Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 13:00:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818799.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_SRR1818799 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818799.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 13:00:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818799.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	346,704
Mapped reads	329,342 / 94.99%
Unmapped reads	17,362 / 5.01%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,882 / 0.83%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	49,976 / 14.41%
Duplication rate	13.8%
Clipped reads	331,588 / 95.64%

2.2. ACGT Content

Number/percentage of A's	6,482,611 / 29.09%
Number/percentage of C's	4,896,656 / 21.97%
Number/percentage of T's	6,282,755 / 28.19%
Number/percentage of G's	4,622,823 / 20.74%
Number/percentage of N's	1,346 / 0.01%
GC Percentage	42.71%

2.3. Coverage

Mean	0.0072

Standard Deviation	0.1244

2.4. Mapping Quality

Mean Mapping Quality	47.61

2.5. Mismatches and indels

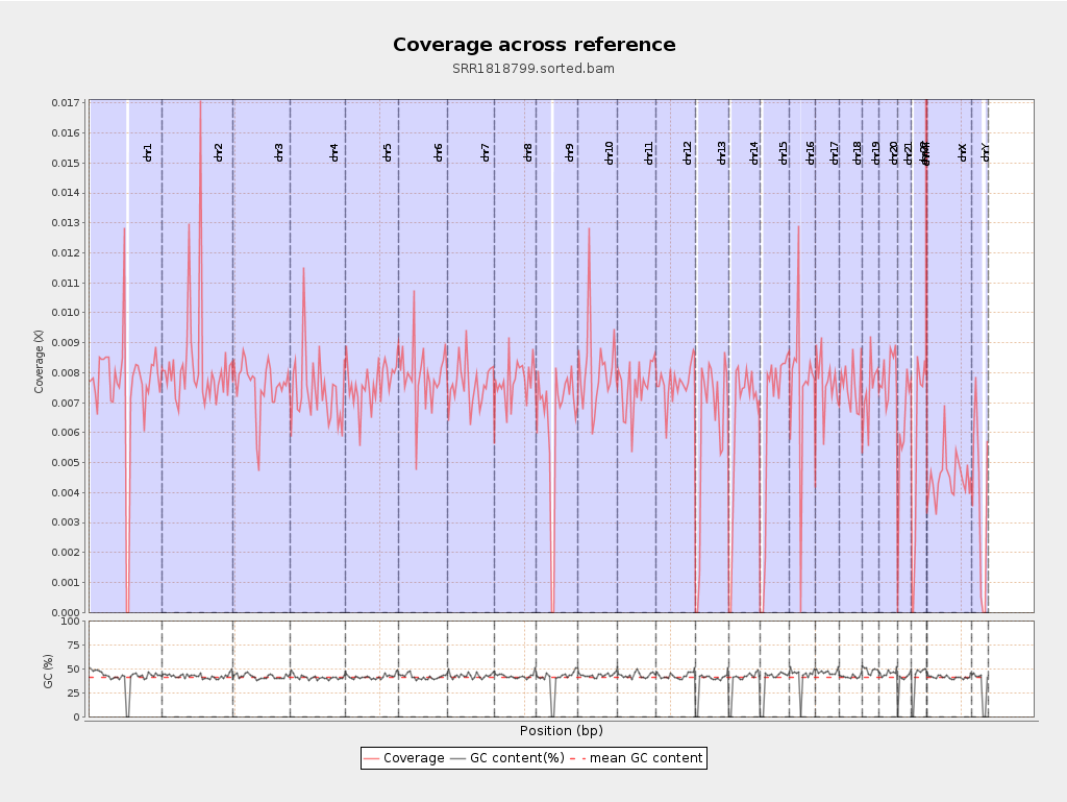
General error rate	0.54%
Mismatches	116,483
Insertions	2,259
Mapped reads with at least one insertion	0.68%
Deletions	5,737
Mapped reads with at least one deletion	1.72%
Homopolymer indels	42.73%

2.6. Chromosome stats

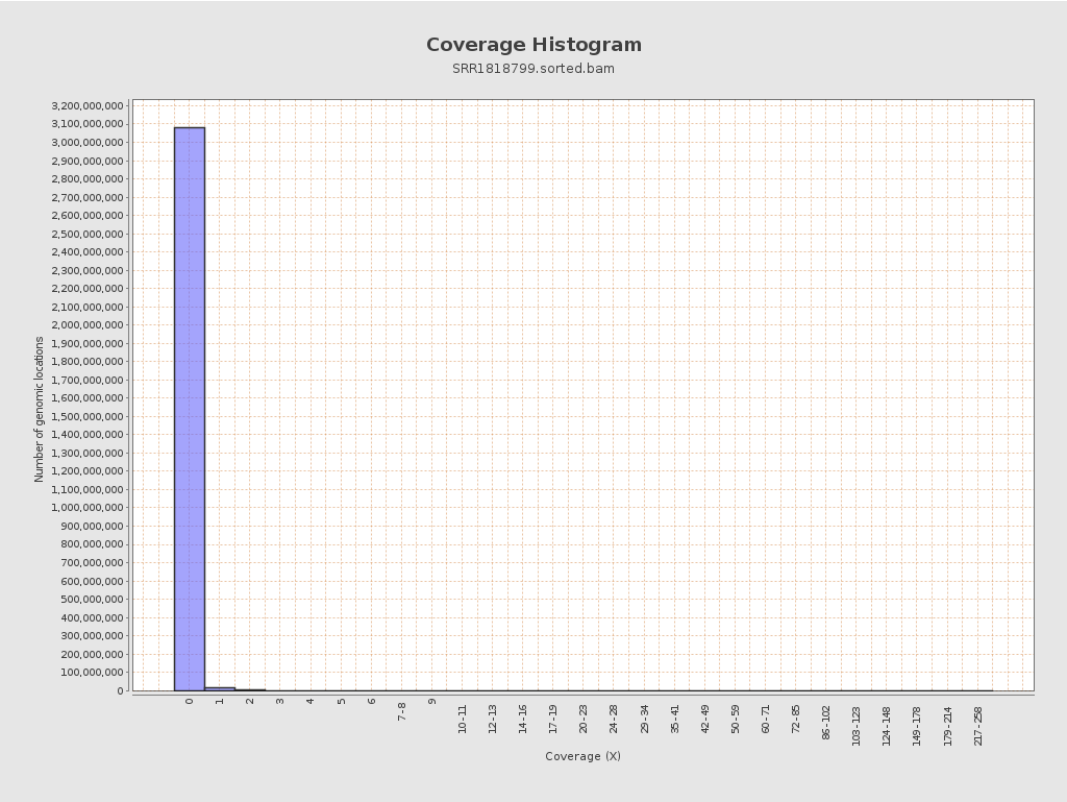
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	1864651	0.0075	0.1615
chr2	243199373	2010023	0.0083	0.1919
chr3	198022430	1502369	0.0076	0.1045
chr4	191154276	1407577	0.0074	0.1132
chr5	180915260	1379223	0.0076	0.106
chr6	171115067	1355571	0.0079	0.1129
chr7	159138663	1215160	0.0076	0.1127

chr8	146364022	1134067	0.0077	0.1109
chr9	141213431	908536	0.0064	0.1047
chr10	135534747	1095346	0.0081	0.129
chr11	135006516	1019192	0.0075	0.1101
chr12	133851895	1020174	0.0076	0.1075
chr13	115169878	707310	0.0061	0.0938
chr14	107349540	676733	0.0063	0.1004
chr15	102531392	657892	0.0064	0.0971
chr16	90354753	686393	0.0076	0.1334
chr17	81195210	623963	0.0077	0.1078
chr18	78077248	589554	0.0076	0.1215
chr19	59128983	437758	0.0074	0.1316
chr20	63025520	500415	0.0079	0.1104
chr21	48129895	291001	0.006	0.095
chr22	51304566	283208	0.0055	0.0928
chrMT	16571	18902	1.1407	1.48
chrX	155270560	701317	0.0045	0.0852
chrY	59373566	209521	0.0035	0.1915

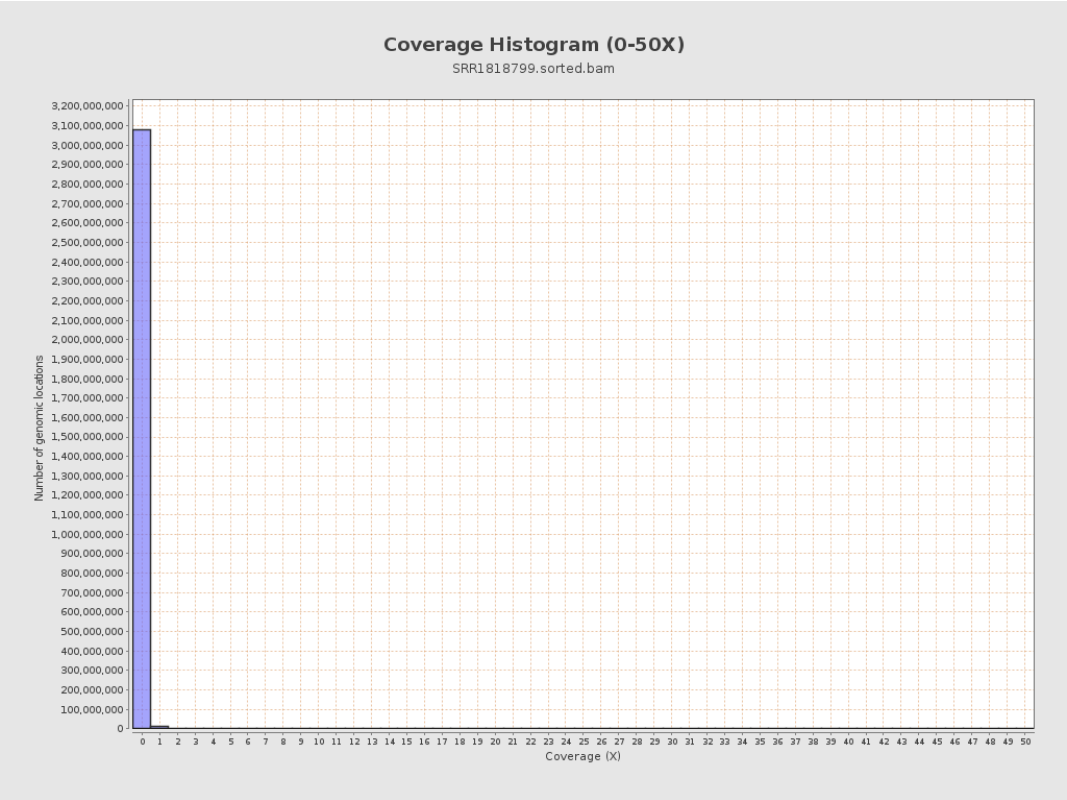
3. Results : Coverage across reference



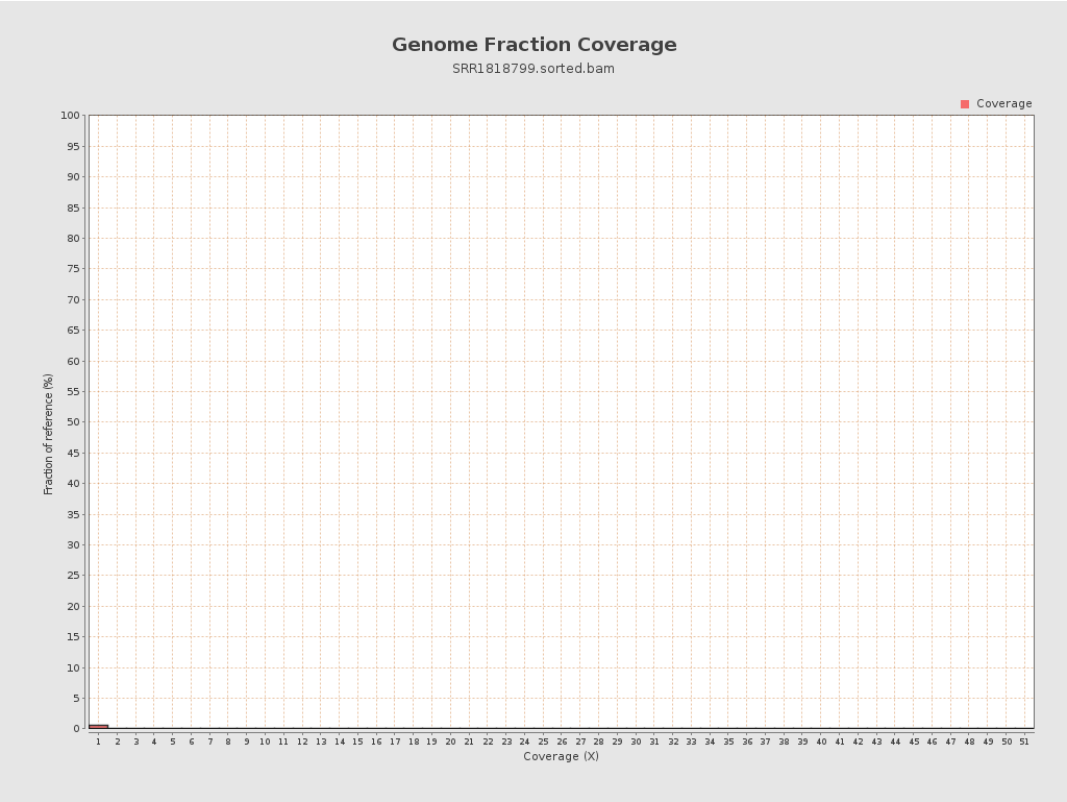
4. Results : Coverage Histogram



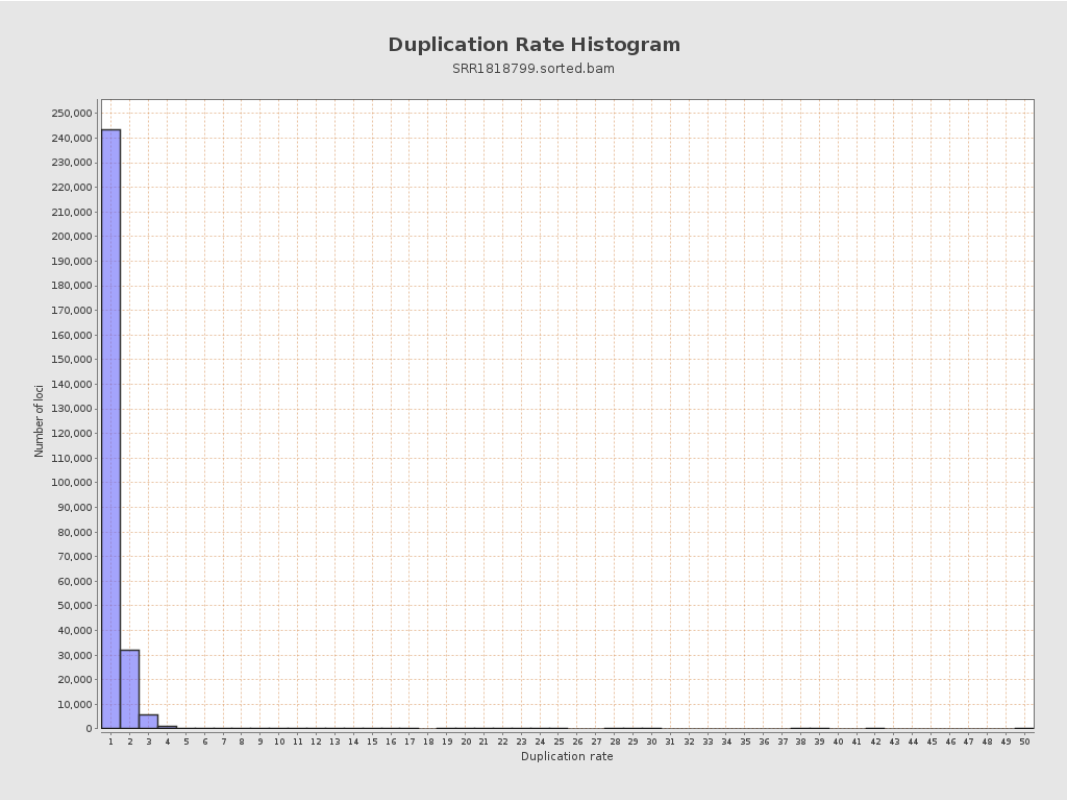
5. Results : Coverage Histogram (0-50X)



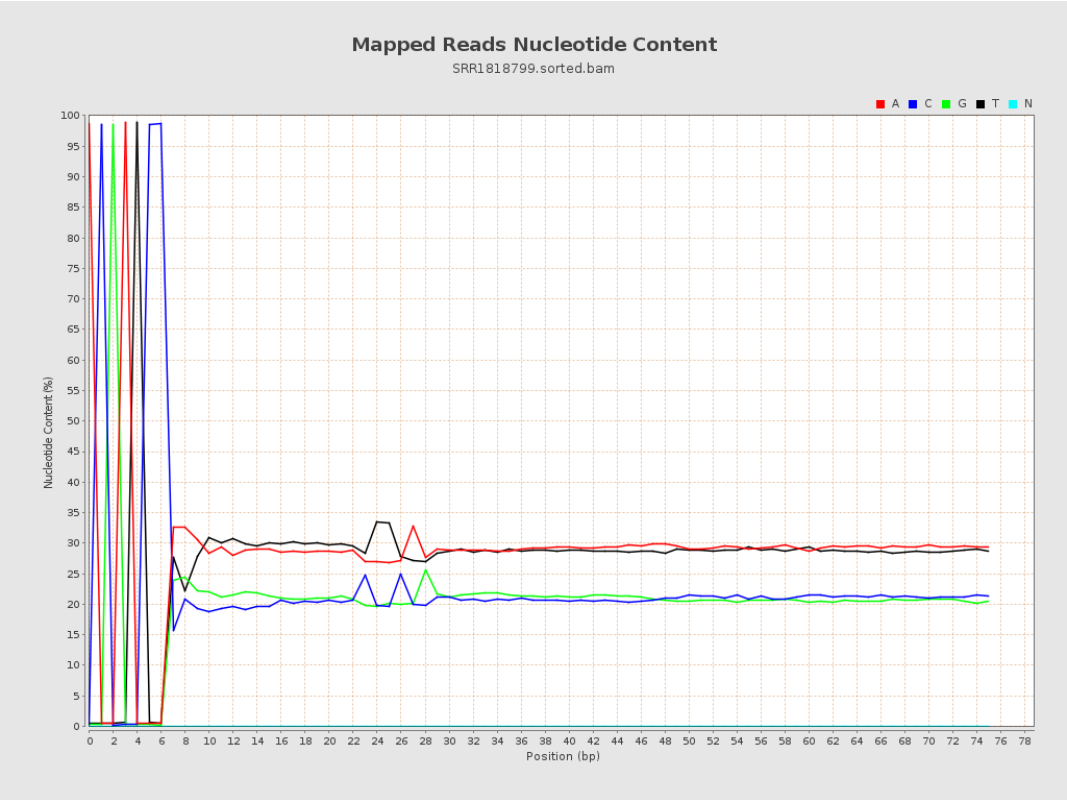
6. Results : Genome Fraction Coverage



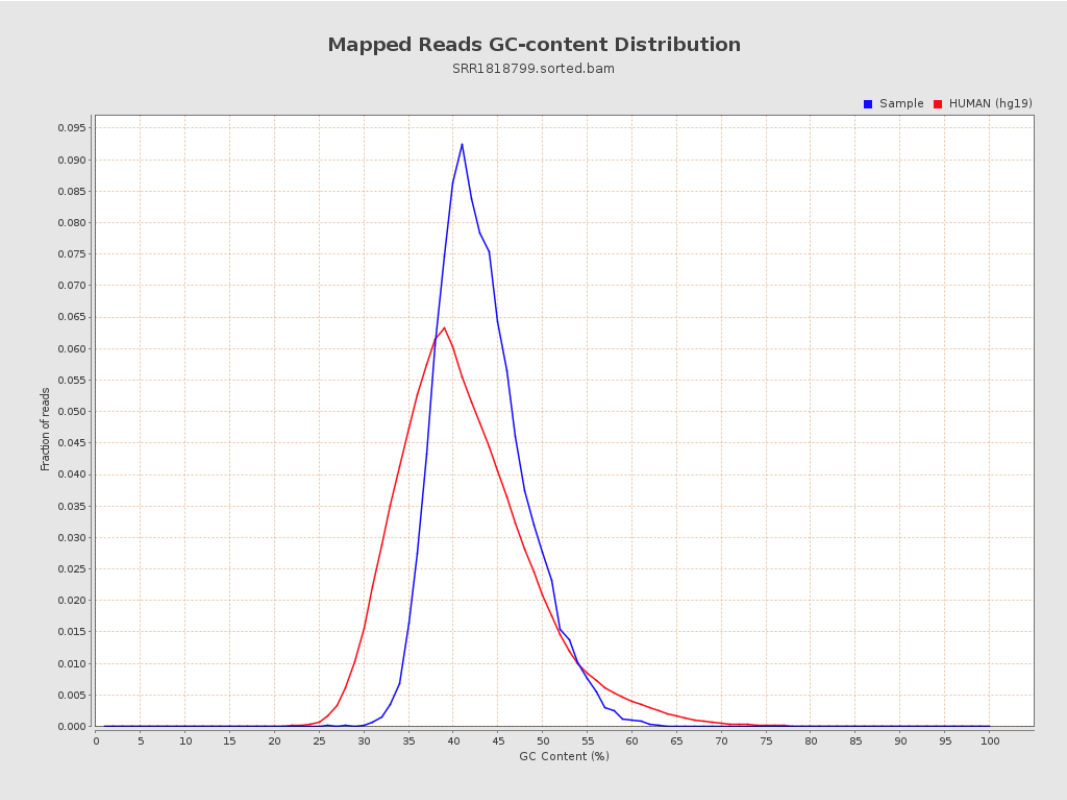
7. Results : Duplication Rate Histogram



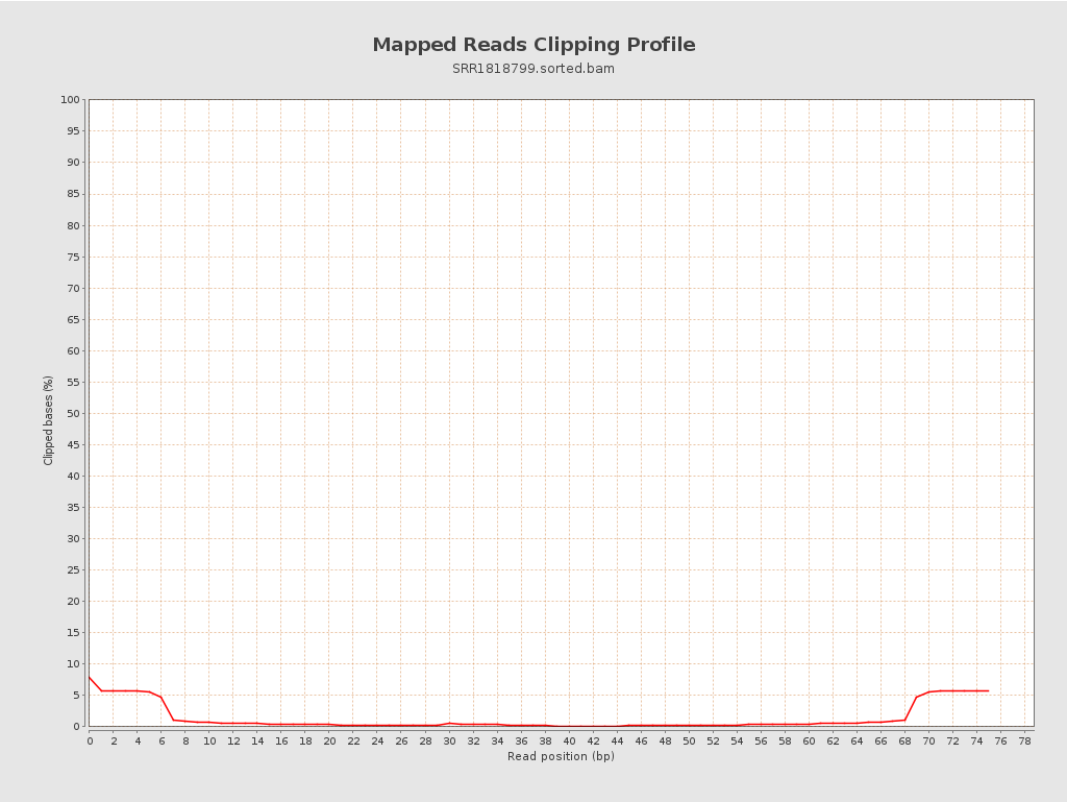
8. Results : Mapped Reads Nucleotide Content



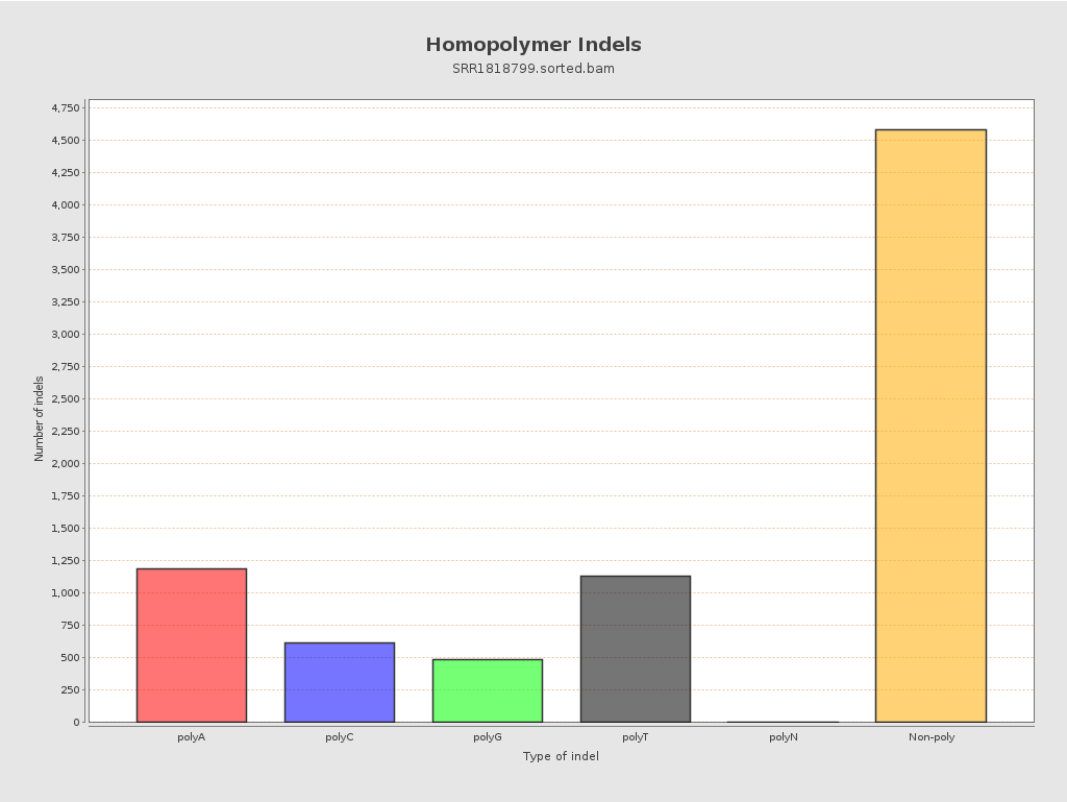
9. Results : Mapped Reads GC-content Distribution



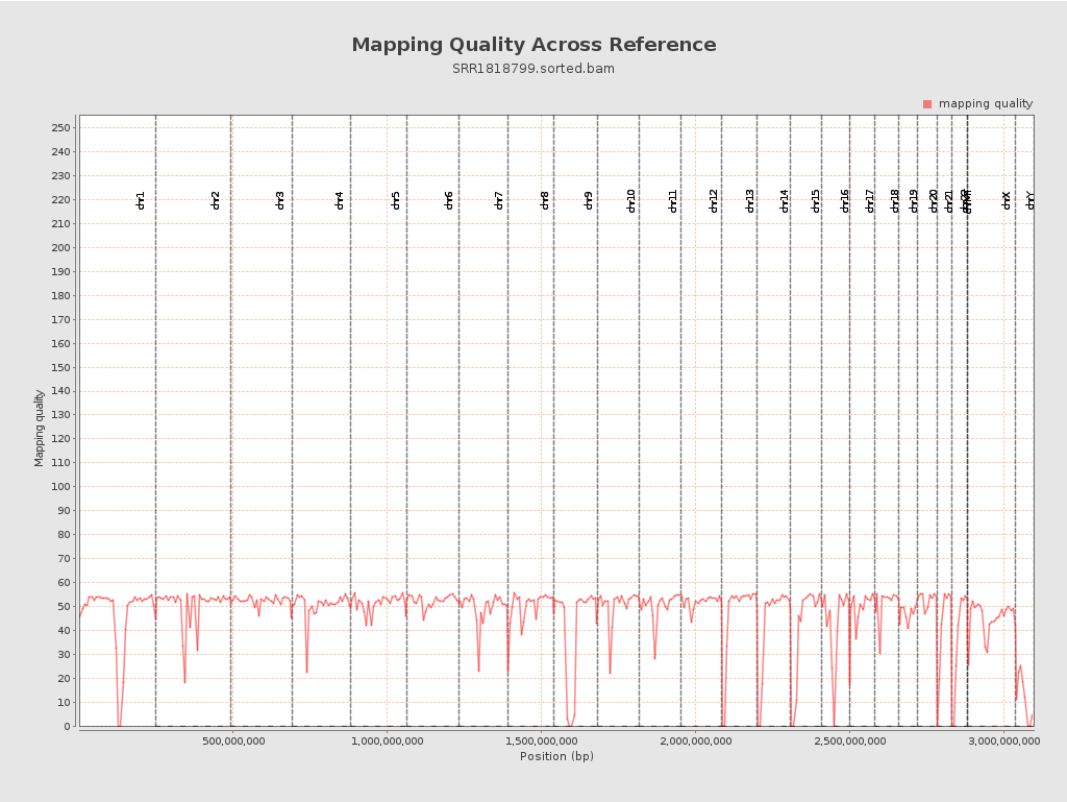
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram