Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 15:54:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1819018.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_SRR1819018 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1819018.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 15:54:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1819018.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,568,827
Mapped reads	2,425,289 / 94.41%
Unmapped reads	143,538 / 5.59%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	24,220 / 0.94%
Read min/max/mean length	30 / 101 / 101.36
Duplicated reads (estimated)	1,044,198 / 40.65%
Duplication rate	33.85%
Clipped reads	2,408,570 / 93.76%

2.2. ACGT Content

Number/percentage of A's	63,717,121 / 28.28%
Number/percentage of C's	44,975,771 / 19.96%
Number/percentage of T's	64,333,251 / 28.55%
Number/percentage of G's	52,268,509 / 23.2%
Number/percentage of N's	10,965 / 0%
GC Percentage	43.16%

2.3. Coverage

Mean	0.0728

Standard Deviation	1.0059

2.4. Mapping Quality

Mean Mapping Quality	49.27

2.5. Mismatches and indels

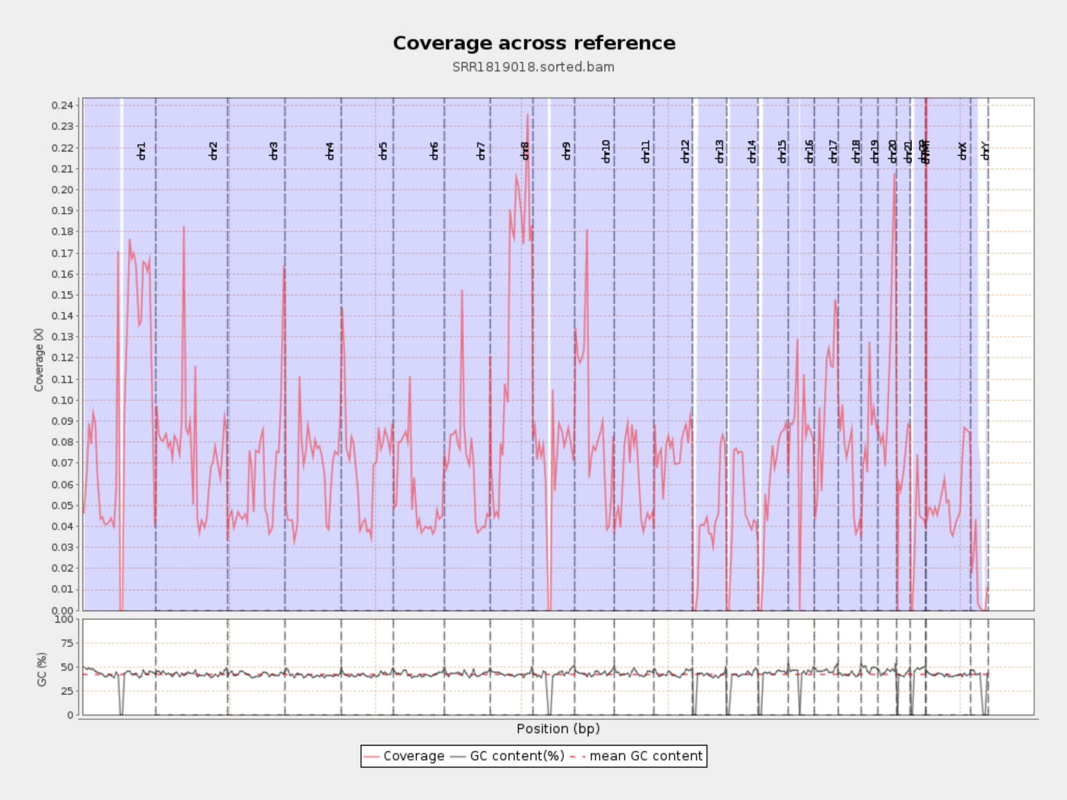
General error rate	0.67%
Mismatches	1,428,255
Insertions	34,312
Mapped reads with at least one insertion	1.37%
Deletions	67,594
Mapped reads with at least one deletion	2.72%
Homopolymer indels	40.84%

2.6. Chromosome stats

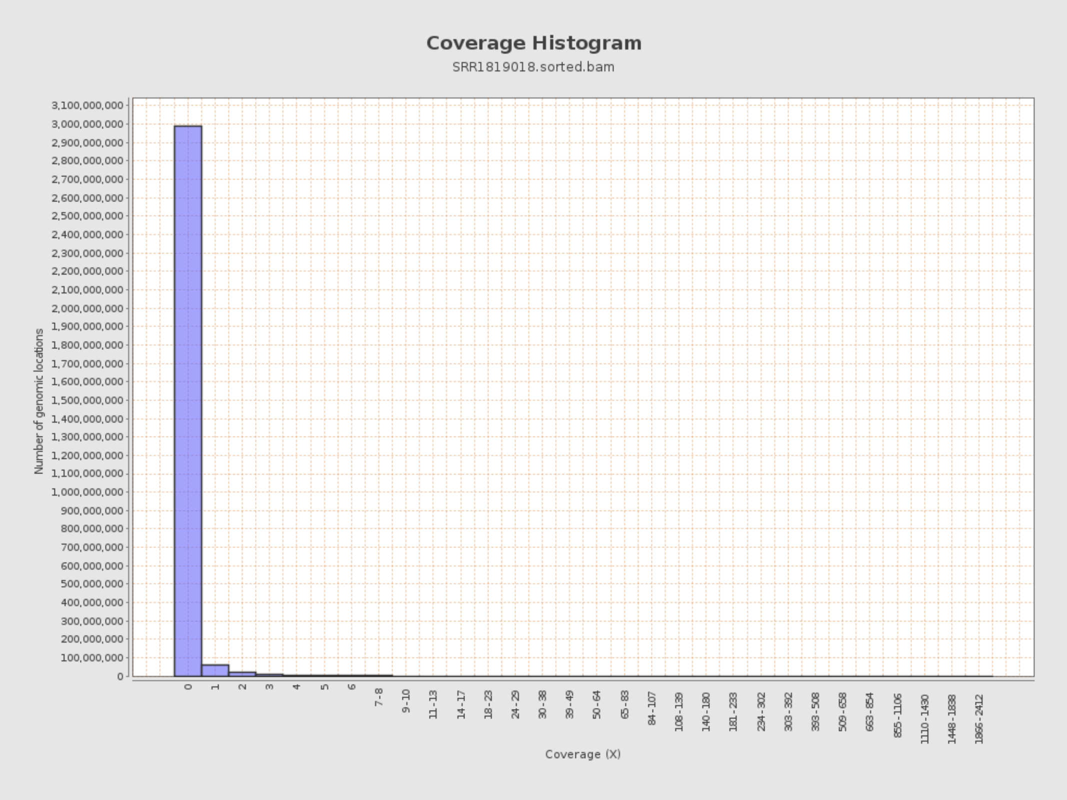
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	23545929	0.0945	1.9344
chr2	243199373	18651713	0.0767	1.3156
chr3	198022430	12349856	0.0624	0.4741
chr4	191154276	12637981	0.0661	0.5869
chr5	180915260	13057647	0.0722	0.5297
chr6	171115067	9516496	0.0556	0.6146
chr7	159138663	10920796	0.0686	1.3852

chr8	146364022	20595295	0.1407	0.8393
chr9	141213431	9931788	0.0703	1.0769
chr10	135534747	12176772	0.0898	1.1924
chr11	135006516	7901437	0.0585	0.6518
chr12	133851895	10397630	0.0777	0.5415
chr13	115169878	4846663	0.0421	0.3791
chr14	107349540	5181614	0.0483	0.485
chr15	102531392	5941663	0.0579	0.4563
chr16	90354753	7437631	0.0823	1.0126
chr17	81195210	8085088	0.0996	0.7761
chr18	78077248	5357536	0.0686	1.2371
chr19	59128983	5002918	0.0846	1.8381
chr20	63025520	7443657	0.1181	0.7236
chr21	48129895	3150379	0.0655	0.5541
chr22	51304566	1869670	0.0364	0.3957
chrMT	16571	148343	8.952	7.6437
chrX	155270560	8528040	0.0549	0.6444
chrY	59373566	756676	0.0127	0.8563

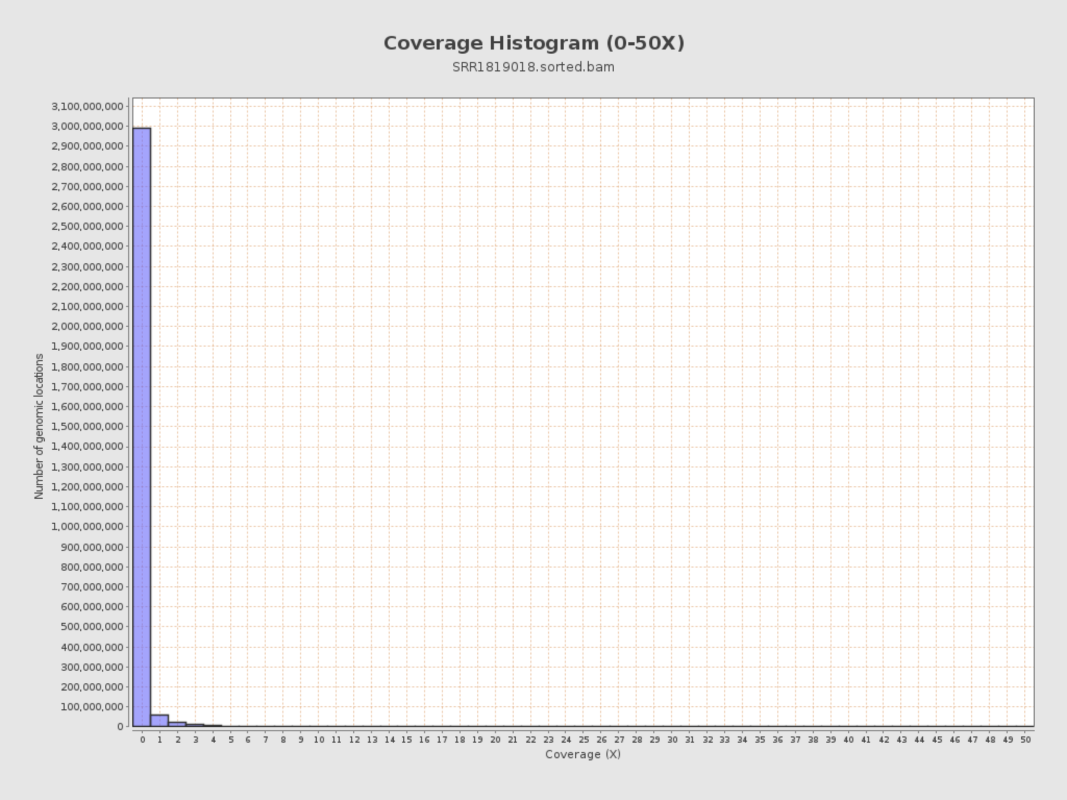
3. Results : Coverage across reference



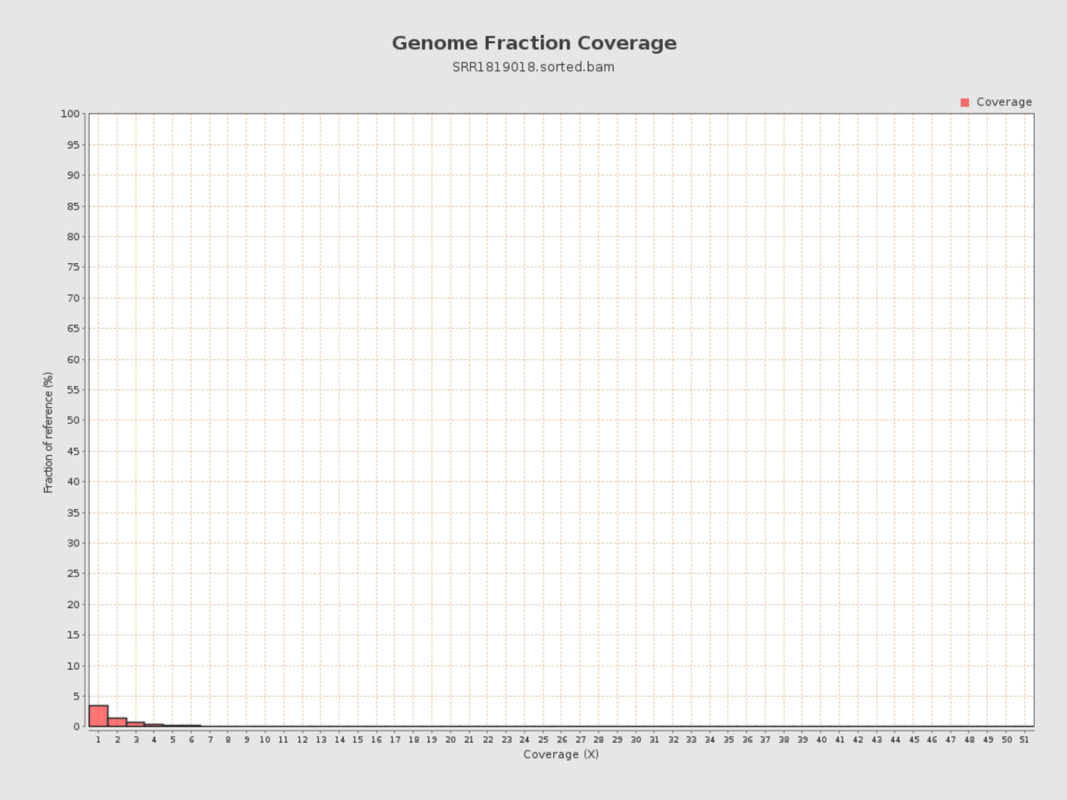
4. Results : Coverage Histogram



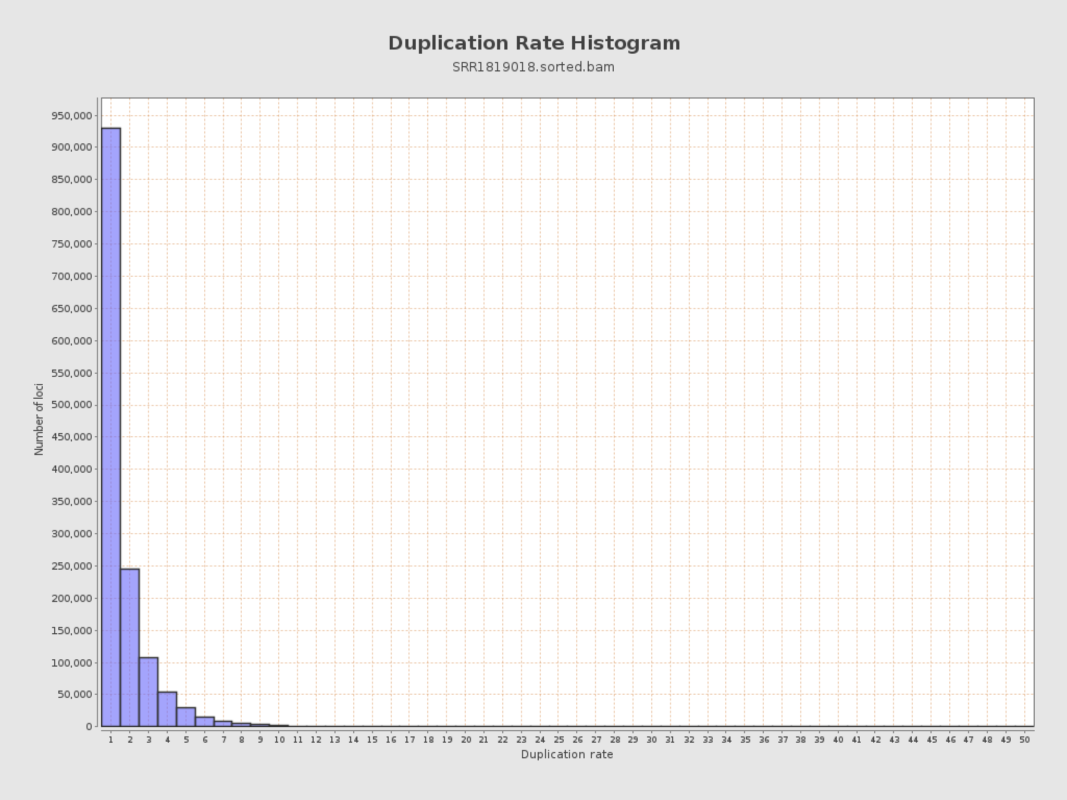
5. Results : Coverage Histogram (0-50X)



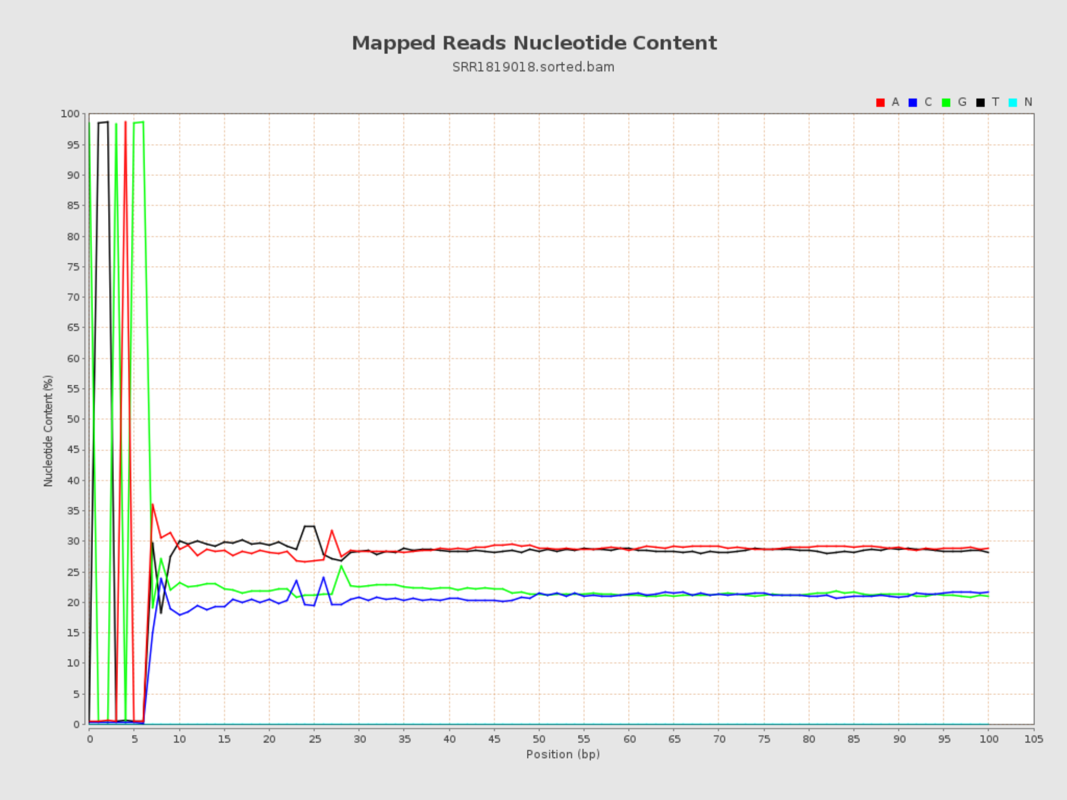
6. Results : Genome Fraction Coverage



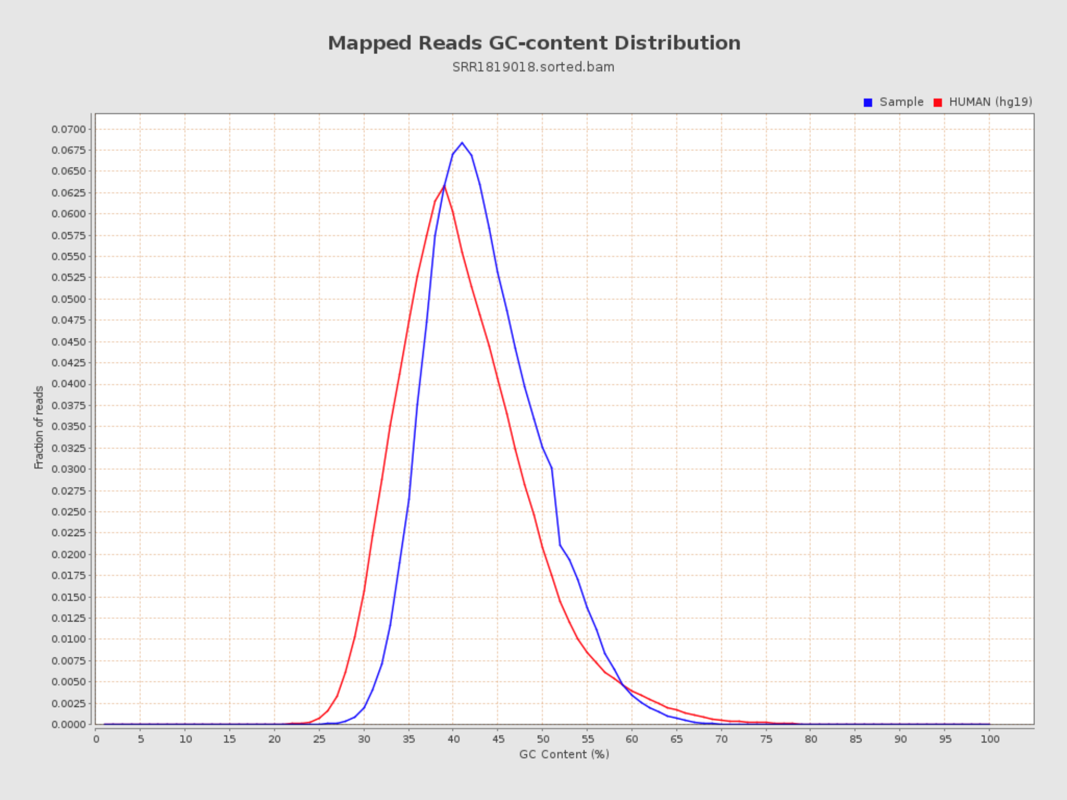
7. Results : Duplication Rate Histogram



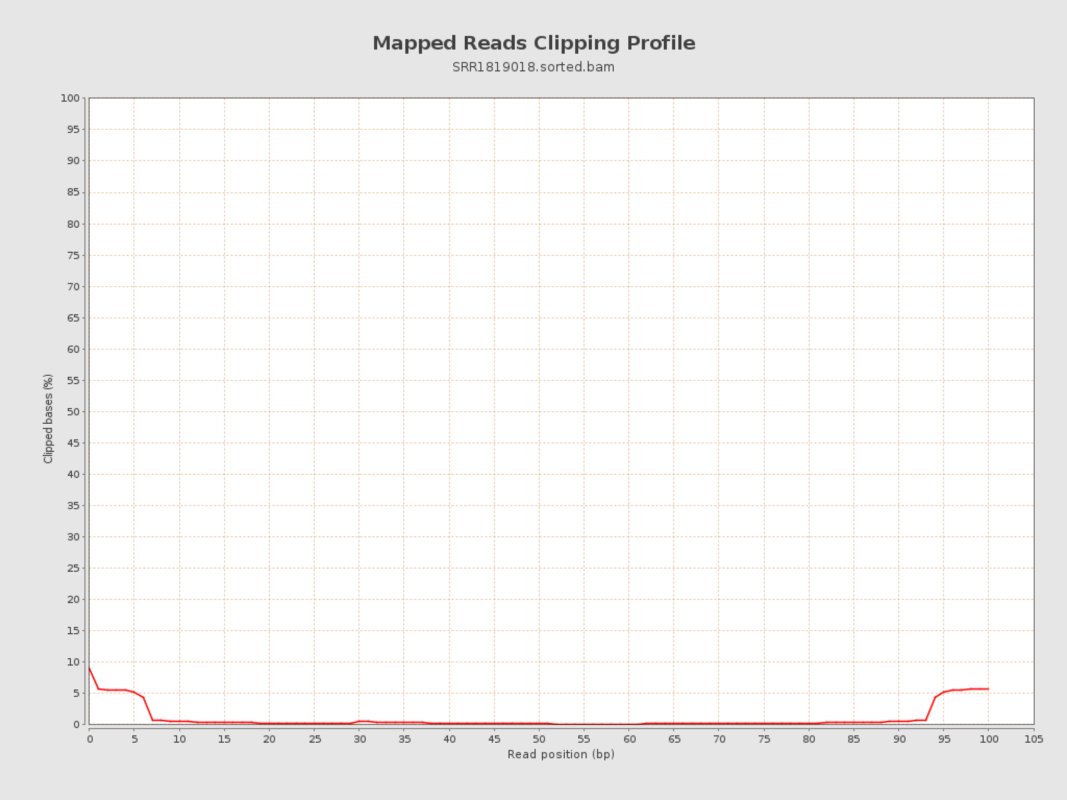
8. Results : Mapped Reads Nucleotide Content



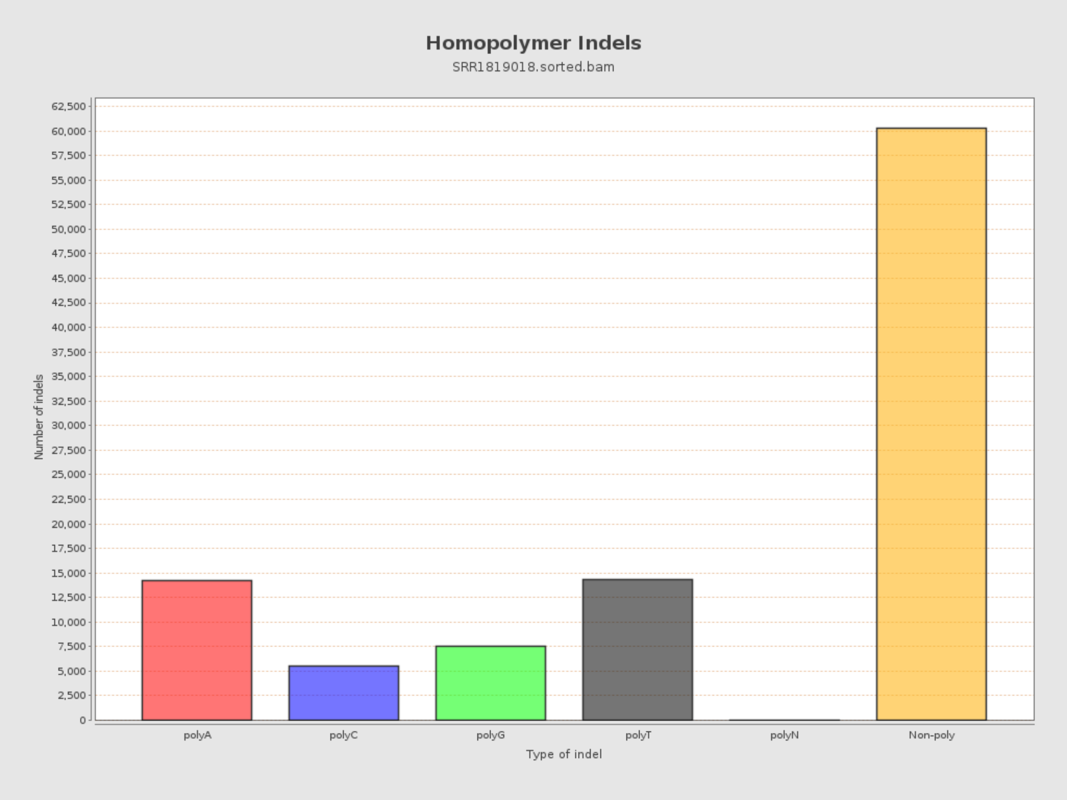
9. Results : Mapped Reads GC-content Distribution



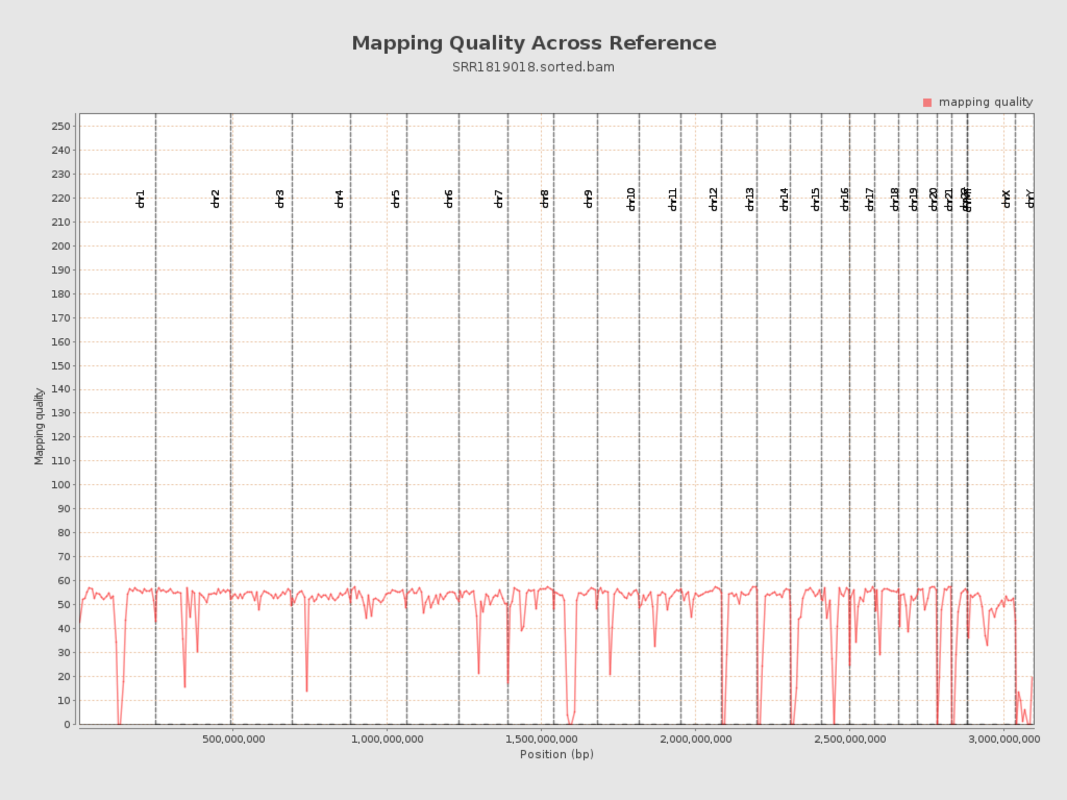
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram