Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 13:30:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818802.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_SRR1818802 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818802.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 13:30:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818802.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	871,428
Mapped reads	840,043 / 96.4%
Unmapped reads	31,385 / 3.6%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,372 / 0.85%
Read min/max/mean length	30 / 76 / 76.29
Duplicated reads (estimated)	284,360 / 32.63%
Duplication rate	29.54%
Clipped reads	841,673 / 96.59%

2.2. ACGT Content

Number/percentage of A's	16,522,621 / 29.04%
Number/percentage of C's	12,232,905 / 21.5%
Number/percentage of T's	16,401,531 / 28.82%
Number/percentage of G's	11,740,353 / 20.63%
Number/percentage of N's	3,644 / 0.01%
GC Percentage	42.13%

2.3. Coverage

Mean	0.0184

Standard Deviation	0.2761

2.4. Mapping Quality

Mean Mapping Quality	47.83

2.5. Mismatches and indels

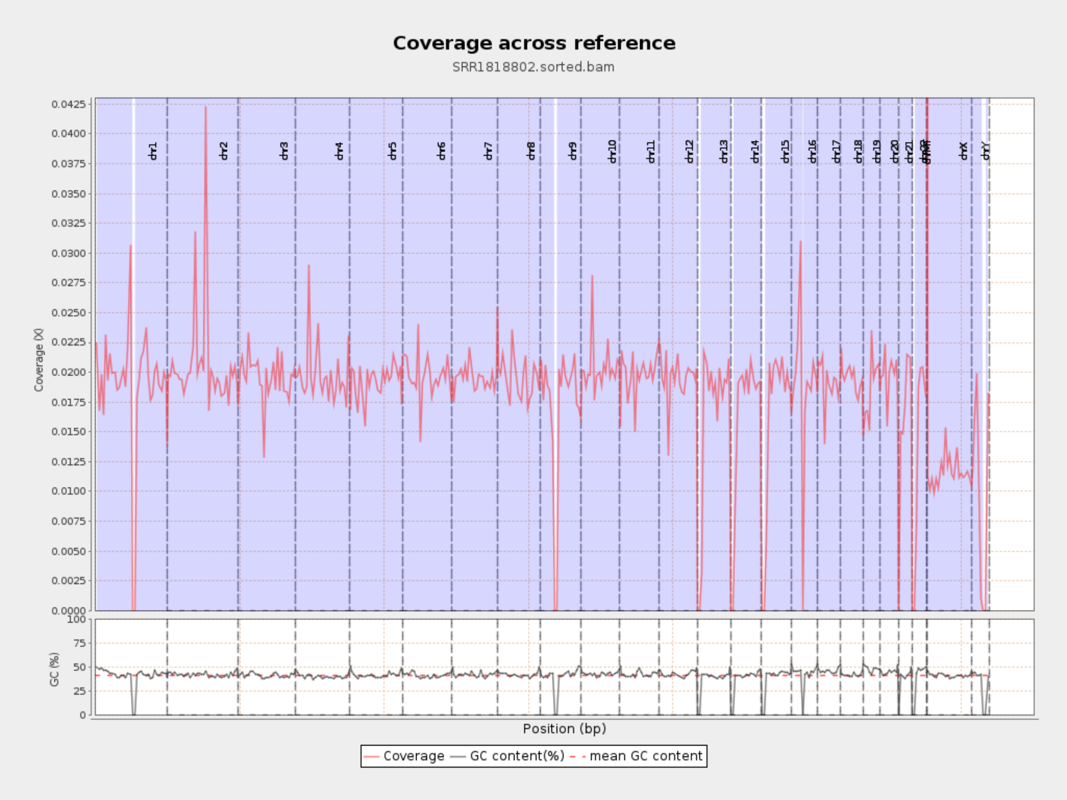
General error rate	0.55%
Mismatches	298,324
Insertions	7,210
Mapped reads with at least one insertion	0.85%
Deletions	14,924
Mapped reads with at least one deletion	1.76%
Homopolymer indels	39.85%

2.6. Chromosome stats

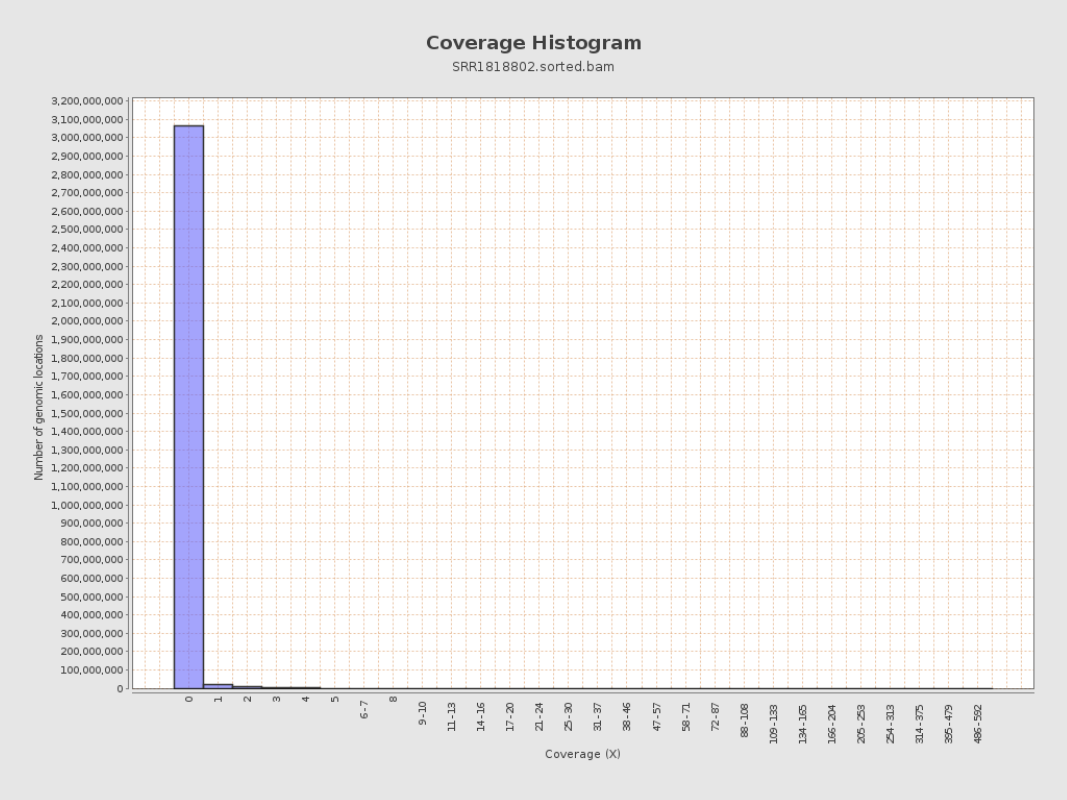
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4700482	0.0189	0.3447
chr2	243199373	5028728	0.0207	0.4503
chr3	198022430	3880223	0.0196	0.2175
chr4	191154276	3774424	0.0197	0.2455
chr5	180915260	3497568	0.0193	0.2246
chr6	171115067	3373283	0.0197	0.2374
chr7	159138663	3103172	0.0195	0.243

chr8	146364022	2860853	0.0195	0.232
chr9	141213431	2401917	0.017	0.2247
chr10	135534747	2767377	0.0204	0.3034
chr11	135006516	2674255	0.0198	0.2397
chr12	133851895	2609399	0.0195	0.2237
chr13	115169878	1851370	0.0161	0.1982
chr14	107349540	1718125	0.016	0.2203
chr15	102531392	1636710	0.016	0.1985
chr16	90354753	1674616	0.0185	0.3191
chr17	81195210	1552215	0.0191	0.2254
chr18	78077248	1522903	0.0195	0.2819
chr19	59128983	1106766	0.0187	0.3108
chr20	63025520	1246647	0.0198	0.2347
chr21	48129895	786394	0.0163	0.2061
chr22	51304566	691033	0.0135	0.1916
chrMT	16571	90095	5.4369	5.6698
chrX	155270560	1803853	0.0116	0.1832
chrY	59373566	573385	0.0097	0.4757

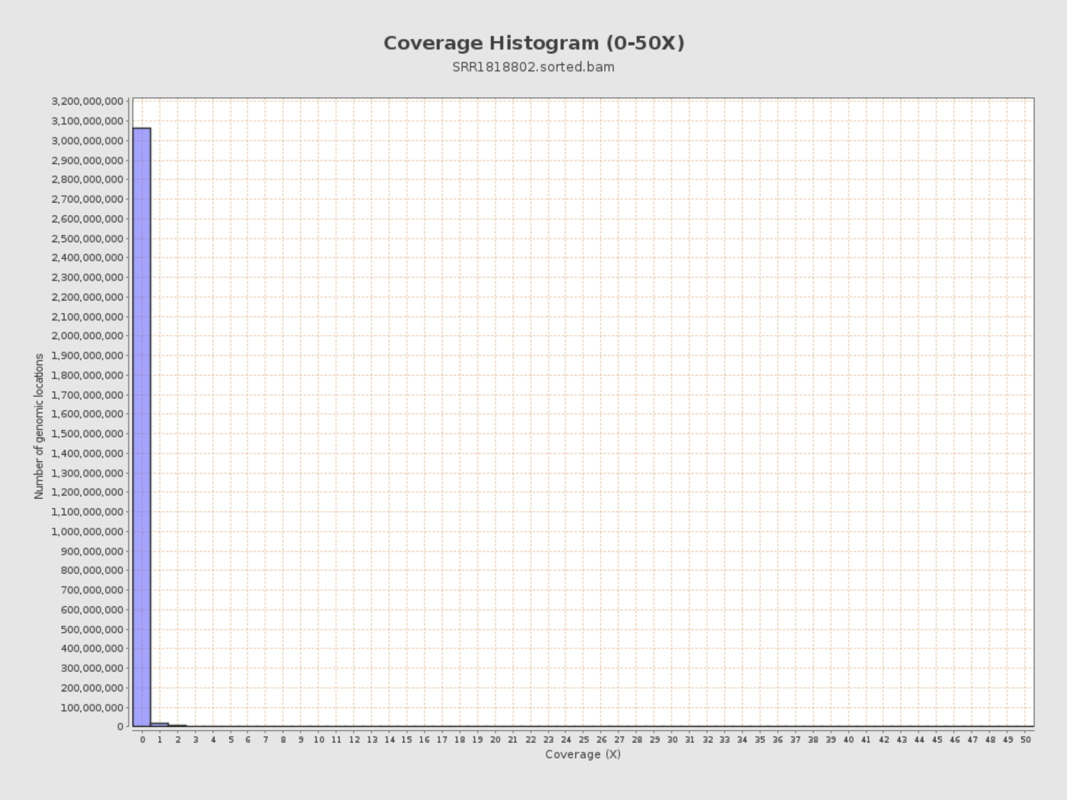
3. Results : Coverage across reference



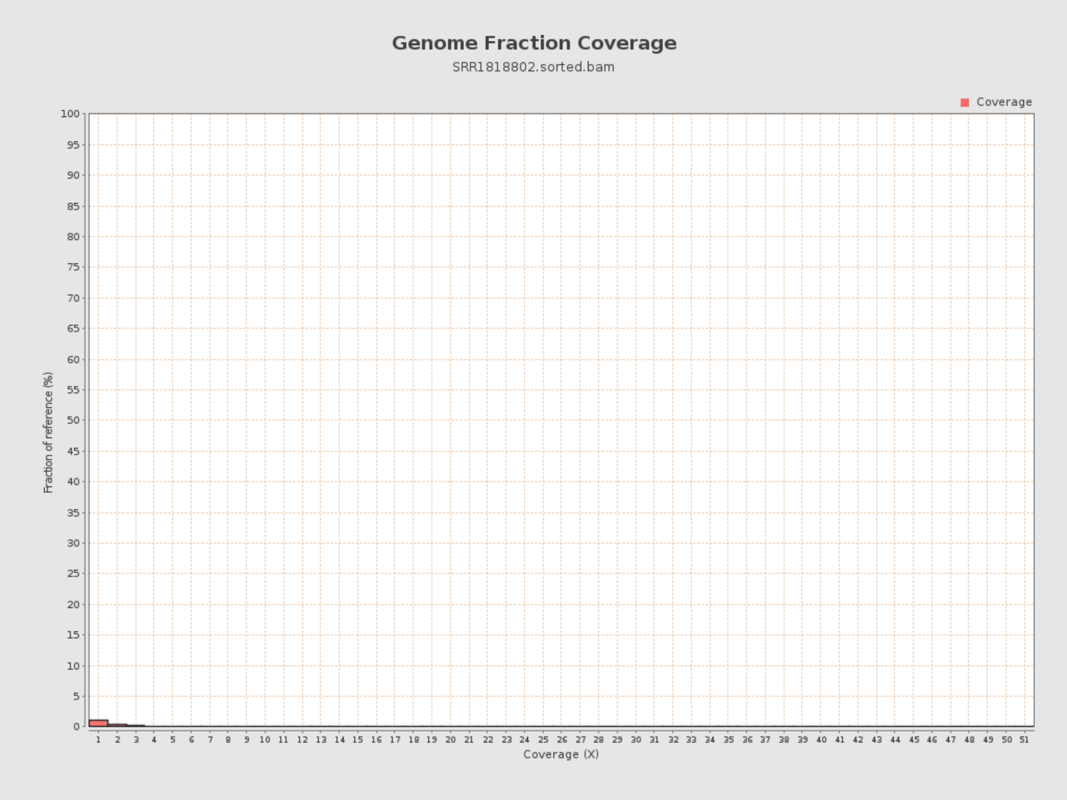
4. Results : Coverage Histogram



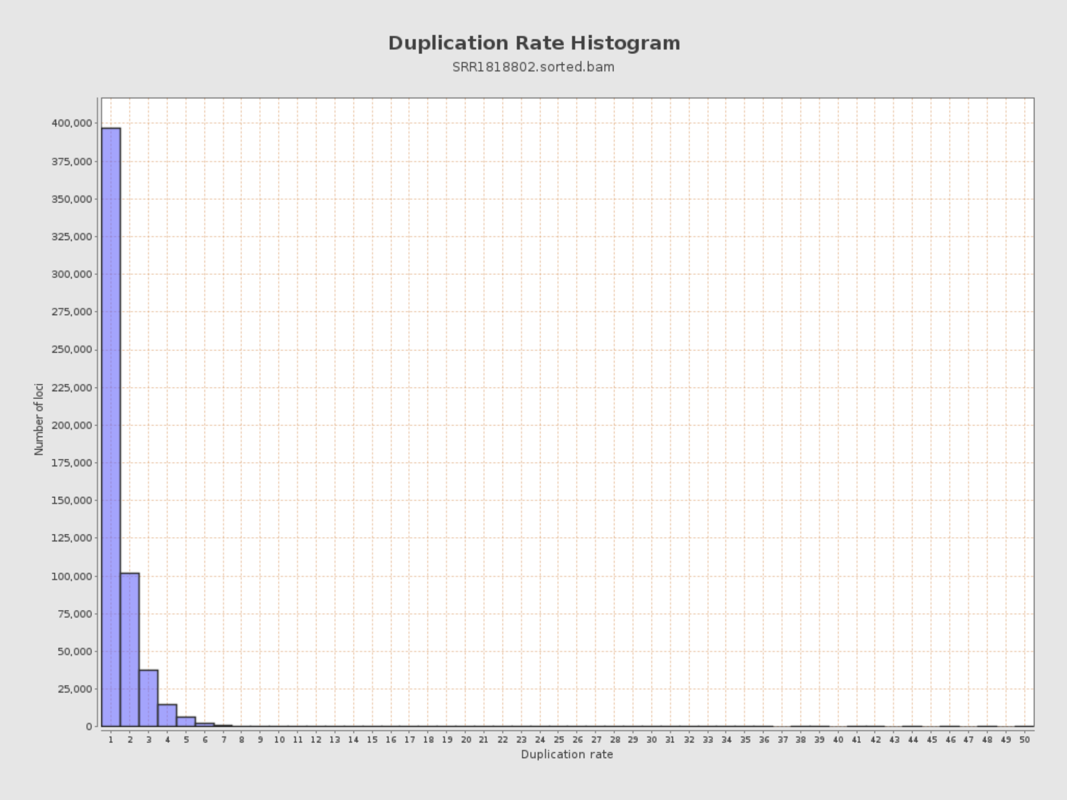
5. Results : Coverage Histogram (0-50X)



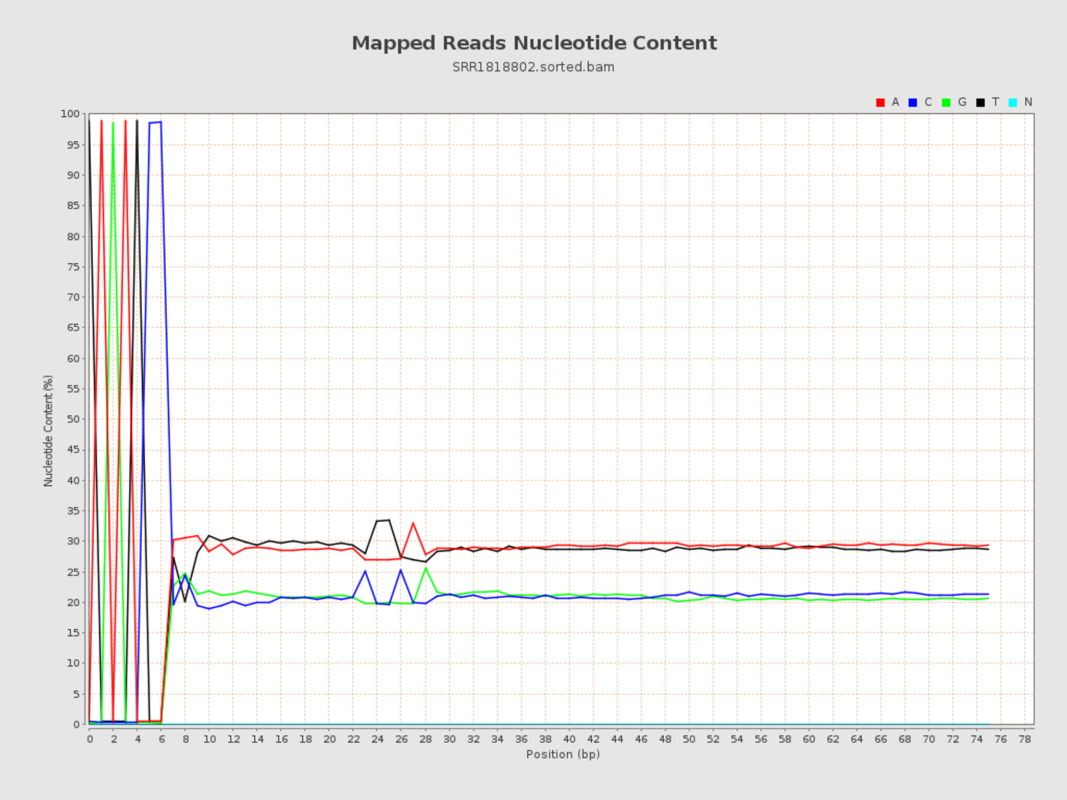
6. Results : Genome Fraction Coverage



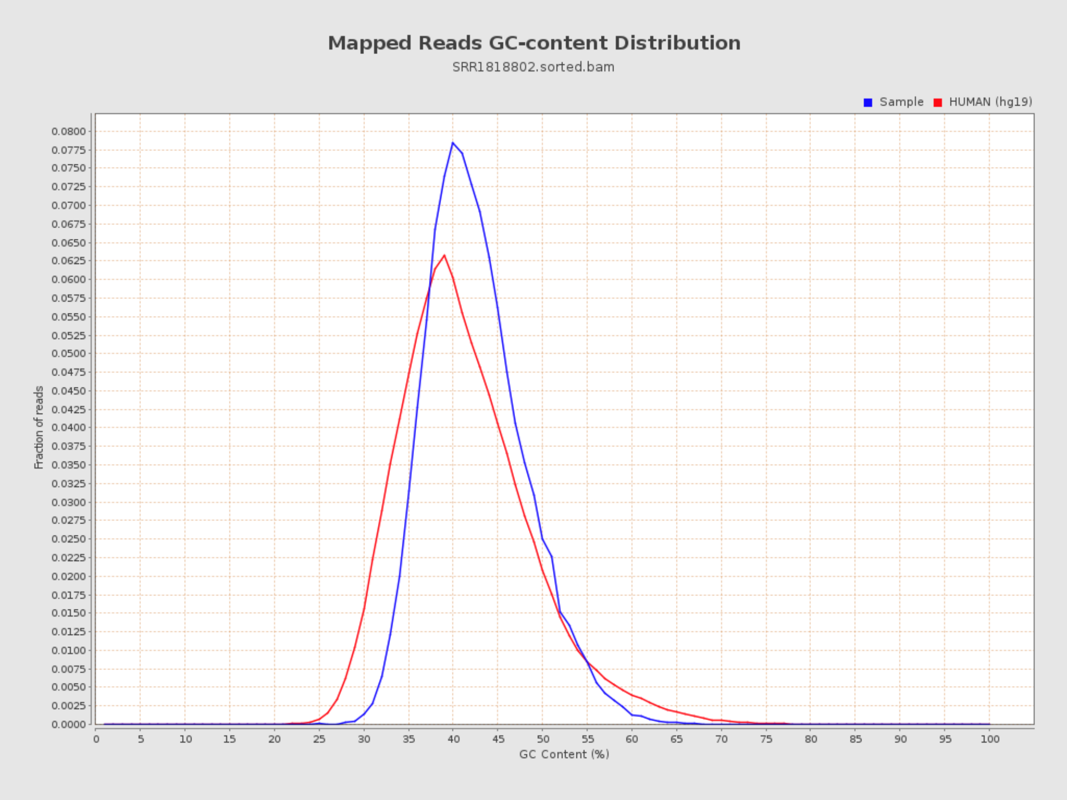
7. Results : Duplication Rate Histogram



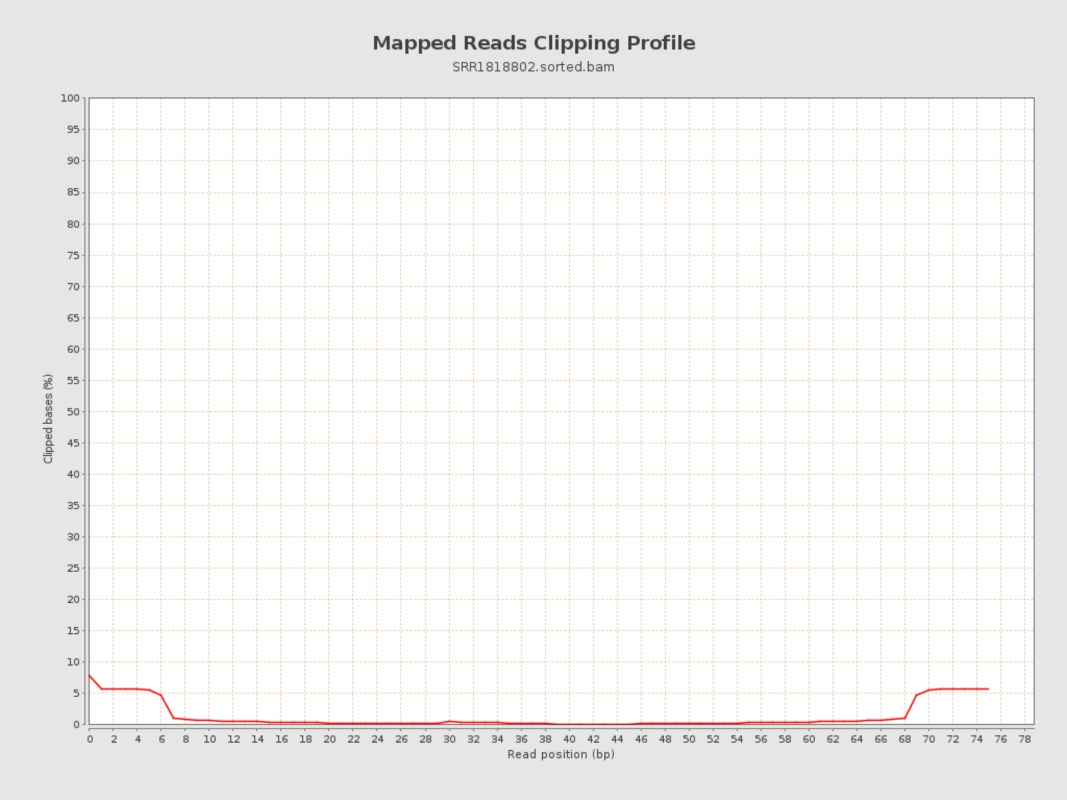
8. Results : Mapped Reads Nucleotide Content



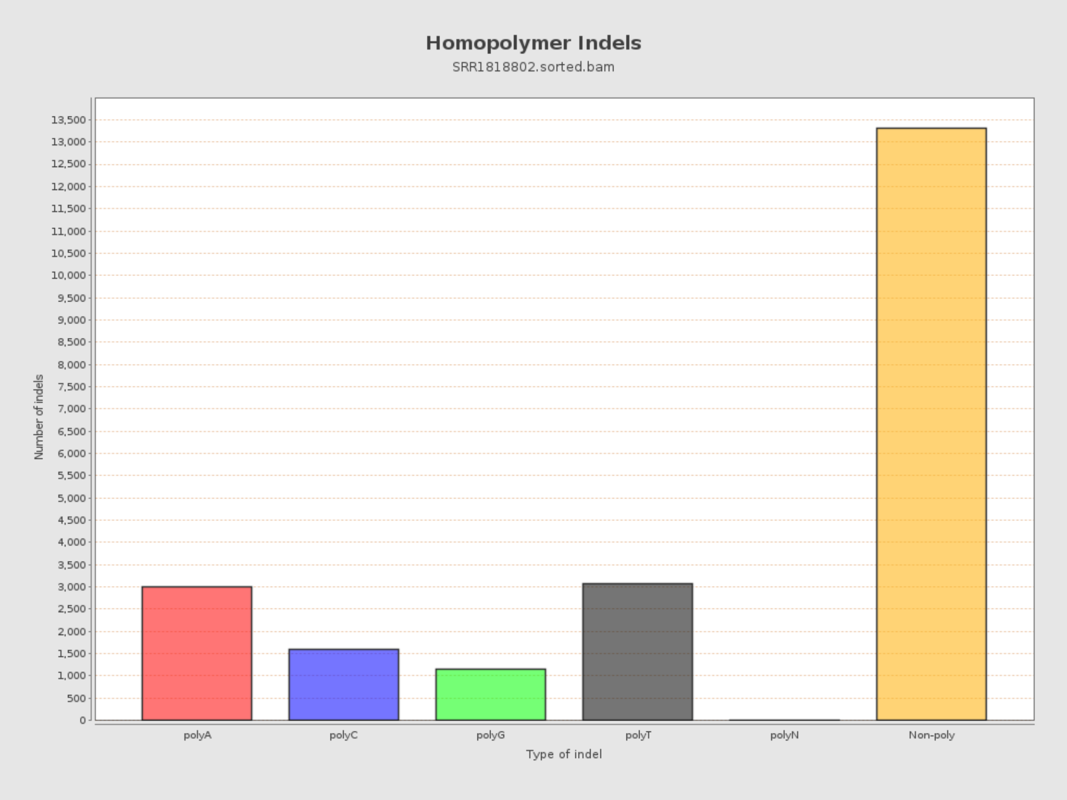
9. Results : Mapped Reads GC-content Distribution



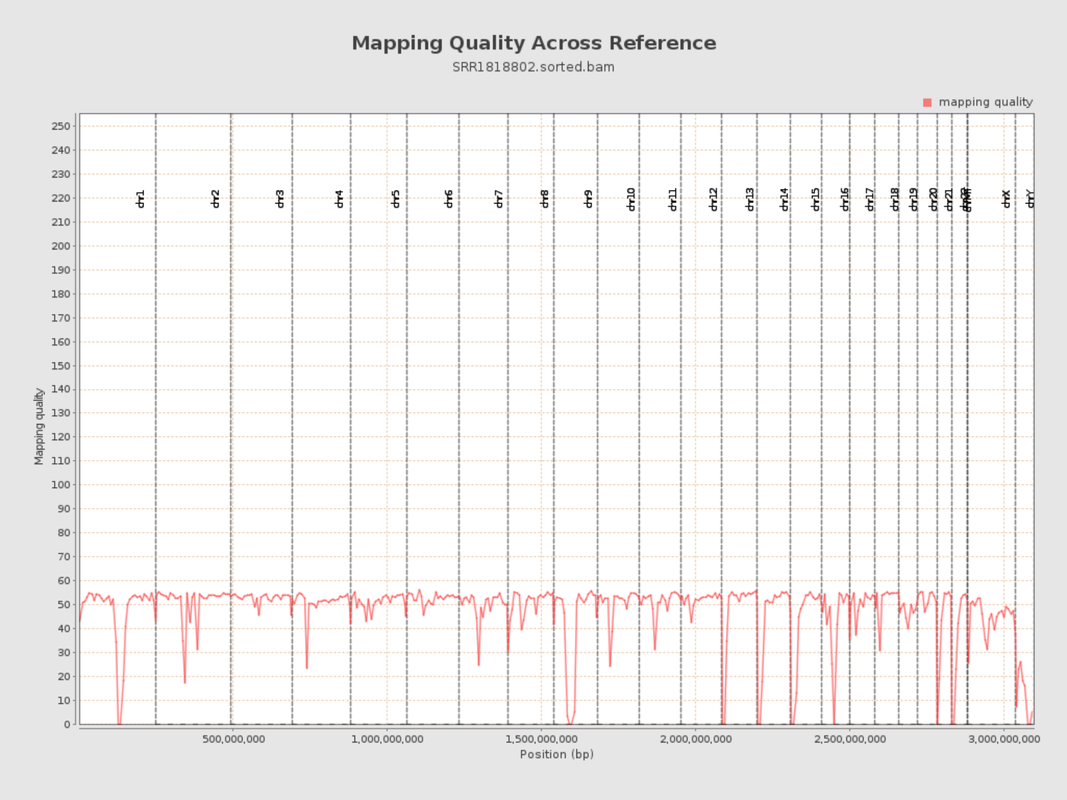
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram