chr20	63025520	3931620	0.0624	0.4483
chr21	48129895	2356370	0.049	0.4166
chr22	51304566	2308413	0.045	0.3884
chrMT	16571	61928	3.7371	3.6111
chrX	155270560	10457168	0.0673	0.5169
chrY	59373566	563385	0.0095	0.483

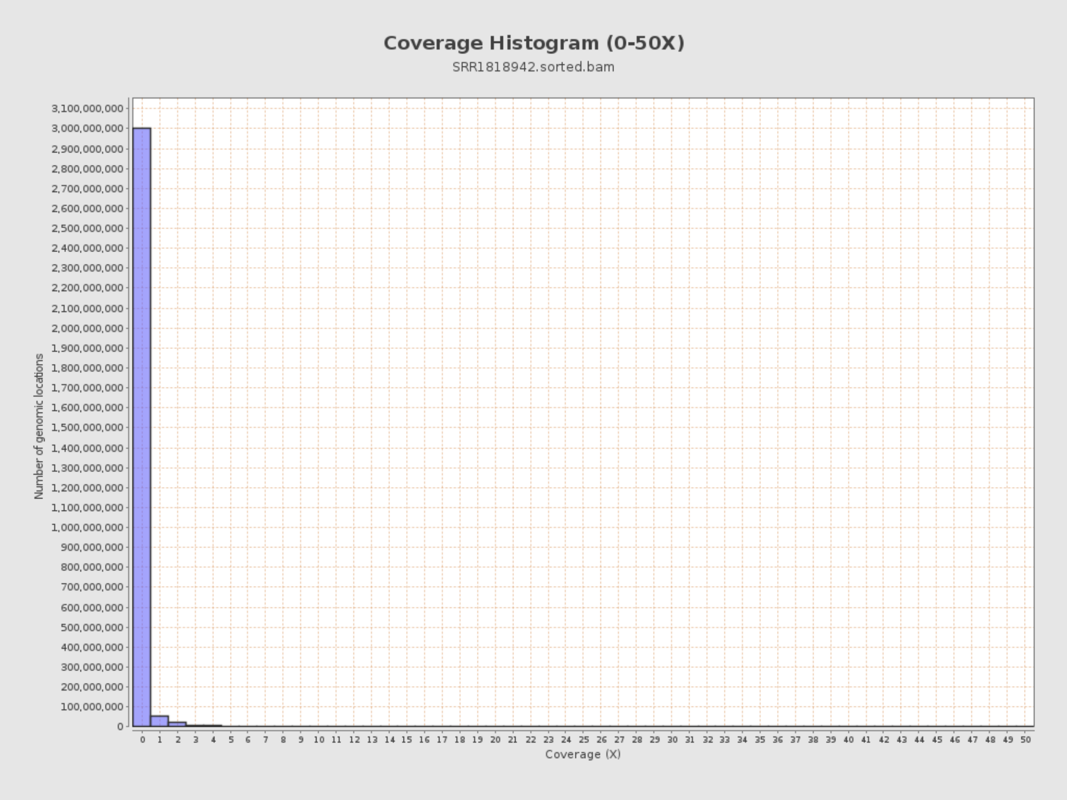
3. Results : Coverage across reference



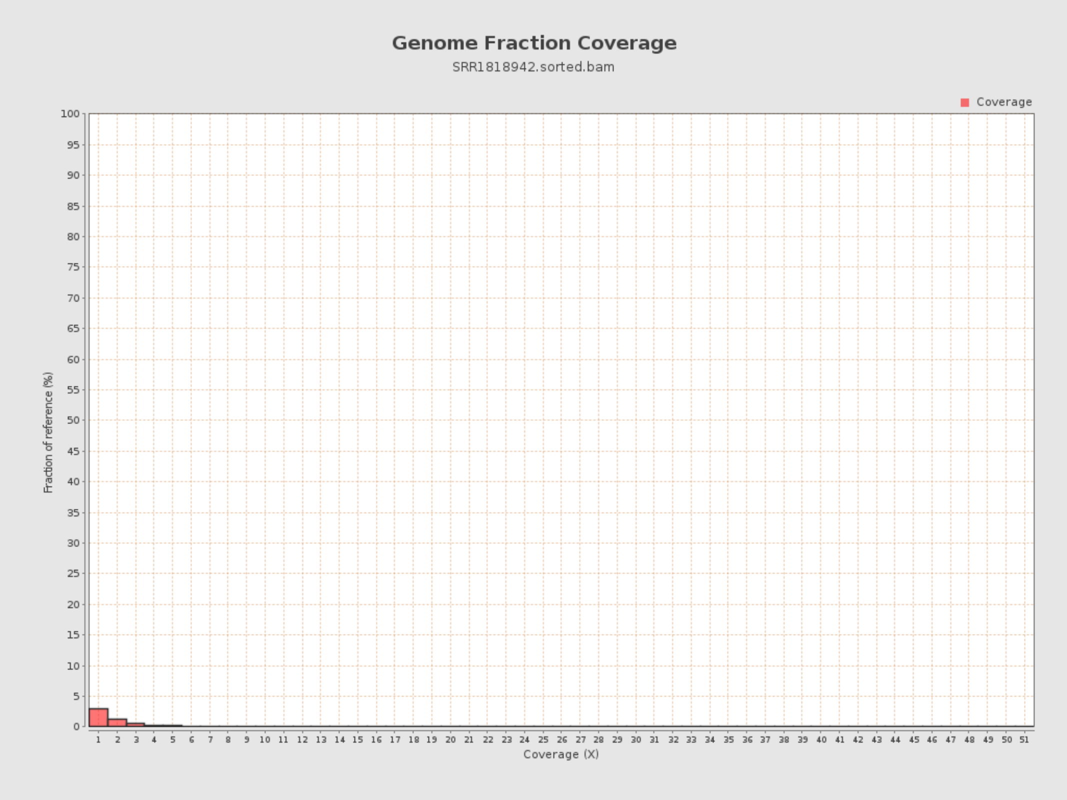
4. Results : Coverage Histogram



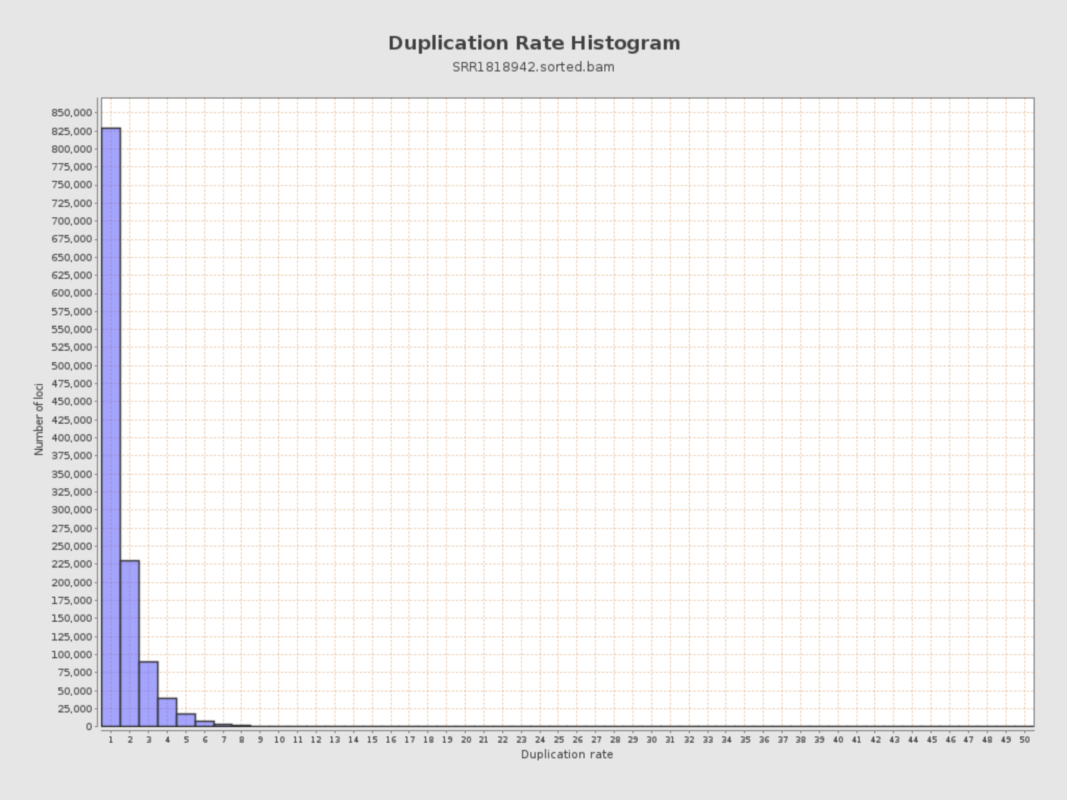
5. Results : Coverage Histogram (0-50X)



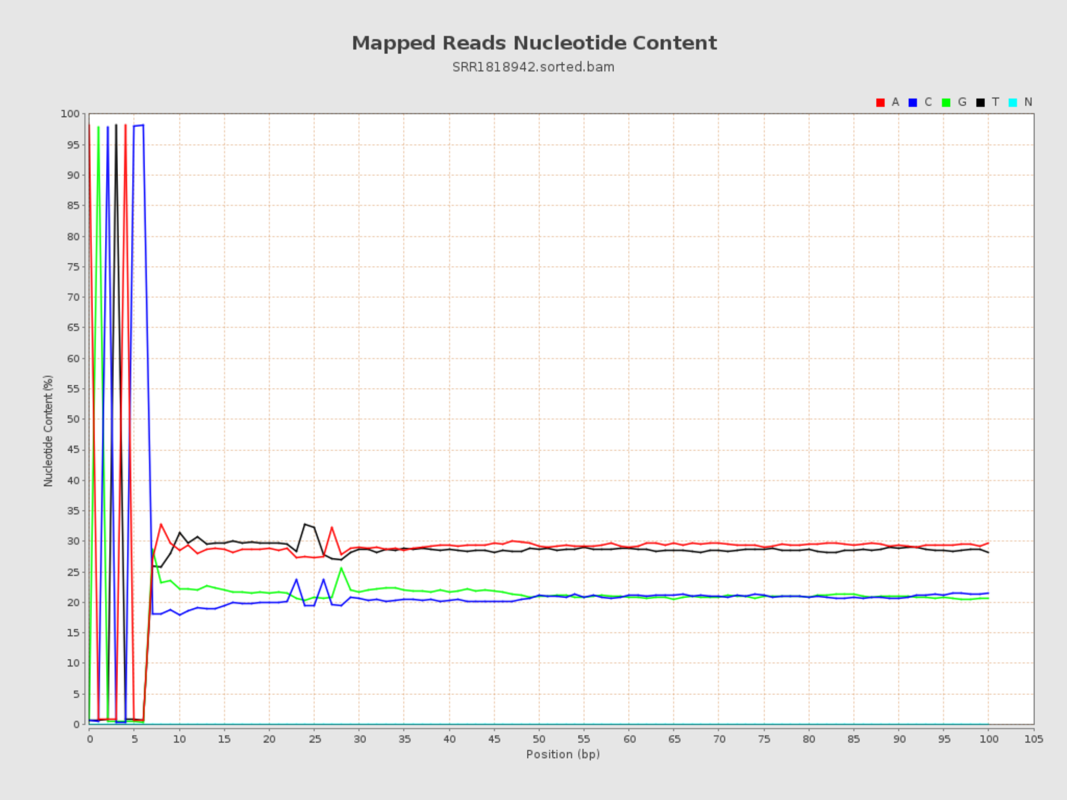
6. Results : Genome Fraction Coverage



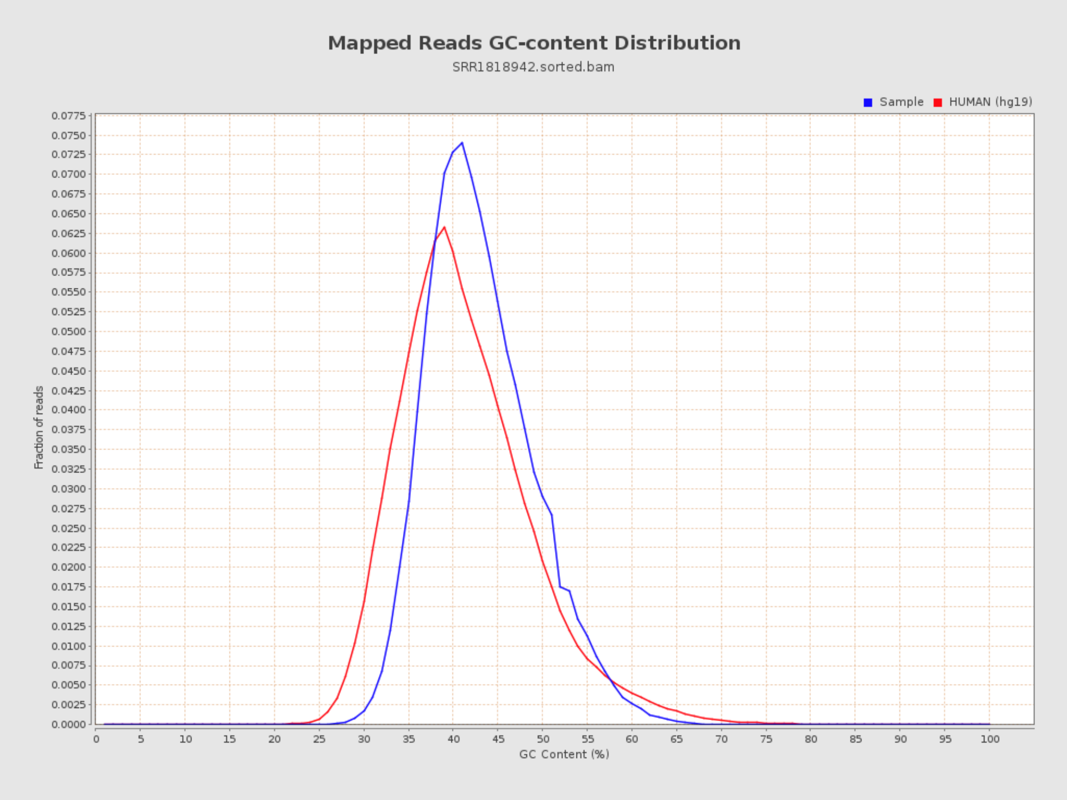
7. Results : Duplication Rate Histogram



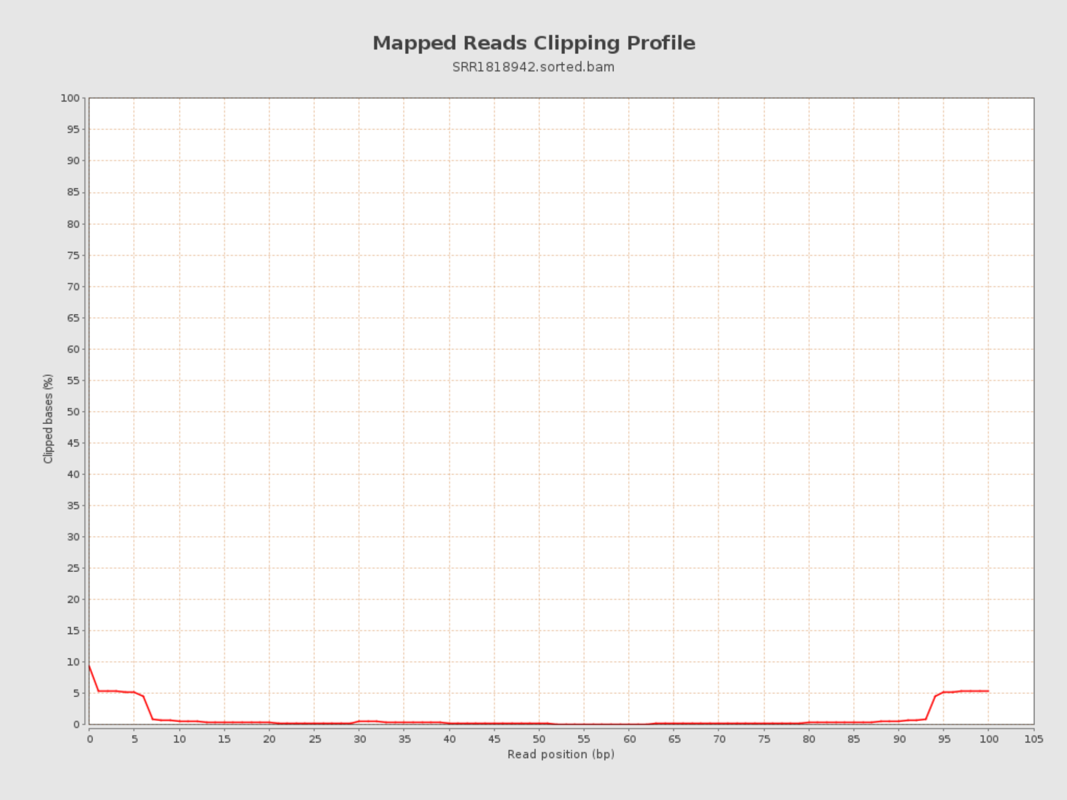
8. Results : Mapped Reads Nucleotide Content



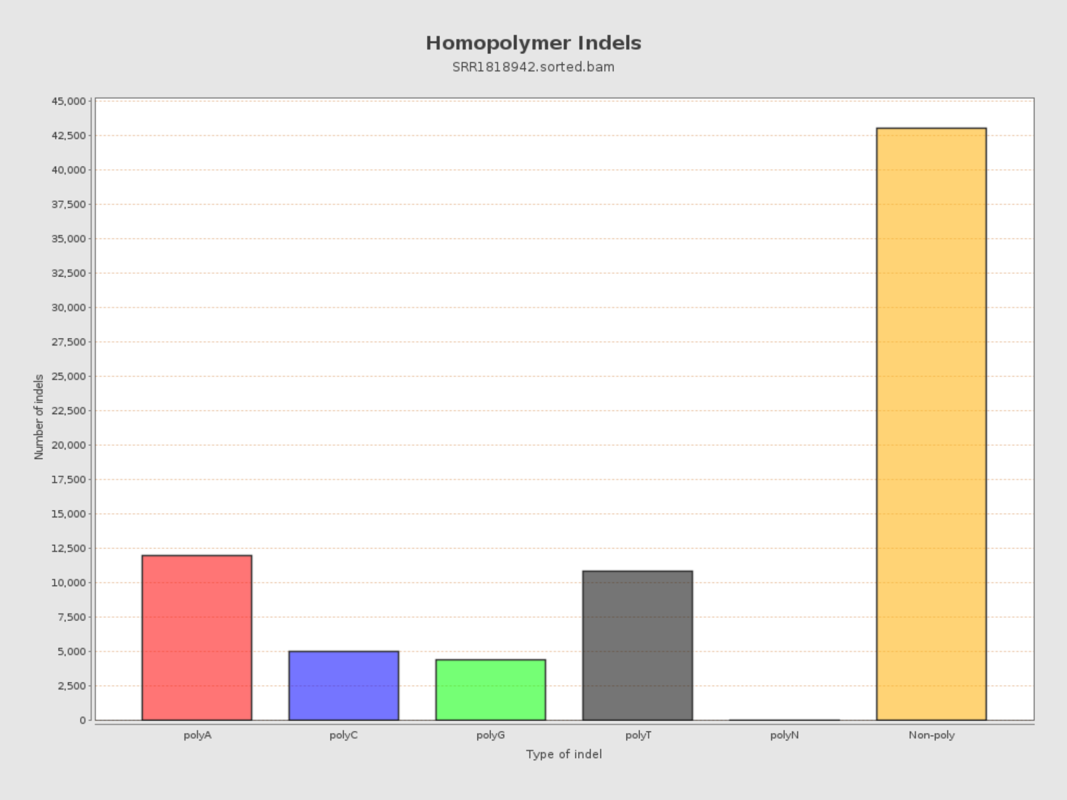
9. Results : Mapped Reads GC-content Distribution



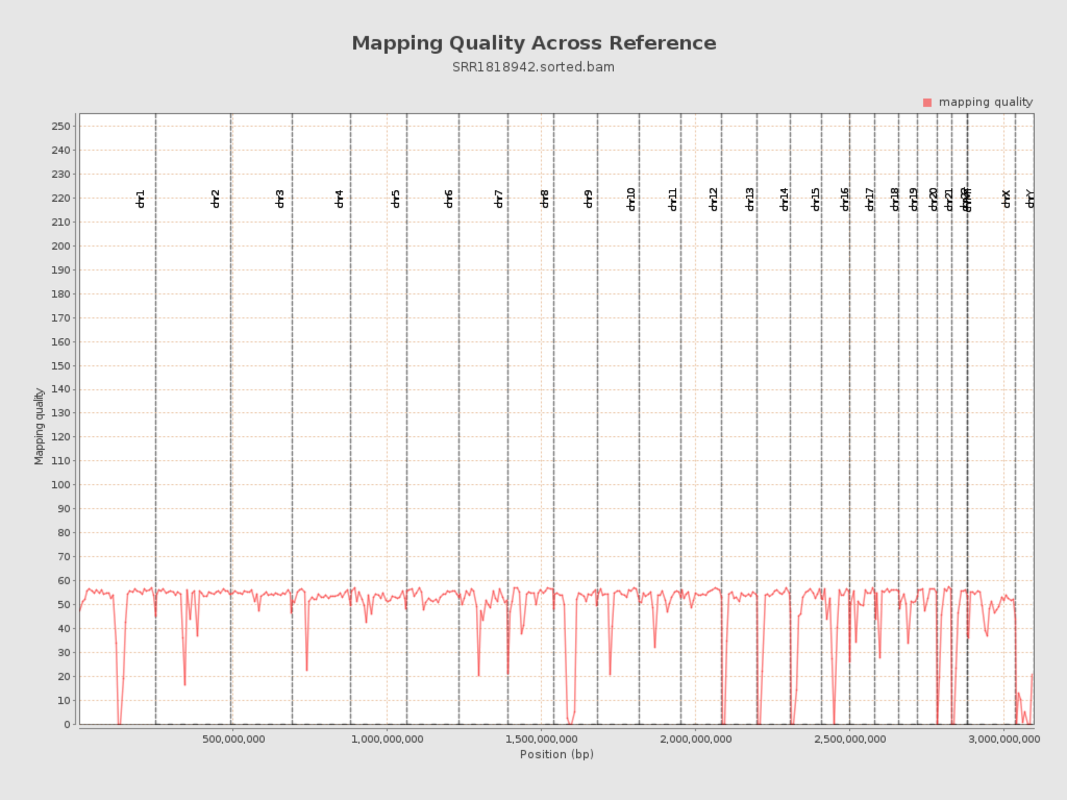
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram