Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 00:43:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1819114.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_SRR1819114 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1819114.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 00:43:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1819114.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	967,884
Mapped reads	827,434 / 85.49%
Unmapped reads	140,450 / 14.51%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,826 / 0.29%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	22,149 / 2.29%
Duplication rate	1.87%
Clipped reads	828,012 / 85.55%

2.2. ACGT Content

Number/percentage of A's	11,968,766 / 25.22%
Number/percentage of C's	9,215,039 / 19.42%
Number/percentage of T's	14,903,670 / 31.41%
Number/percentage of G's	11,368,110 / 23.95%
Number/percentage of N's	587 / 0%
GC Percentage	43.37%

2.3. Coverage

Mean	0.0153

Standard Deviation	0.1751

2.4. Mapping Quality

Mean Mapping Quality	43.46

2.5. Mismatches and indels

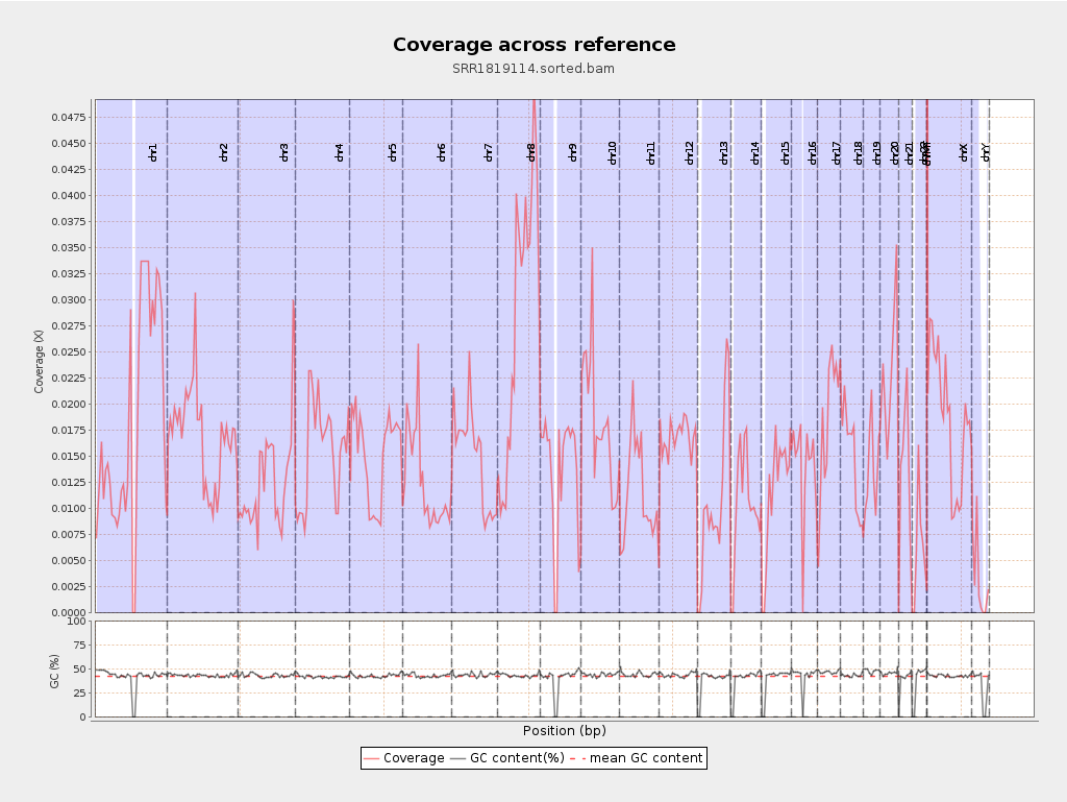
General error rate	0.54%
Mismatches	250,504
Insertions	3,588
Mapped reads with at least one insertion	0.43%
Deletions	8,952
Mapped reads with at least one deletion	1.07%
Homopolymer indels	41.37%

2.6. Chromosome stats

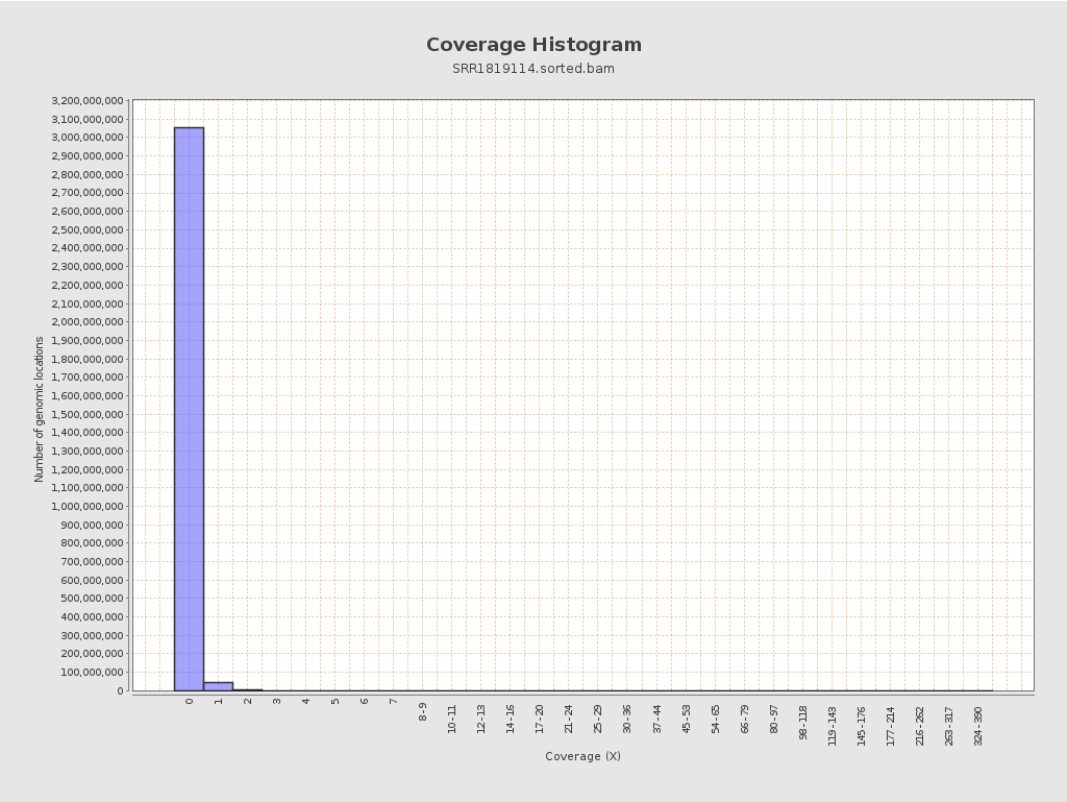
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	4504819	0.0181	0.3033
chr2	243199373	4111221	0.0169	0.1988
chr3	198022430	2473880	0.0125	0.1182
chr4	191154276	2966561	0.0155	0.1409
chr5	180915260	2749564	0.0152	0.13
chr6	171115067	2131766	0.0125	0.1471
chr7	159138663	2389417	0.015	0.19

chr8	146364022	4150362	0.0284	0.1968
chr9	141213431	1911258	0.0135	0.1575
chr10	135534747	2494010	0.0184	0.192
chr11	135006516	1553623	0.0115	0.1554
chr12	133851895	2266784	0.0169	0.1384
chr13	115169878	1240415	0.0108	0.1097
chr14	107349540	1108915	0.0103	0.1103
chr15	102531392	1171847	0.0114	0.1146
chr16	90354753	1251832	0.0139	0.1318
chr17	81195210	1492331	0.0184	0.148
chr18	78077248	1164736	0.0149	0.2702
chr19	59128983	821845	0.0139	0.2192
chr20	63025520	1461715	0.0232	0.1624
chr21	48129895	637470	0.0132	0.131
chr22	51304566	320033	0.0062	0.0818
chrMT	16571	3810	0.2299	0.4989
chrX	155270560	2913929	0.0188	0.1567
chrY	59373566	179227	0.003	0.1067

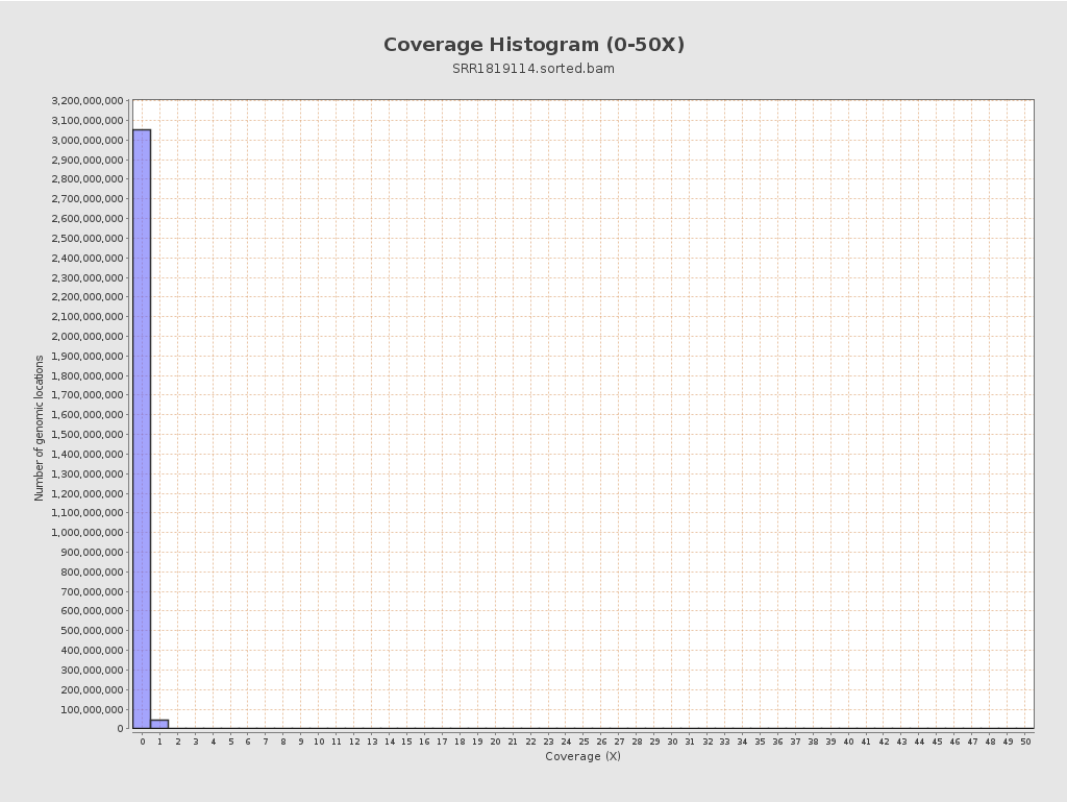
3. Results : Coverage across reference



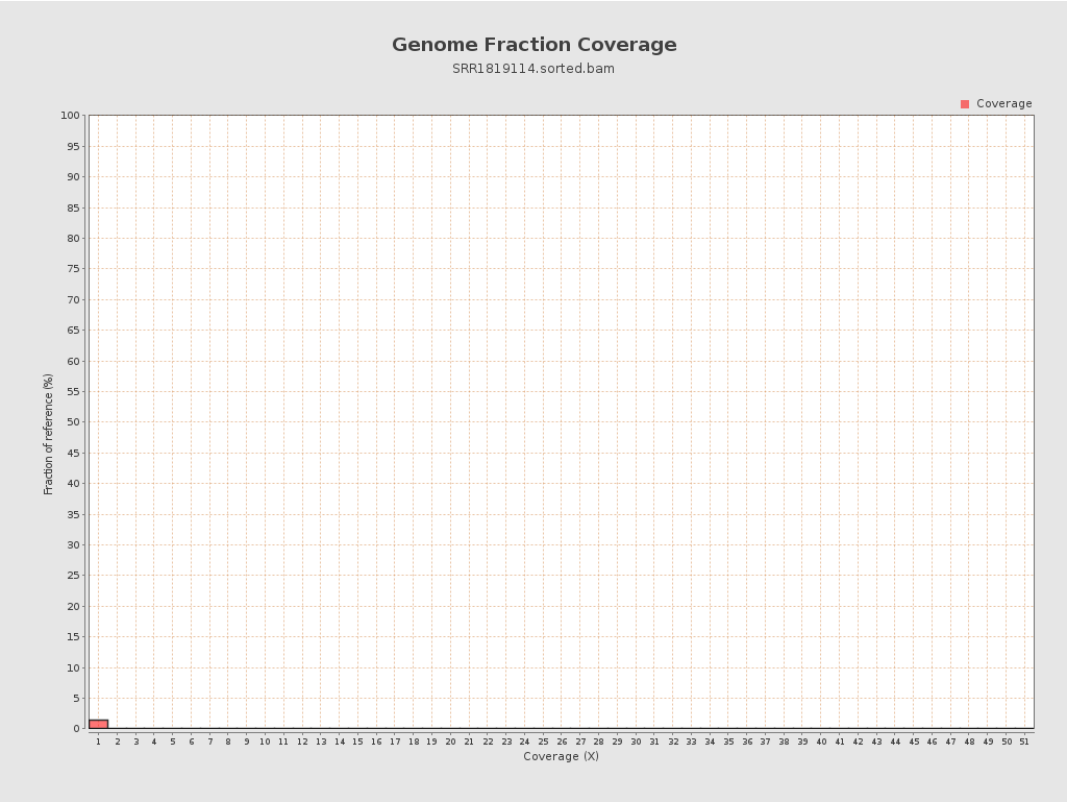
4. Results : Coverage Histogram



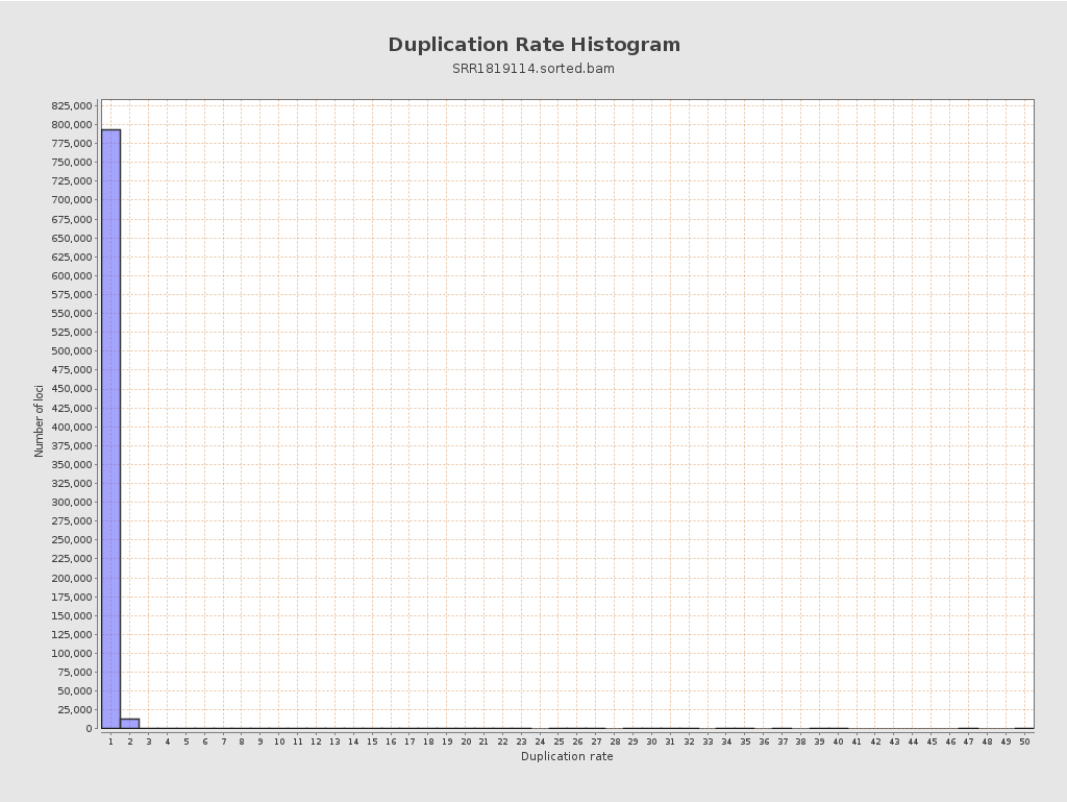
5. Results : Coverage Histogram (0-50X)



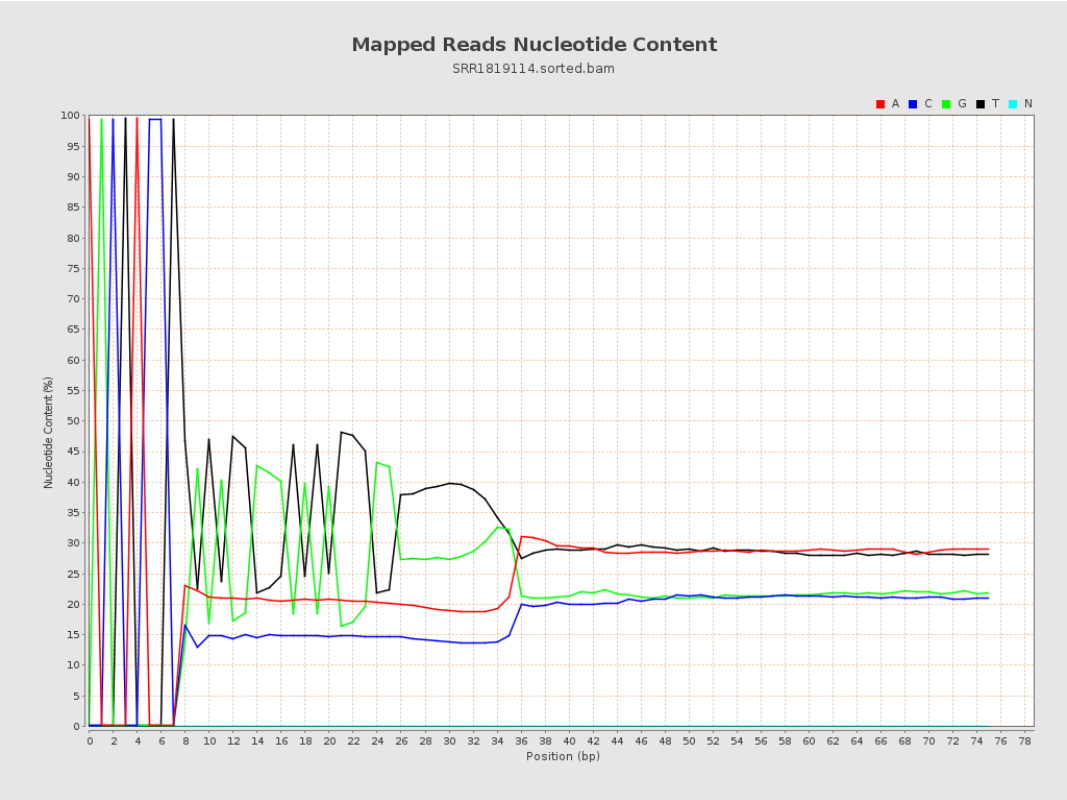
6. Results : Genome Fraction Coverage



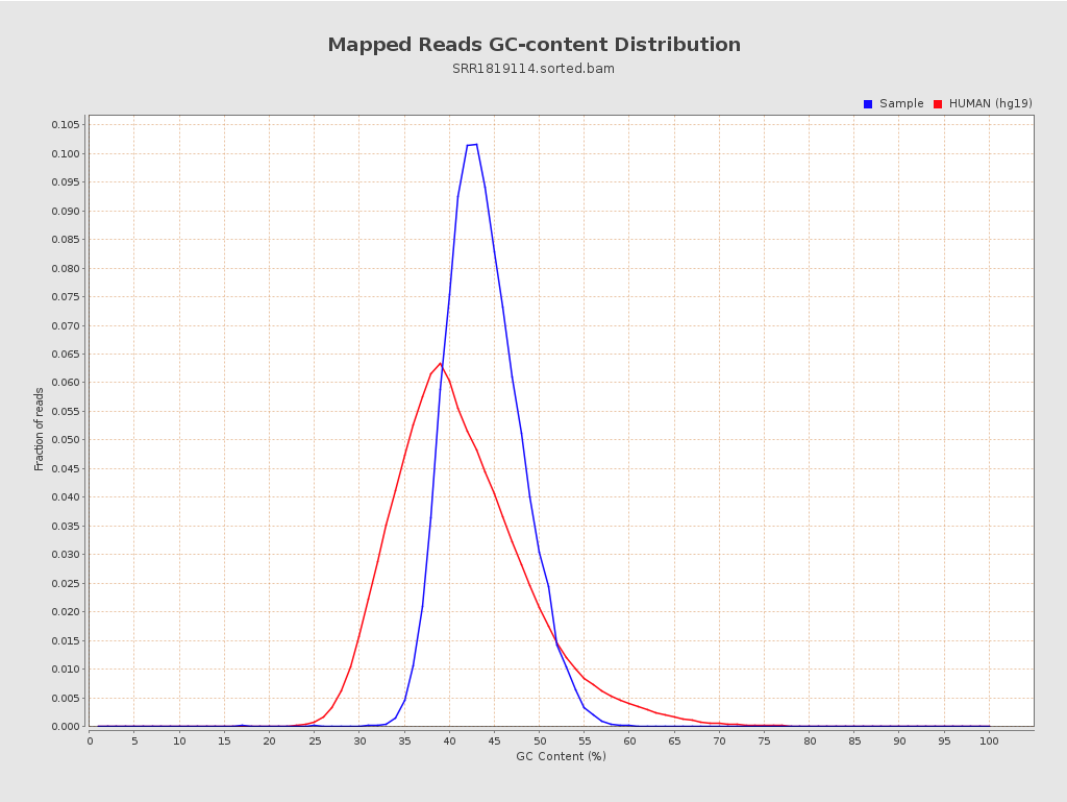
7. Results : Duplication Rate Histogram



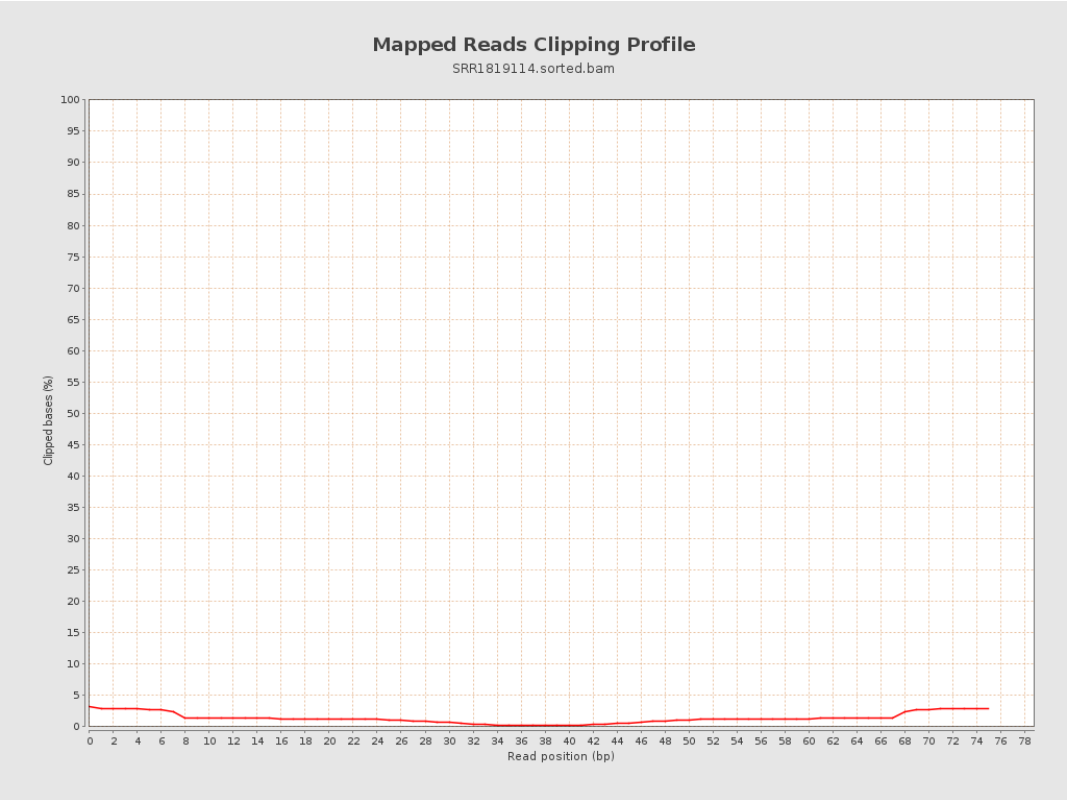
8. Results : Mapped Reads Nucleotide Content



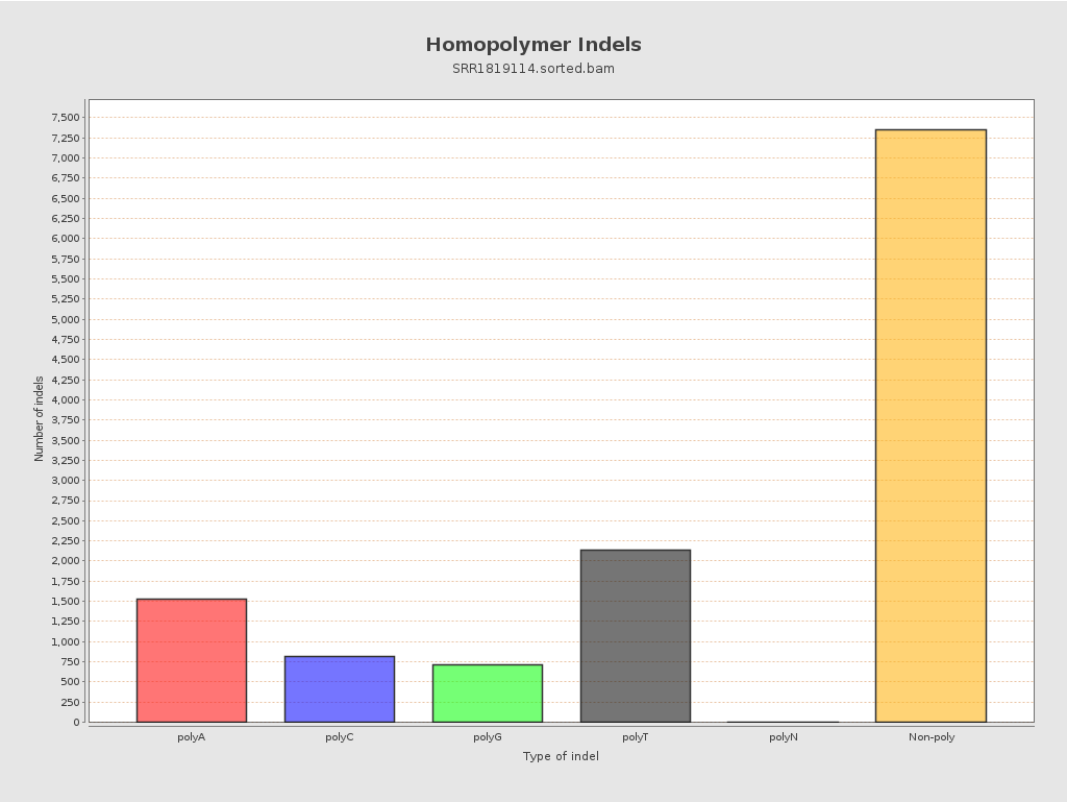
9. Results : Mapped Reads GC-content Distribution



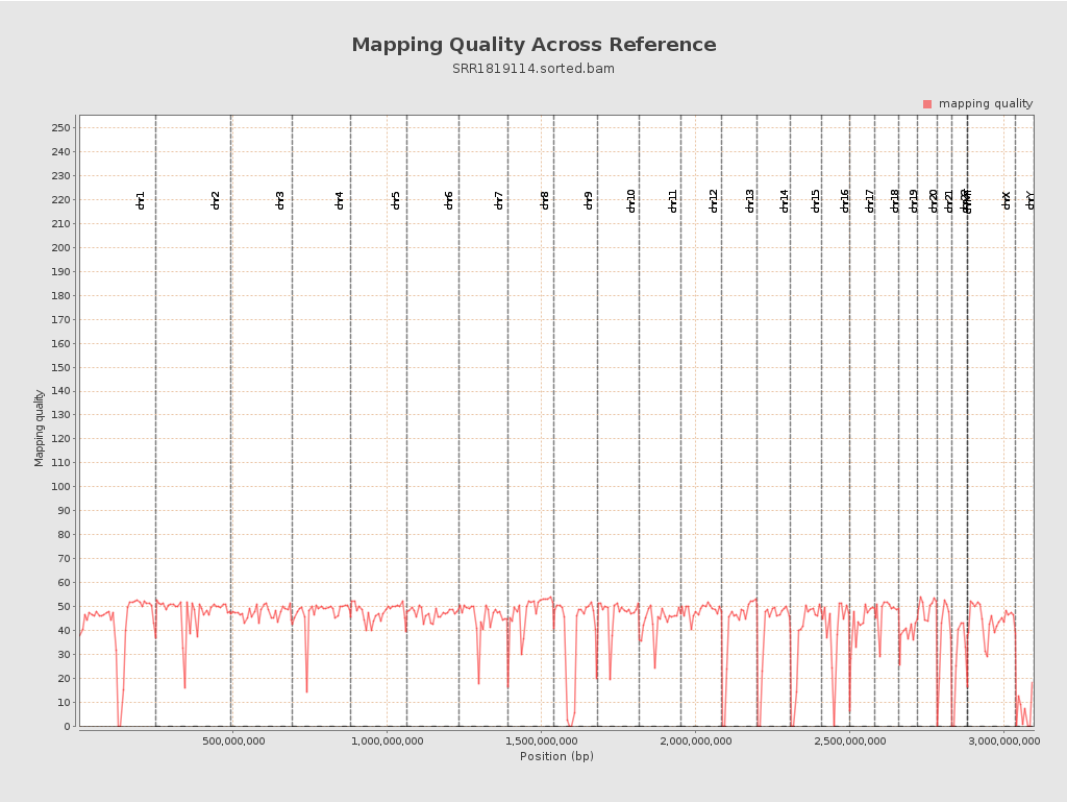
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram