Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 01:34:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818736.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_SRR1818736 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818736.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 01:34:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818736.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,190,346
Mapped reads	1,159,934 / 97.45%
Unmapped reads	30,412 / 2.55%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,239 / 0.78%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	459,782 / 38.63%
Duplication rate	35.39%
Clipped reads	1,161,453 / 97.57%

2.2. ACGT Content

Number/percentage of A's	22,821,066 / 28.97%
Number/percentage of C's	16,057,249 / 20.38%
Number/percentage of T's	22,393,612 / 28.42%
Number/percentage of G's	17,507,295 / 22.22%
Number/percentage of N's	4,519 / 0.01%
GC Percentage	42.6%

2.3. Coverage

Mean	0.0255

Standard Deviation	0.335

2.4. Mapping Quality

Mean Mapping Quality	47.6

2.5. Mismatches and indels

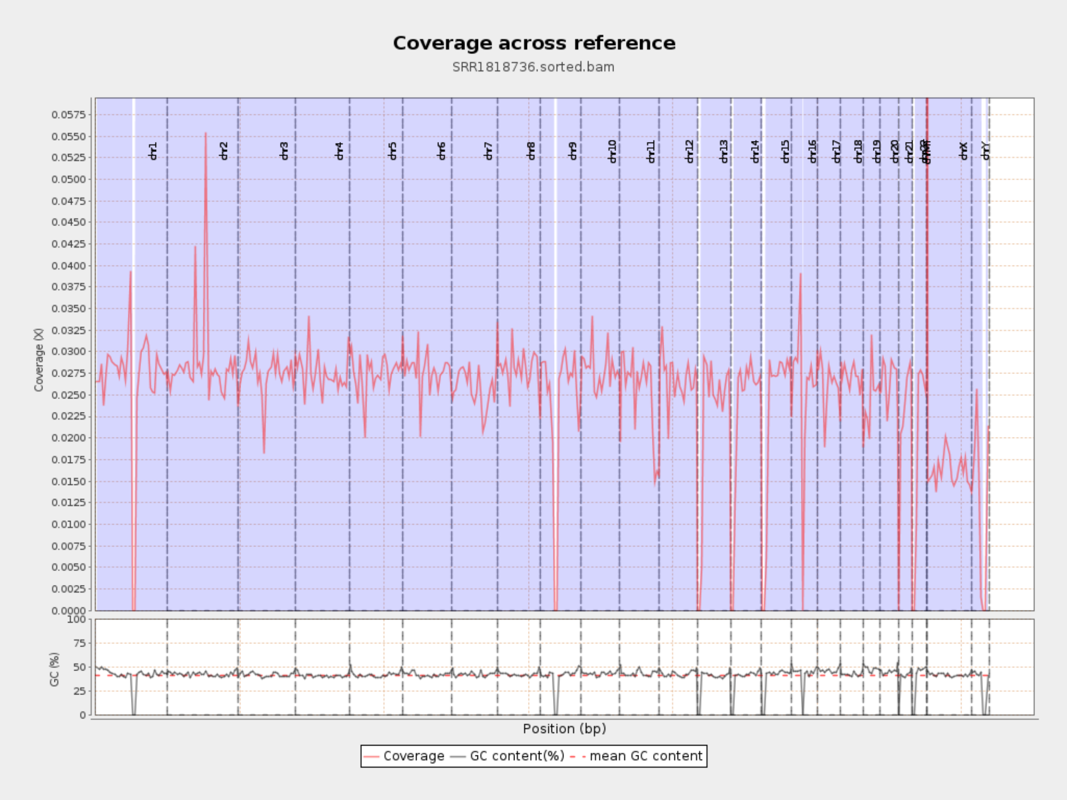
General error rate	0.52%
Mismatches	388,633
Insertions	9,023
Mapped reads with at least one insertion	0.76%
Deletions	20,529
Mapped reads with at least one deletion	1.75%
Homopolymer indels	39.91%

2.6. Chromosome stats

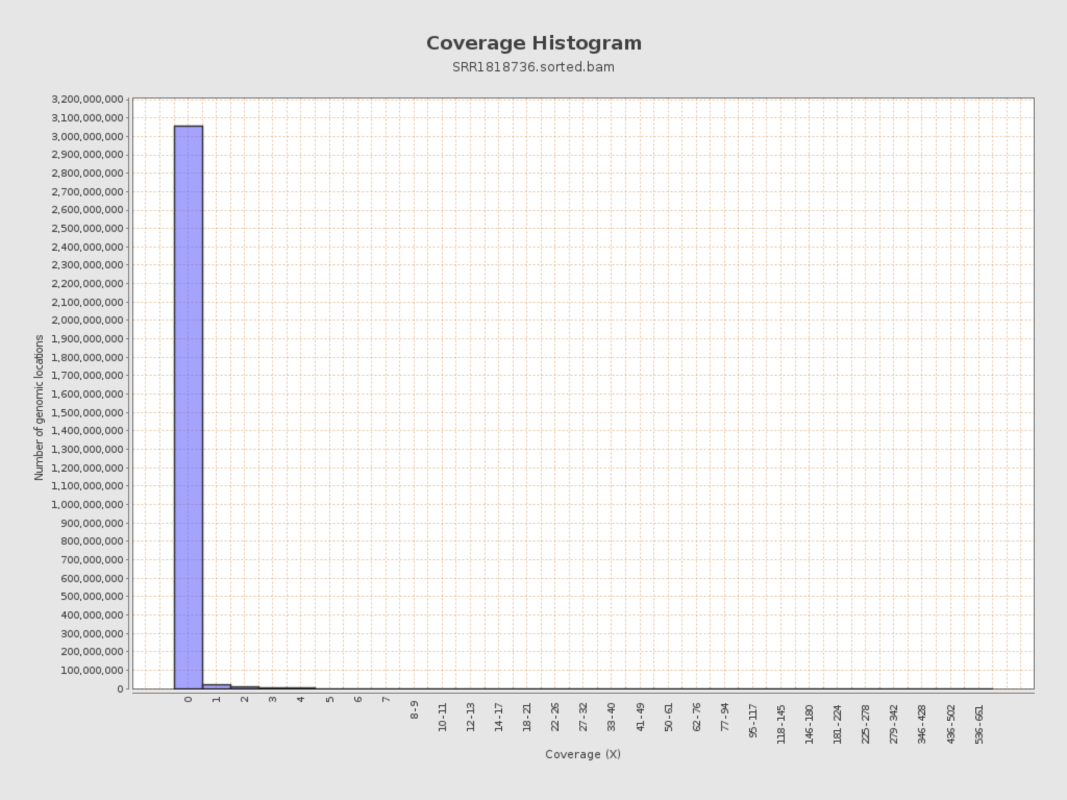
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6632227	0.0266	0.4146
chr2	243199373	7022799	0.0289	0.5215
chr3	198022430	5435070	0.0274	0.2731
chr4	191154276	5265811	0.0275	0.3062
chr5	180915260	4972670	0.0275	0.2832
chr6	171115067	4756288	0.0278	0.2956
chr7	159138663	4105434	0.0258	0.299

chr8	146364022	4109100	0.0281	0.3091
chr9	141213431	3368154	0.0239	0.2901
chr10	135534747	3802216	0.0281	0.3635
chr11	135006516	3446860	0.0255	0.2898
chr12	133851895	3612710	0.027	0.2828
chr13	115169878	2524590	0.0219	0.2461
chr14	107349540	2418700	0.0225	0.2772
chr15	102531392	2298571	0.0224	0.2507
chr16	90354753	2292928	0.0254	0.3741
chr17	81195210	2118233	0.0261	0.28
chr18	78077248	2127316	0.0272	0.3793
chr19	59128983	1456857	0.0246	0.3719
chr20	63025520	1685154	0.0267	0.2833
chr21	48129895	1075205	0.0223	0.2561
chr22	51304566	967990	0.0189	0.2486
chrMT	16571	64614	3.8992	4.5969
chrX	155270560	2534621	0.0163	0.2271
chrY	59373566	722634	0.0122	0.5212

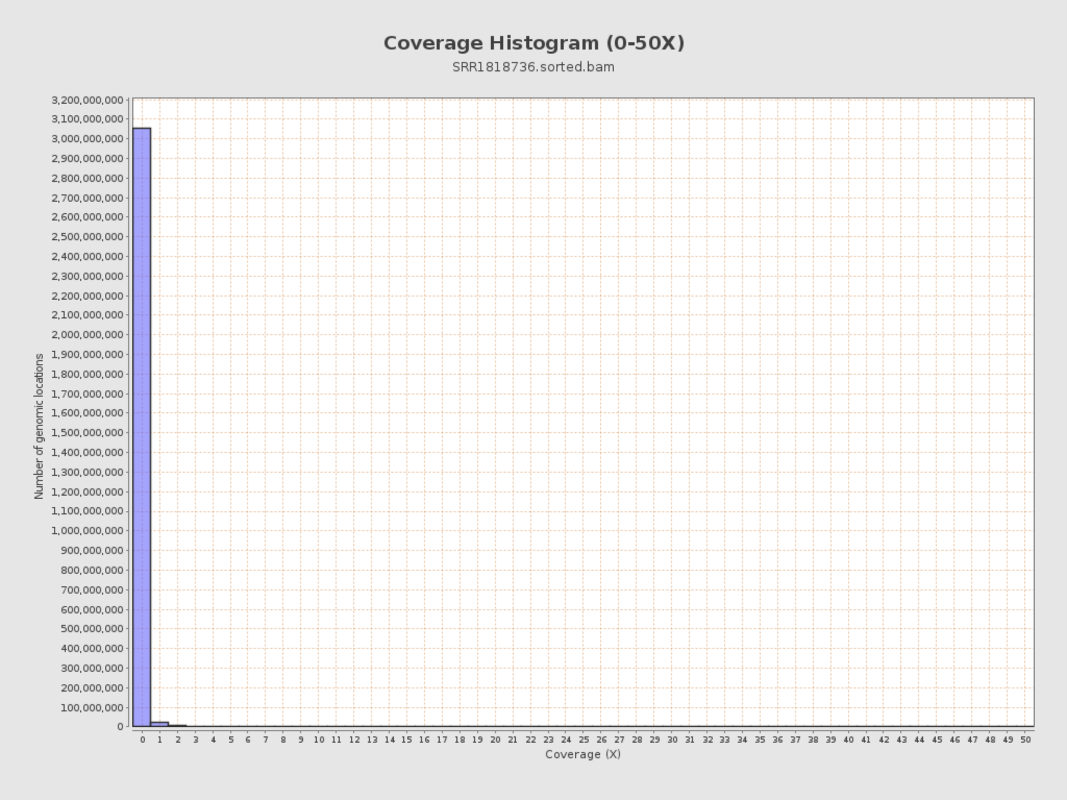
3. Results : Coverage across reference



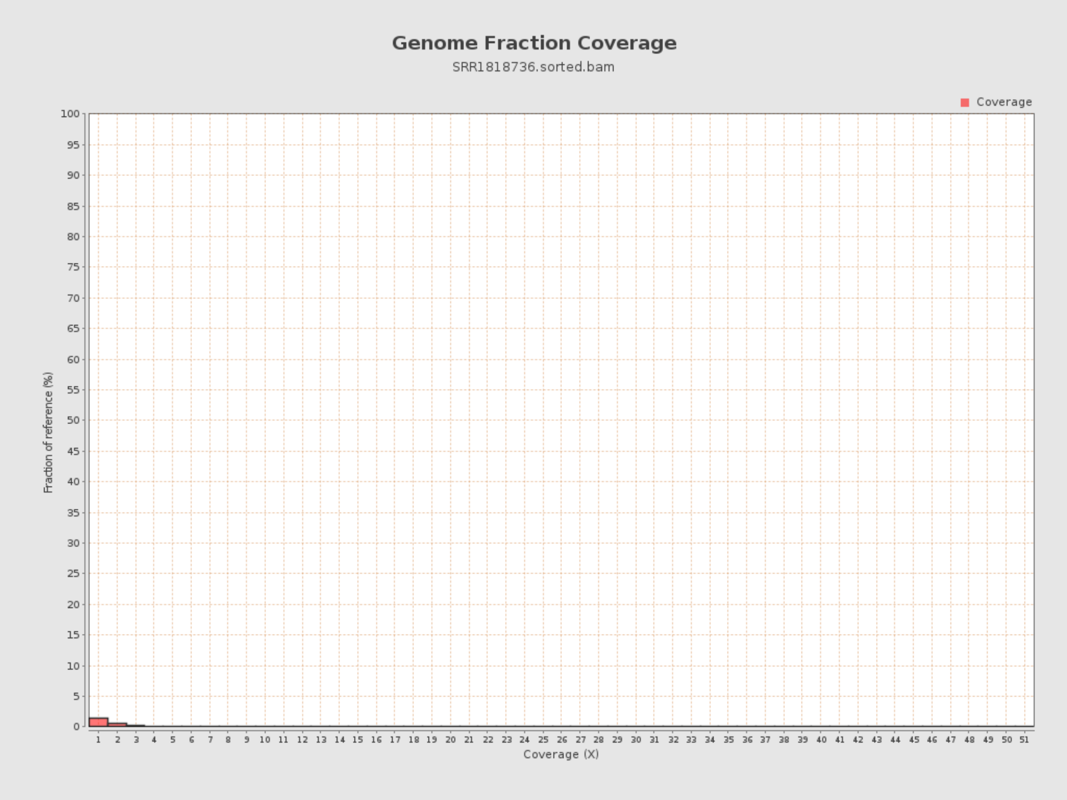
4. Results : Coverage Histogram



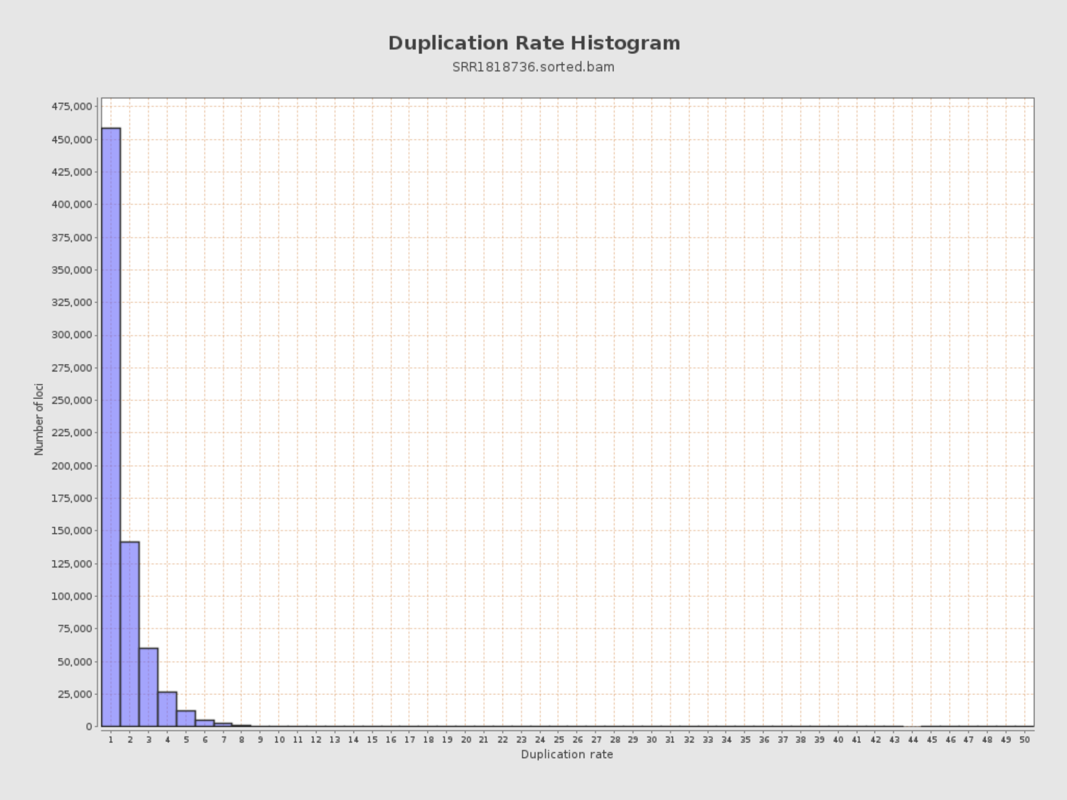
5. Results : Coverage Histogram (0-50X)



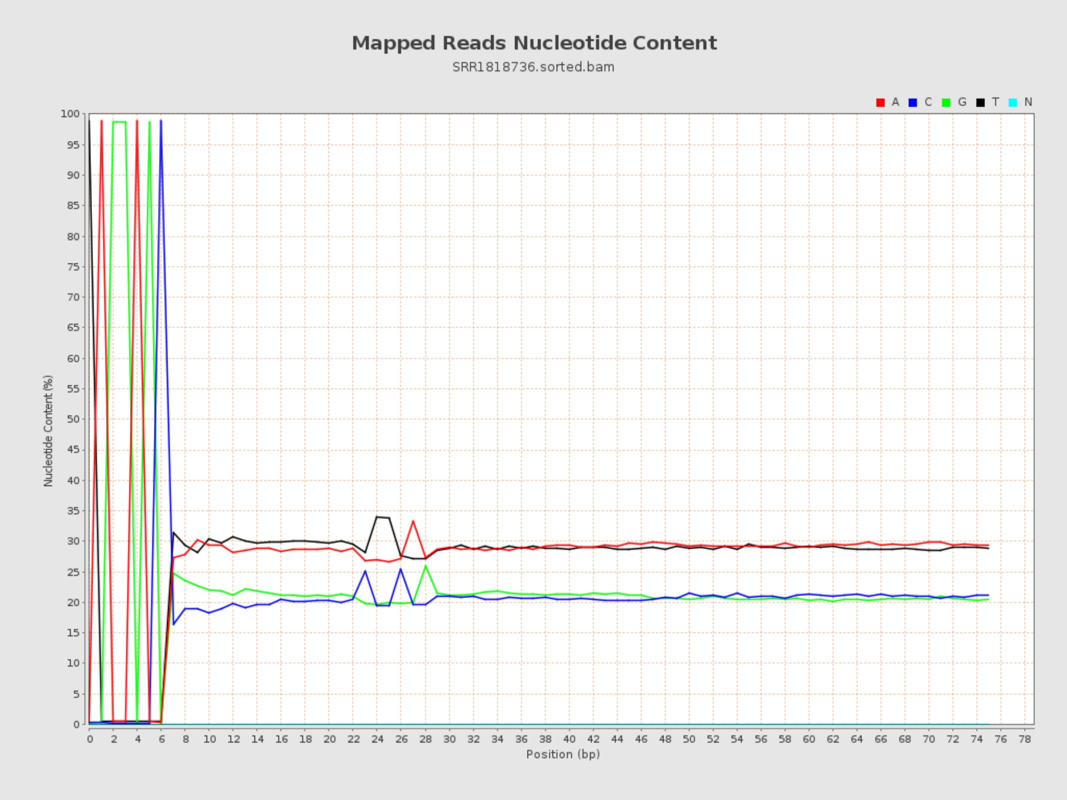
6. Results : Genome Fraction Coverage



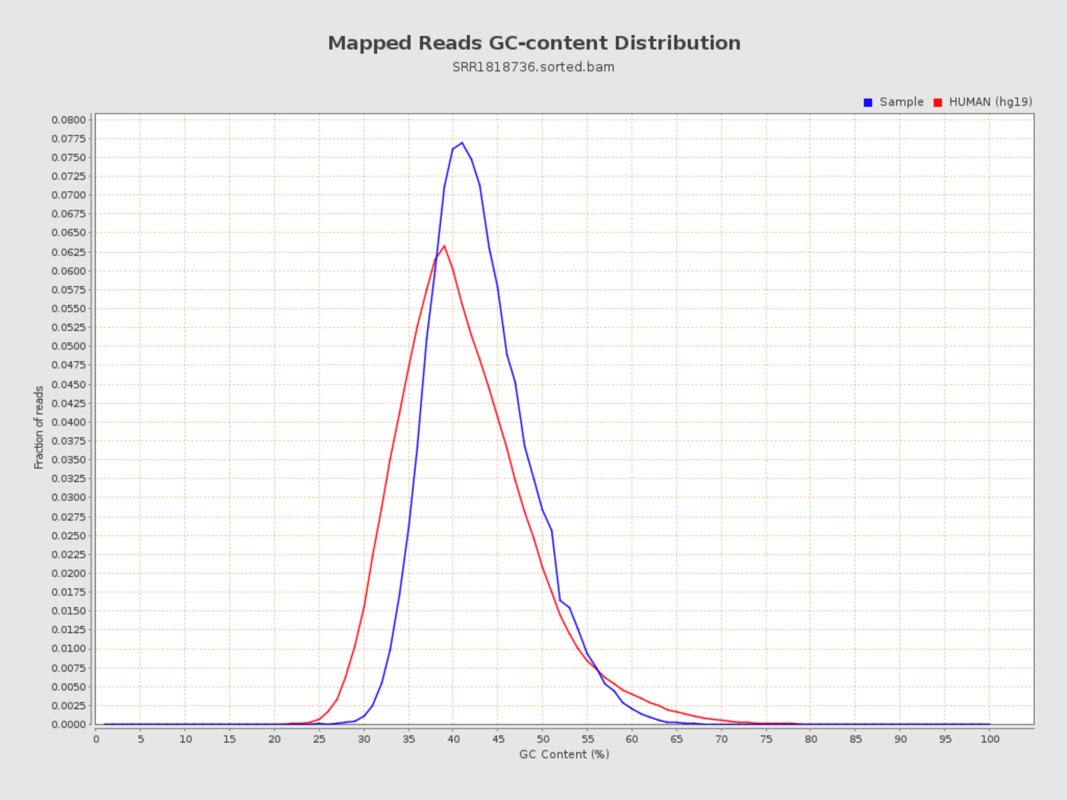
7. Results : Duplication Rate Histogram



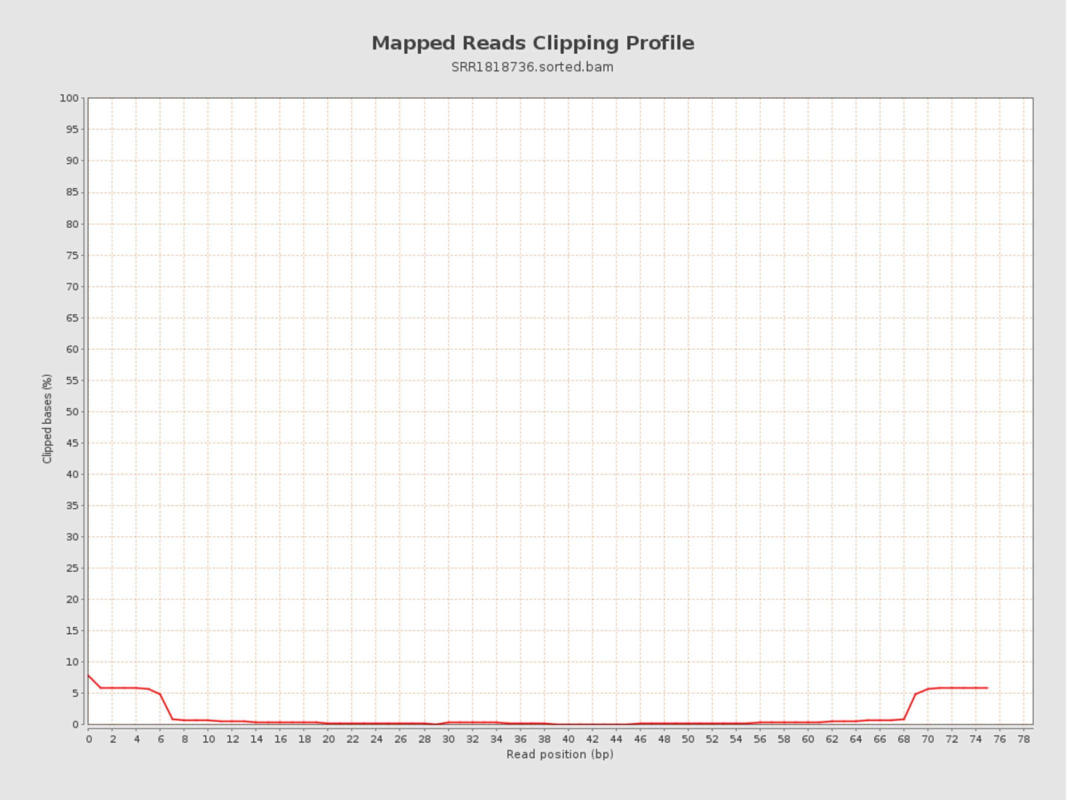
8. Results : Mapped Reads Nucleotide Content



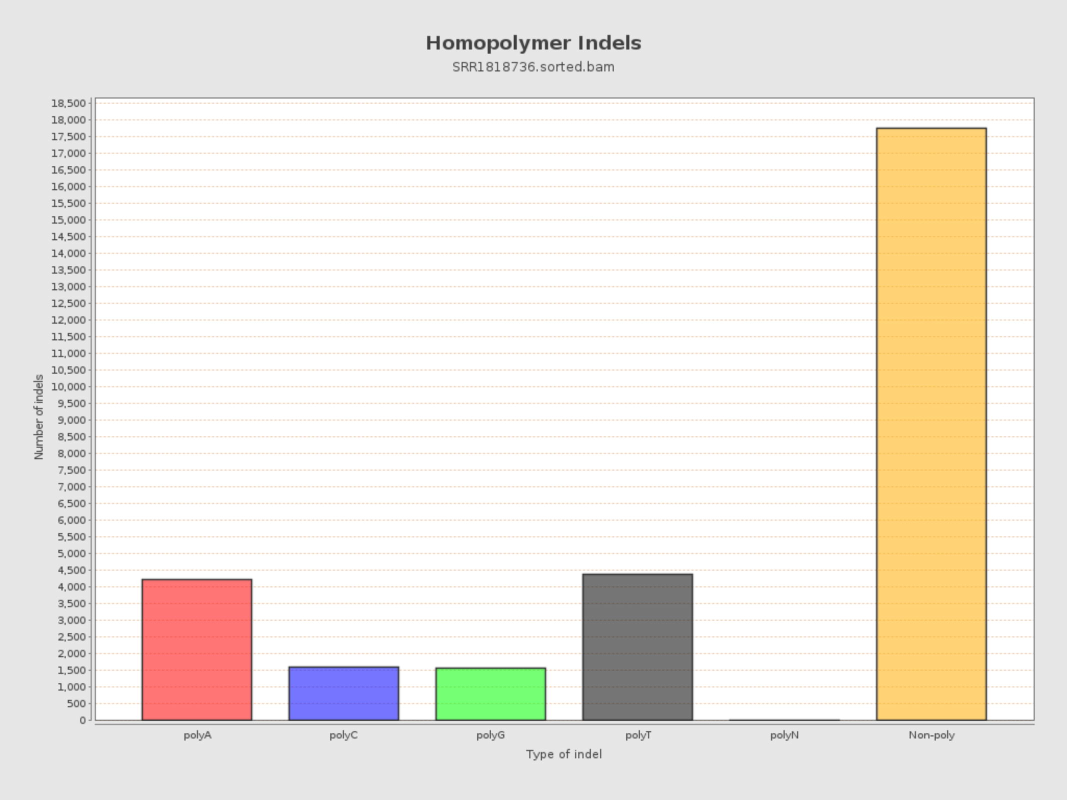
9. Results : Mapped Reads GC-content Distribution



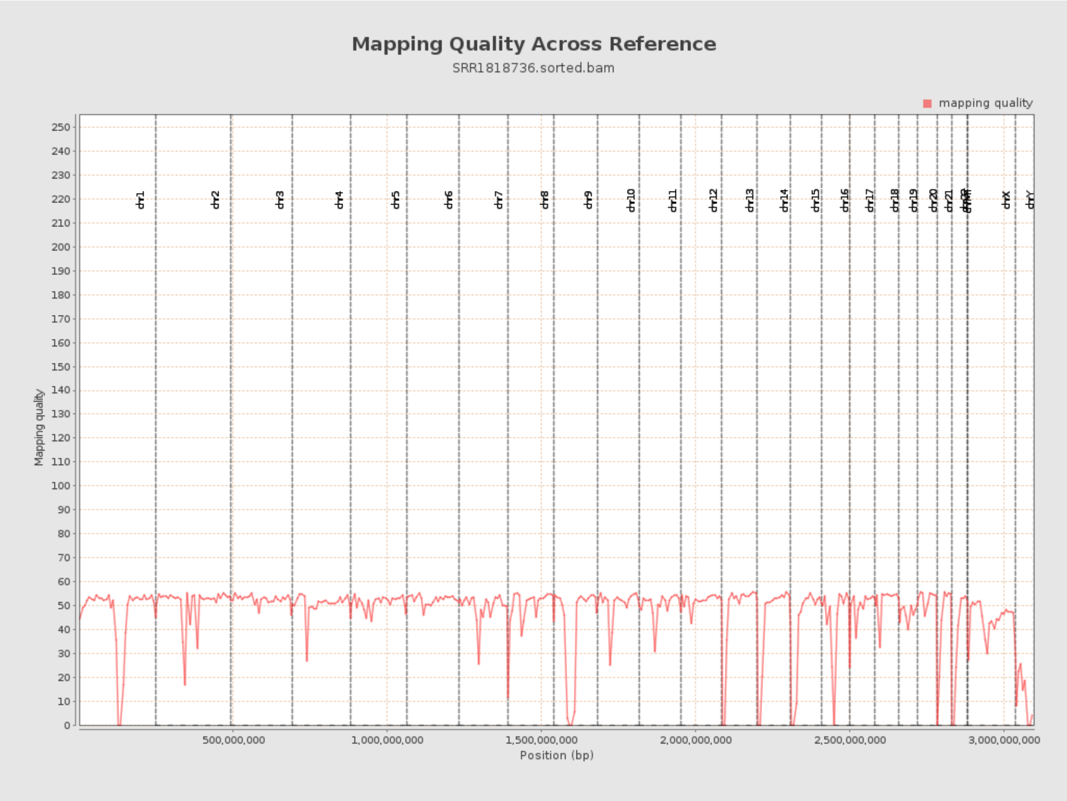
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram