Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 17:13:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818822.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_SRR1818822 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818822.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 17:13:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818822.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,092,769
Mapped reads	2,032,278 / 97.11%
Unmapped reads	60,491 / 2.89%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,836 / 0.8%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	992,372 / 47.42%
Duplication rate	39.61%
Clipped reads	2,009,776 / 96.03%

2.2. ACGT Content

Number/percentage of A's	40,090,565 / 29.03%
Number/percentage of C's	27,270,092 / 19.75%
Number/percentage of T's	39,891,871 / 28.89%
Number/percentage of G's	30,818,625 / 22.32%
Number/percentage of N's	8,665 / 0.01%
GC Percentage	42.07%

2.3. Coverage

Mean	0.0446

Standard Deviation	0.5847

2.4. Mapping Quality

Mean Mapping Quality	47.8

2.5. Mismatches and indels

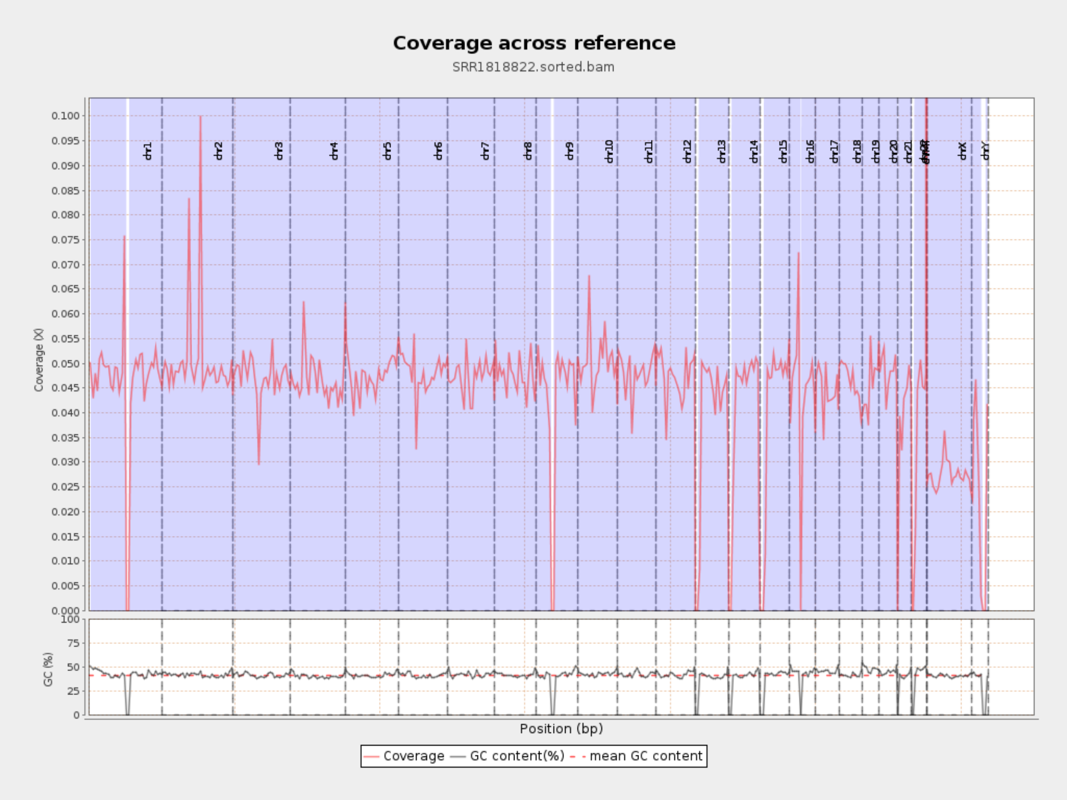
General error rate	0.56%
Mismatches	739,751
Insertions	19,365
Mapped reads with at least one insertion	0.94%
Deletions	36,695
Mapped reads with at least one deletion	1.79%
Homopolymer indels	40.67%

2.6. Chromosome stats

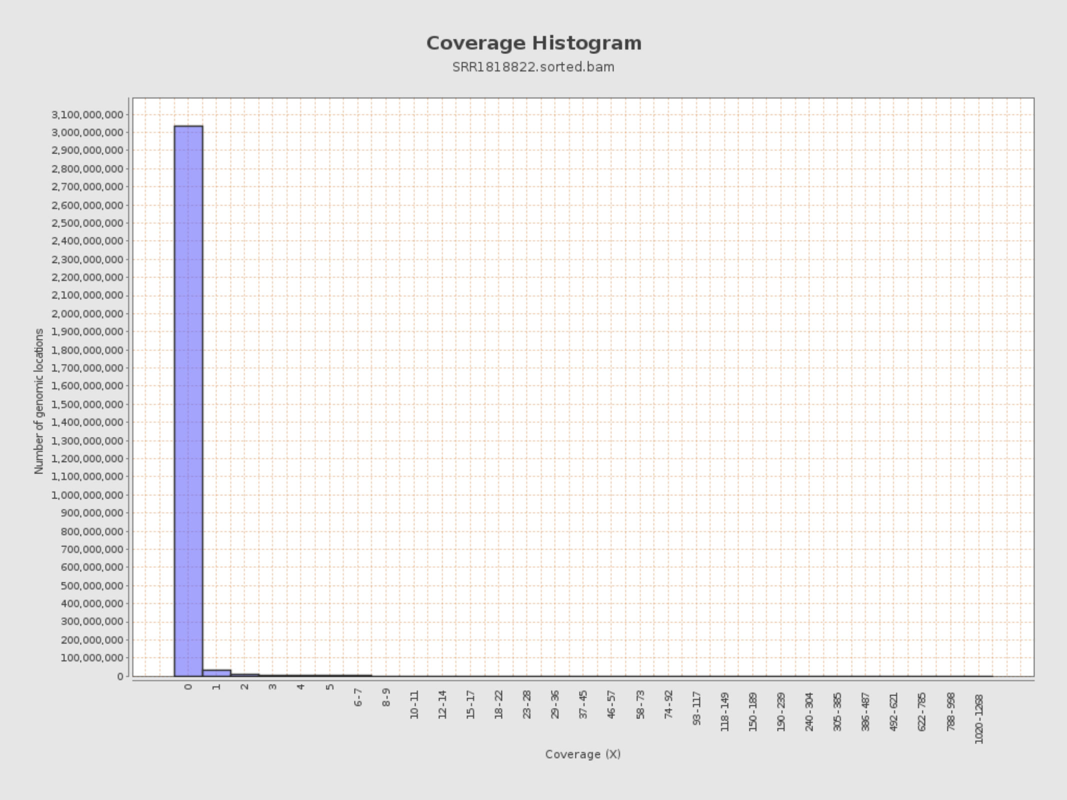
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11453030	0.0459	0.7993
chr2	243199373	12375534	0.0509	0.9757
chr3	198022430	9343511	0.0472	0.4347
chr4	191154276	8886667	0.0465	0.4761
chr5	180915260	8565639	0.0473	0.448
chr6	171115067	8241689	0.0482	0.476
chr7	159138663	7543471	0.0474	0.4981

chr8	146364022	6984500	0.0477	0.4724
chr9	141213431	5977174	0.0423	0.4714
chr10	135534747	6830828	0.0504	0.666
chr11	135006516	6484472	0.048	0.4869
chr12	133851895	6332711	0.0473	0.4558
chr13	115169878	4428792	0.0385	0.384
chr14	107349540	4336160	0.0404	0.4625
chr15	102531392	4027258	0.0393	0.3952
chr16	90354753	4016240	0.0444	0.6892
chr17	81195210	3623435	0.0446	0.4438
chr18	78077248	3647300	0.0467	0.6141
chr19	59128983	2696383	0.0456	0.6741
chr20	63025520	3049369	0.0484	0.4818
chr21	48129895	1841325	0.0383	0.4163
chr22	51304566	1651176	0.0322	0.3952
chrMT	16571	195651	11.8068	11.7312
chrX	155270560	4284074	0.0276	0.3549
chrY	59373566	1323650	0.0223	1.0209

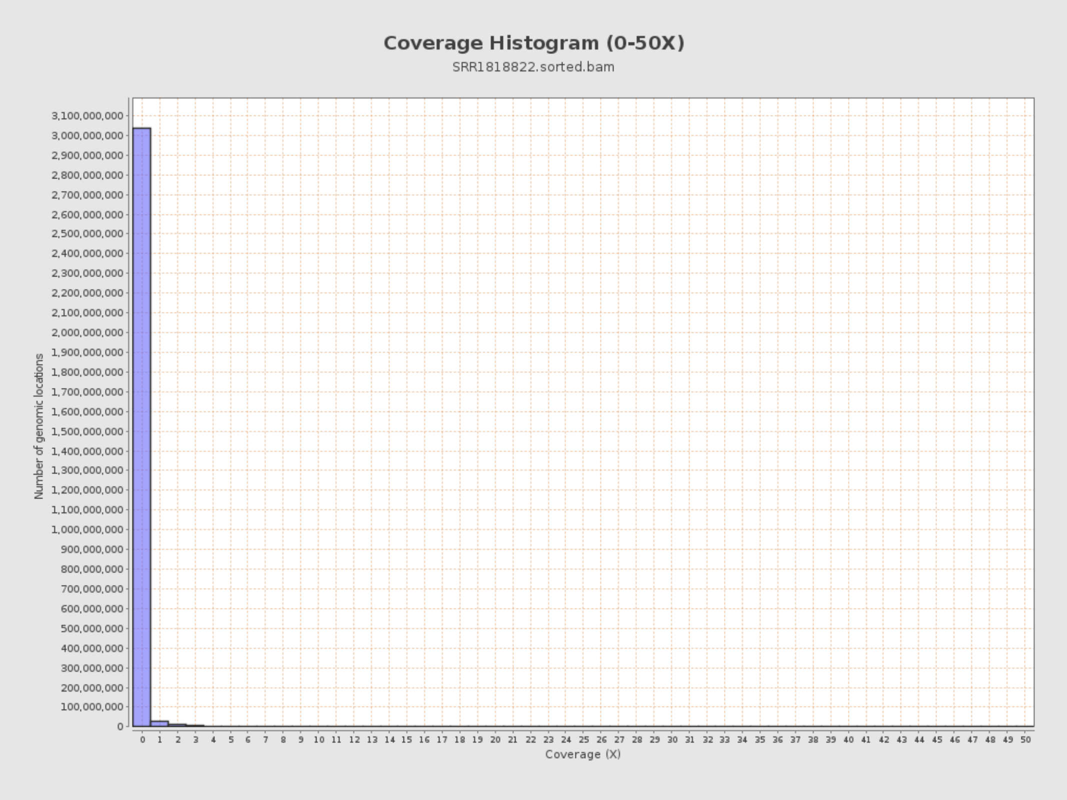
3. Results : Coverage across reference



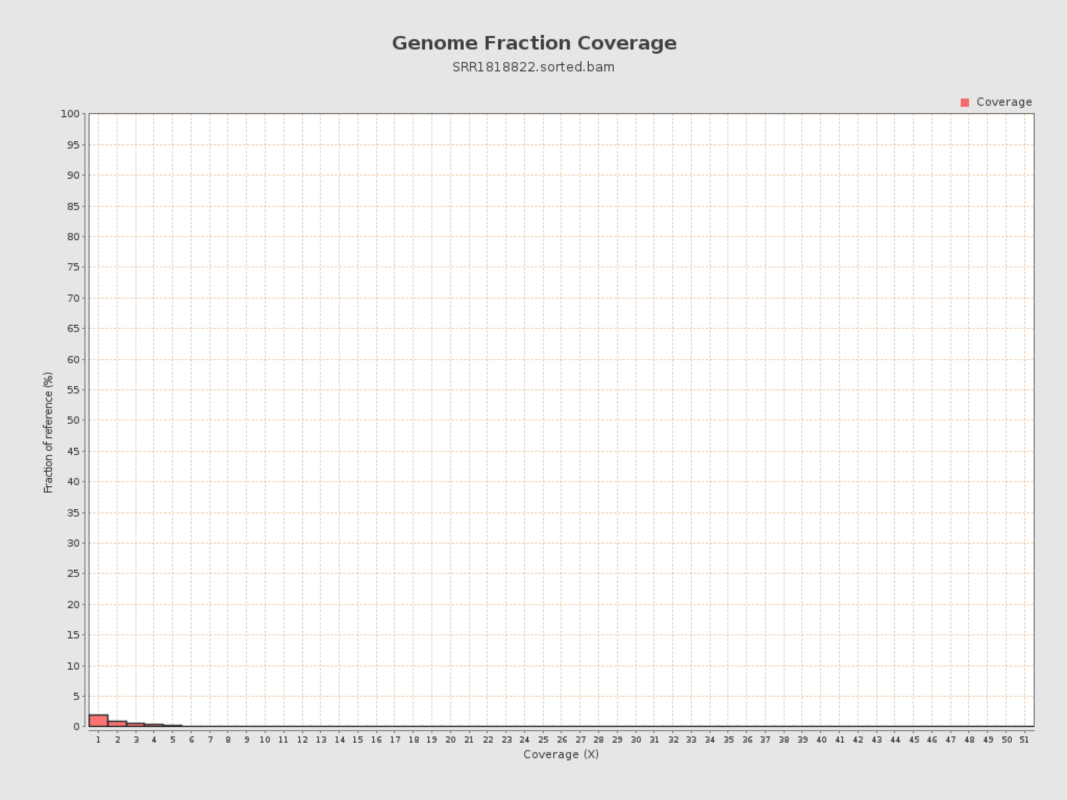
4. Results : Coverage Histogram



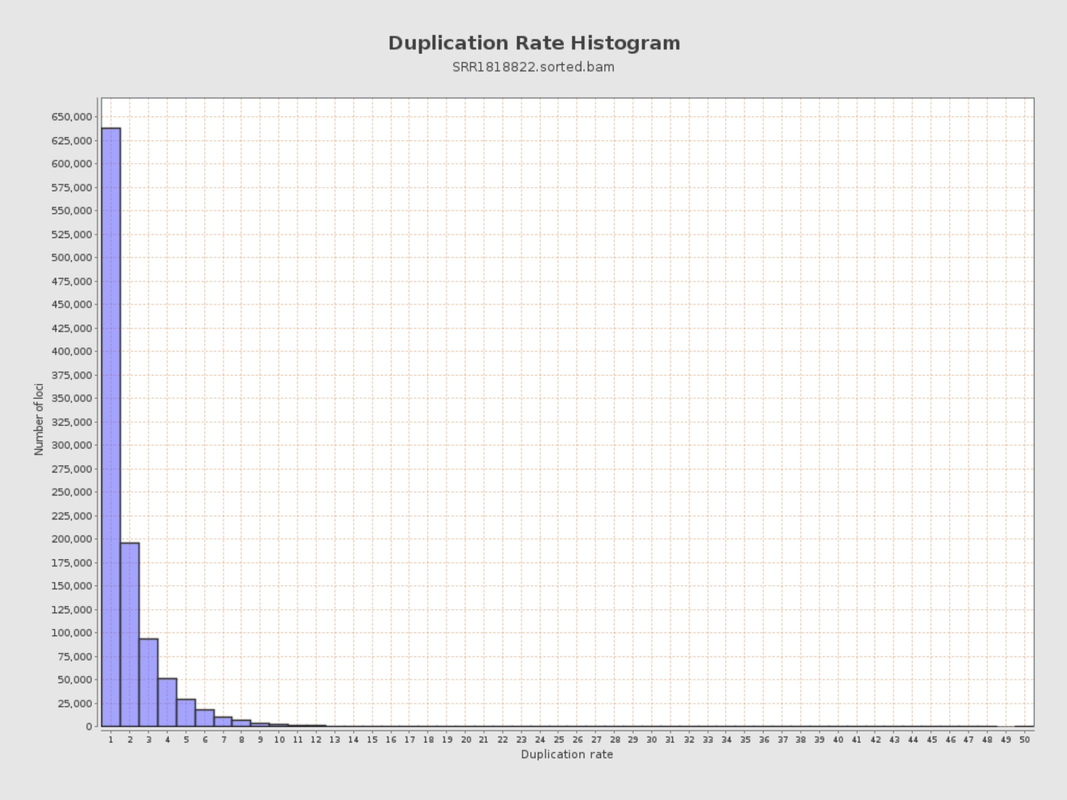
5. Results : Coverage Histogram (0-50X)



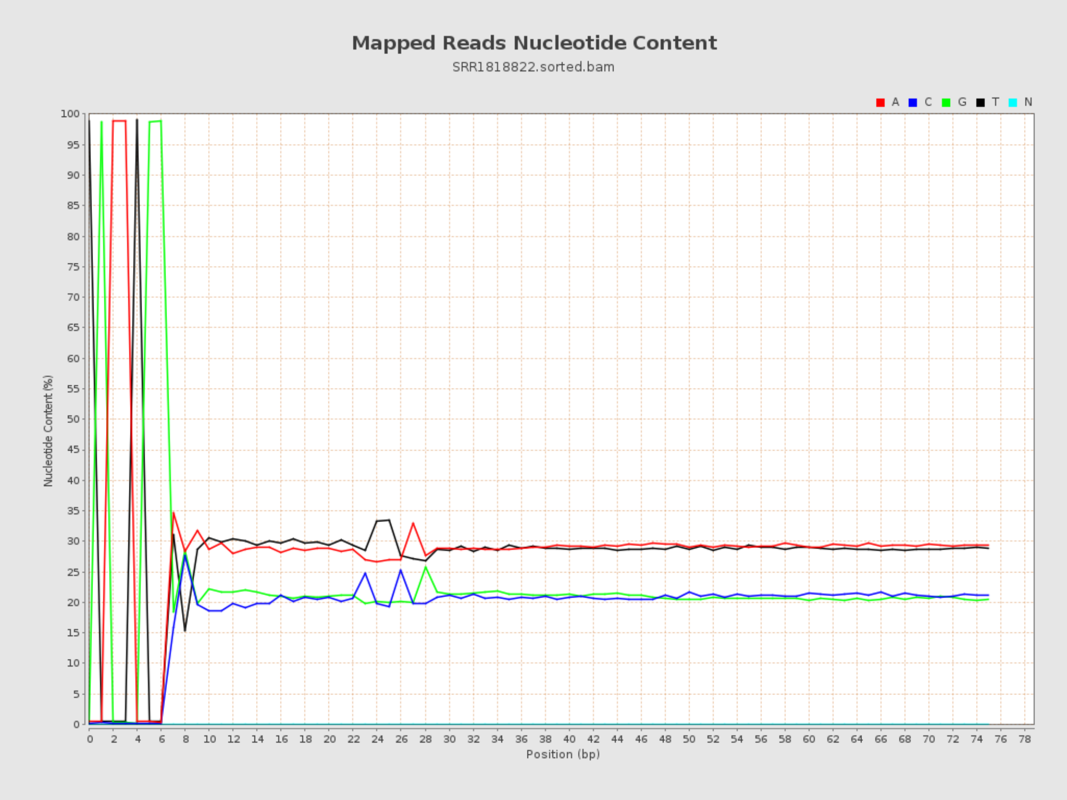
6. Results : Genome Fraction Coverage



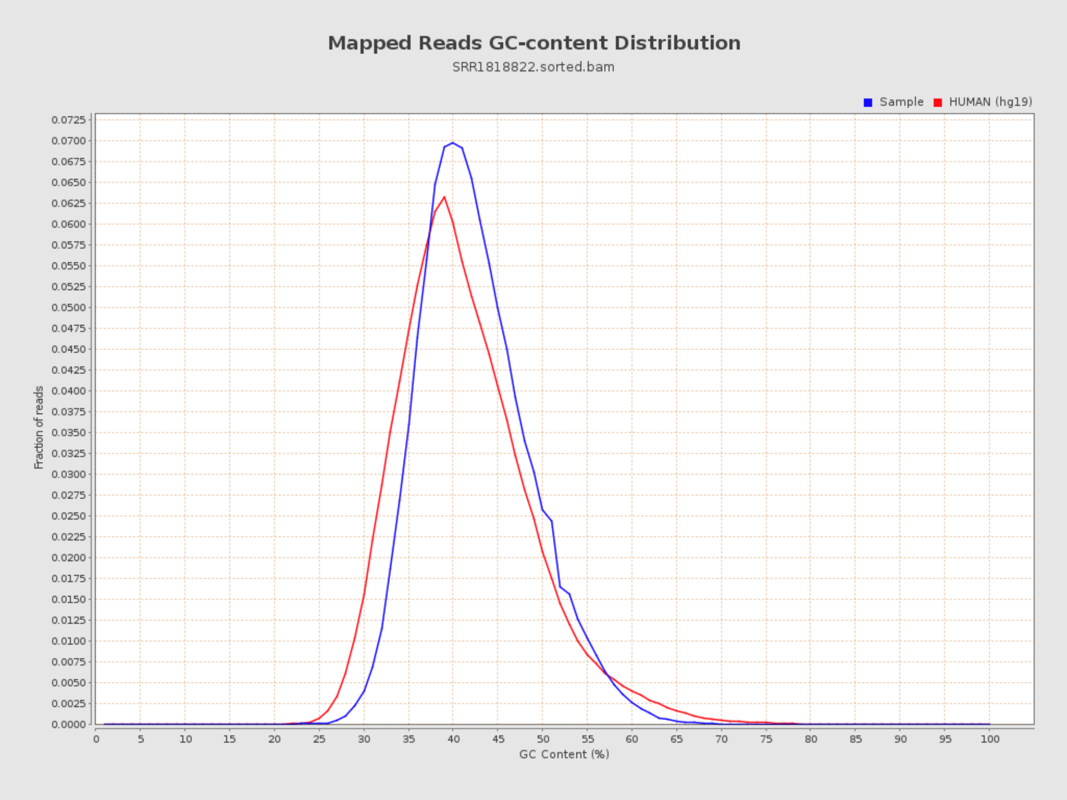
7. Results : Duplication Rate Histogram



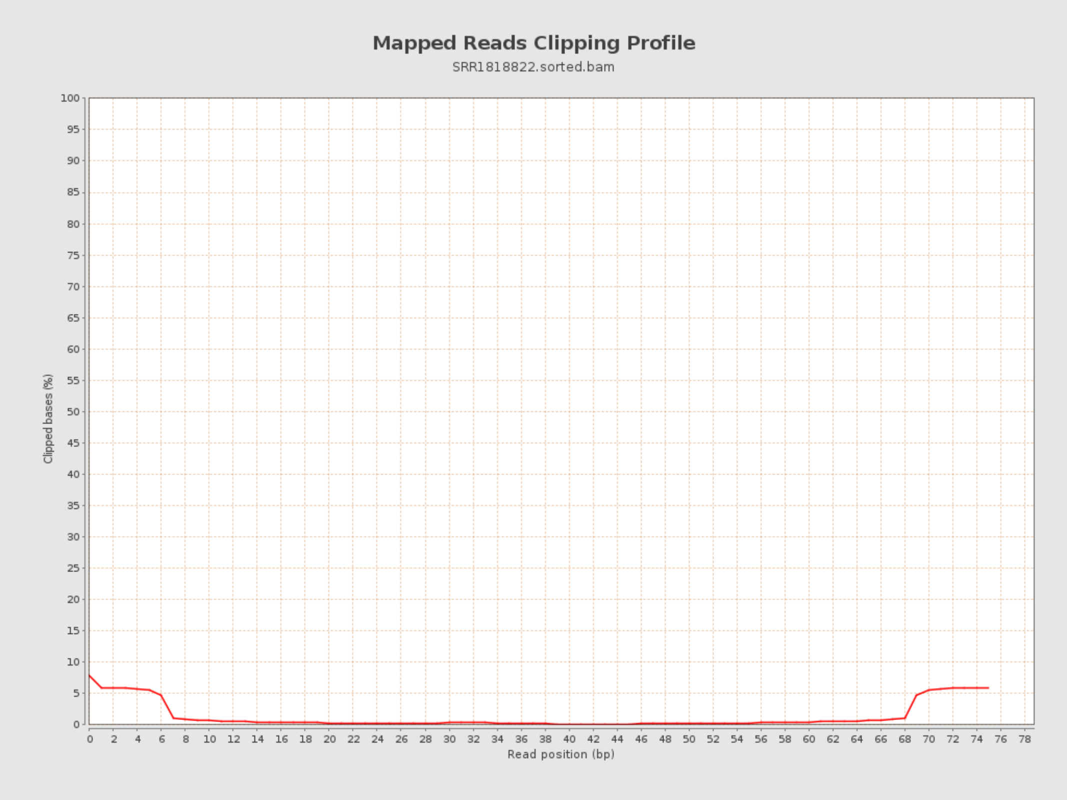
8. Results : Mapped Reads Nucleotide Content



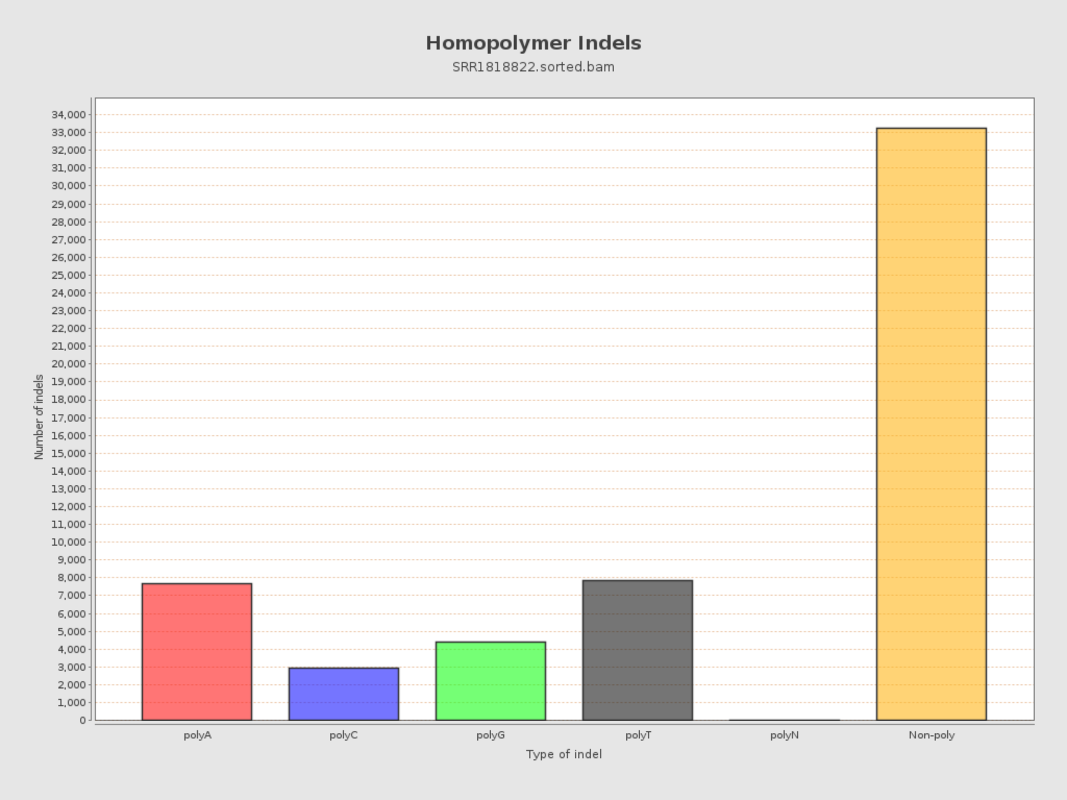
9. Results : Mapped Reads GC-content Distribution



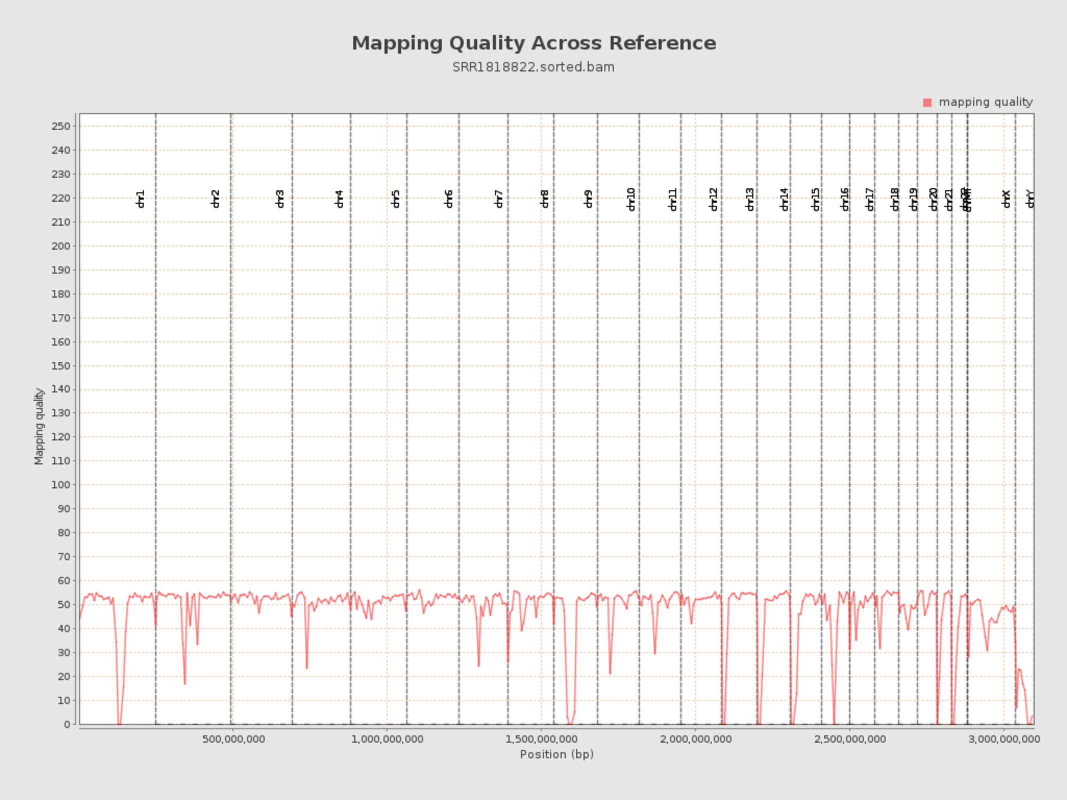
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram