Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 11:25:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818960.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_SRR1818960 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818960.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 11:25:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818960.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	454,210
Mapped reads	422,492 / 93.02%
Unmapped reads	31,718 / 6.98%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,271 / 1.38%
Read min/max/mean length	30 / 101 / 101.53
Duplicated reads (estimated)	66,371 / 14.61%
Duplication rate	13.77%
Clipped reads	427,198 / 94.05%

2.2. ACGT Content

Number/percentage of A's	11,360,933 / 29.17%
Number/percentage of C's	8,491,519 / 21.8%
Number/percentage of T's	11,224,291 / 28.82%
Number/percentage of G's	7,865,294 / 20.2%
Number/percentage of N's	1,838 / 0%
GC Percentage	42%

2.3. Coverage

Mean	0.0126

Standard Deviation	0.1839

2.4. Mapping Quality

Mean Mapping Quality	49.15

2.5. Mismatches and indels

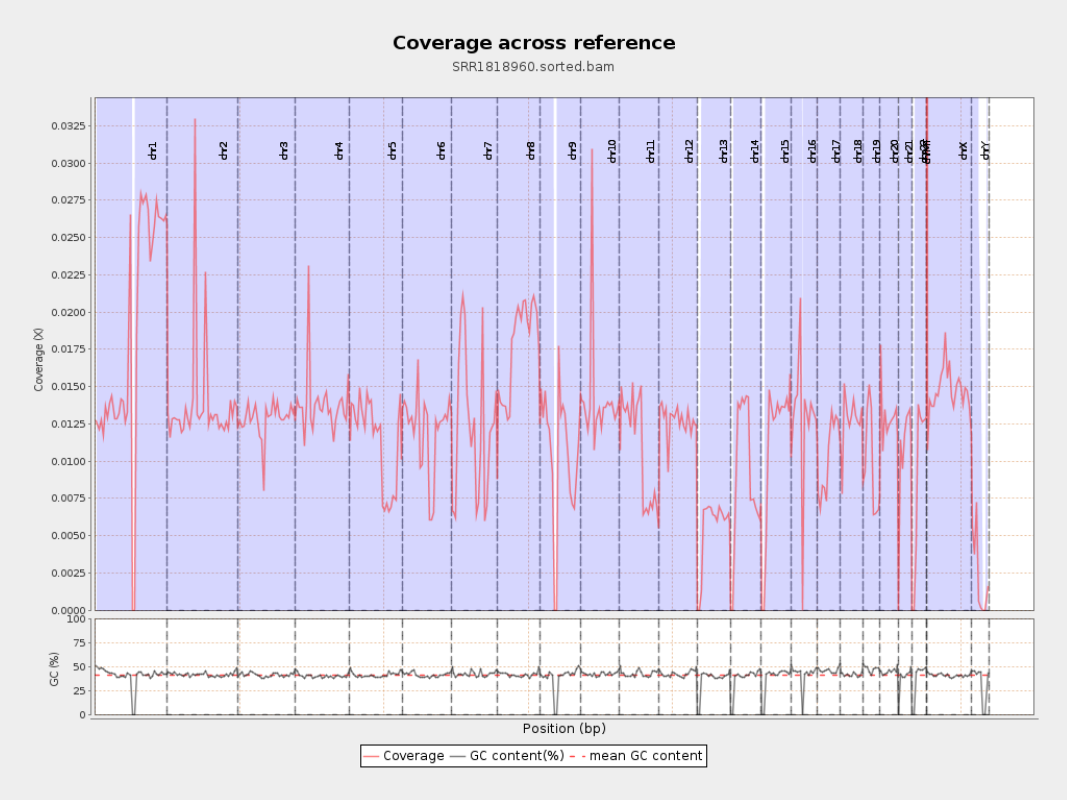
General error rate	0.75%
Mismatches	278,813
Insertions	5,268
Mapped reads with at least one insertion	1.21%
Deletions	12,234
Mapped reads with at least one deletion	2.83%
Homopolymer indels	43.04%

2.6. Chromosome stats

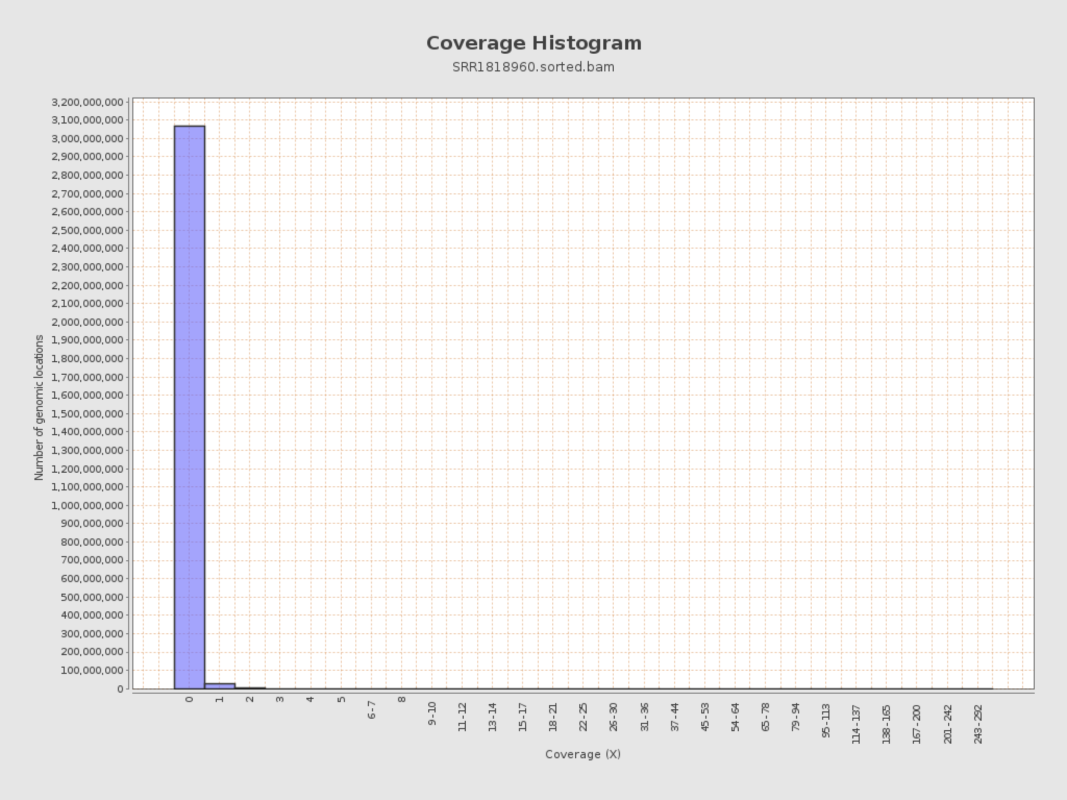
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4566938	0.0183	0.3064
chr2	243199373	3362374	0.0138	0.2377
chr3	198022430	2539350	0.0128	0.1375
chr4	191154276	2638917	0.0138	0.1506
chr5	180915260	2050840	0.0113	0.1322
chr6	171115067	2052162	0.012	0.1417
chr7	159138663	1963903	0.0123	0.1643

chr8	146364022	2593291	0.0177	0.1783
chr9	141213431	1468603	0.0104	0.1961
chr10	135534747	1929036	0.0142	0.2215
chr11	135006516	1481471	0.011	0.1443
chr12	133851895	1705173	0.0127	0.139
chr13	115169878	628524	0.0055	0.0879
chr14	107349540	967650	0.009	0.1233
chr15	102531392	1135643	0.0111	0.1281
chr16	90354753	1155547	0.0128	0.1824
chr17	81195210	828052	0.0102	0.1309
chr18	78077248	982886	0.0126	0.2255
chr19	59128983	590596	0.01	0.2724
chr20	63025520	817867	0.013	0.1446
chr21	48129895	515633	0.0107	0.136
chr22	51304566	464057	0.009	0.1199
chrMT	16571	103865	6.2679	4.9825
chrX	155270560	2290807	0.0148	0.1674
chrY	59373566	132847	0.0022	0.1397

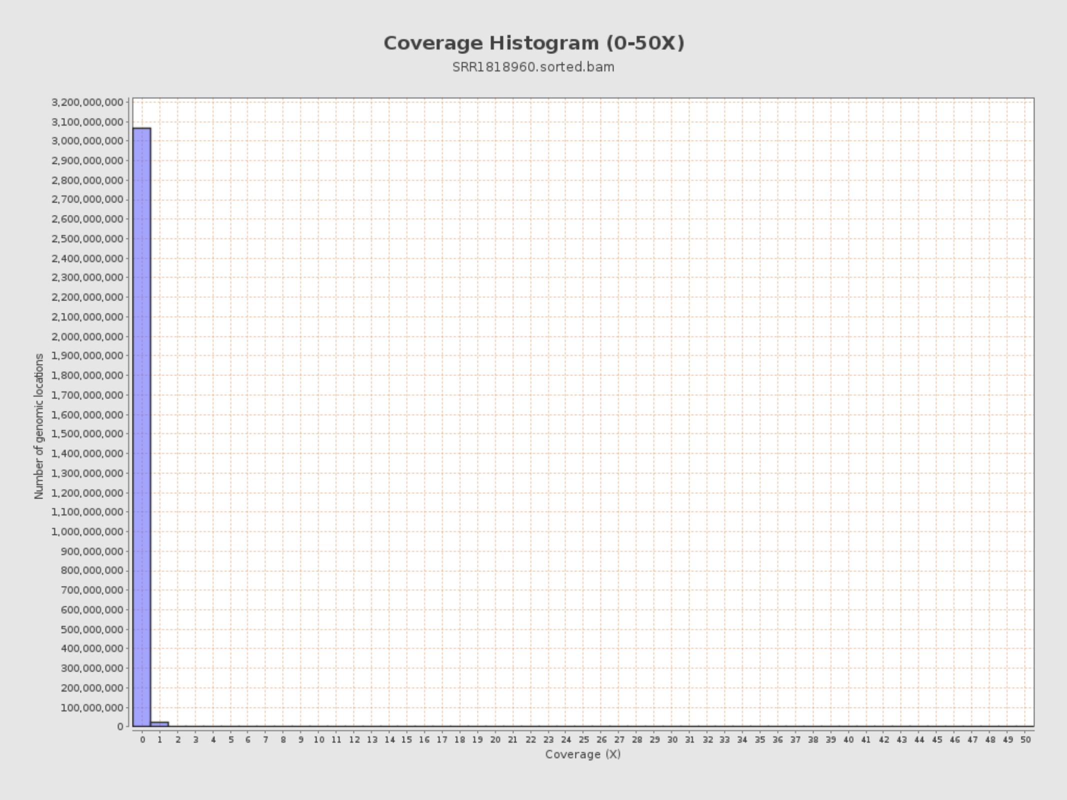
3. Results : Coverage across reference



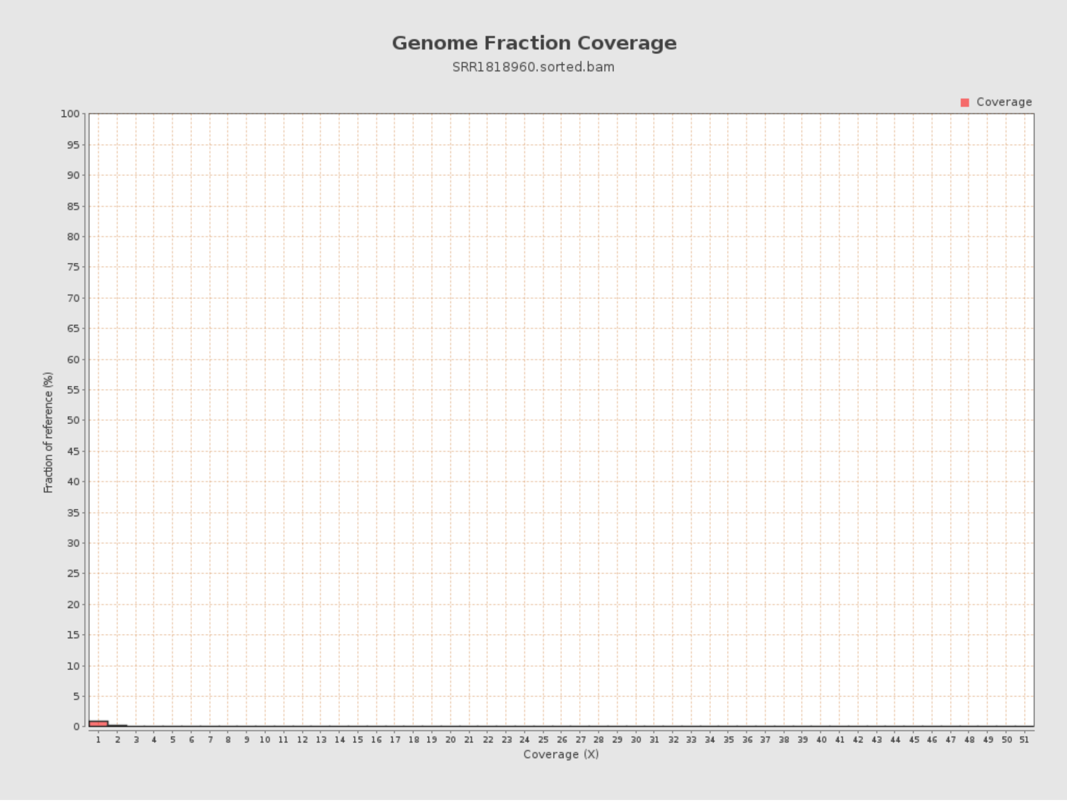
4. Results : Coverage Histogram



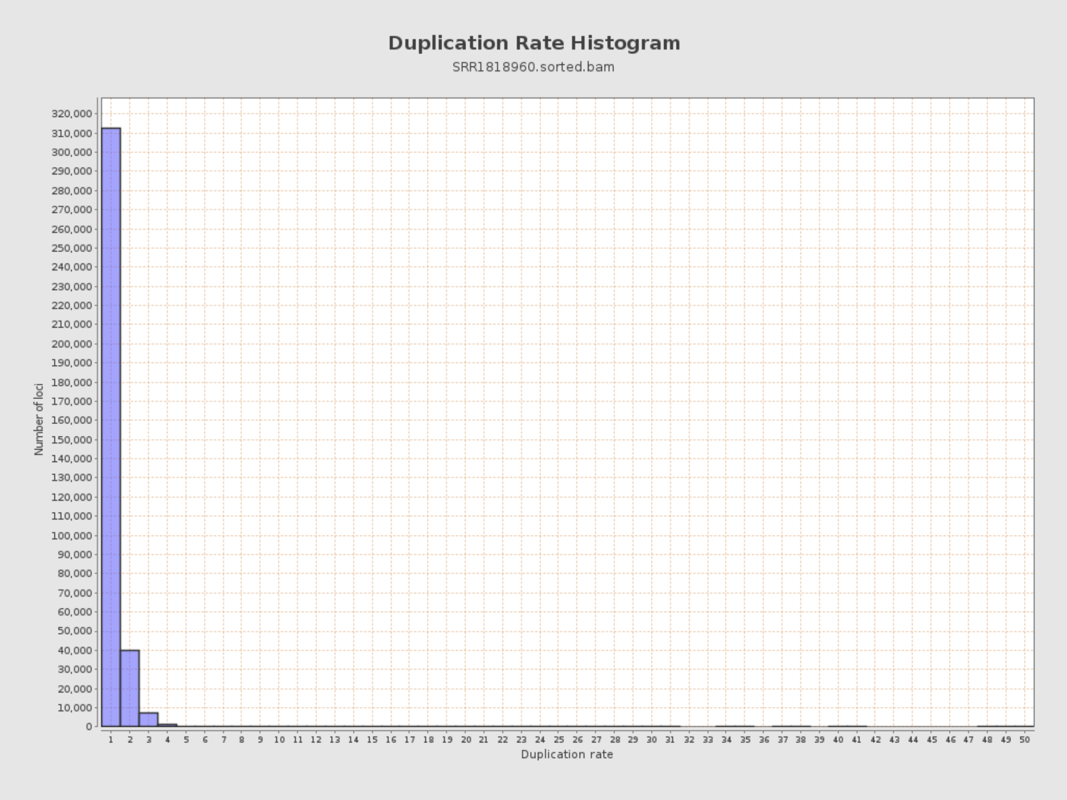
5. Results : Coverage Histogram (0-50X)



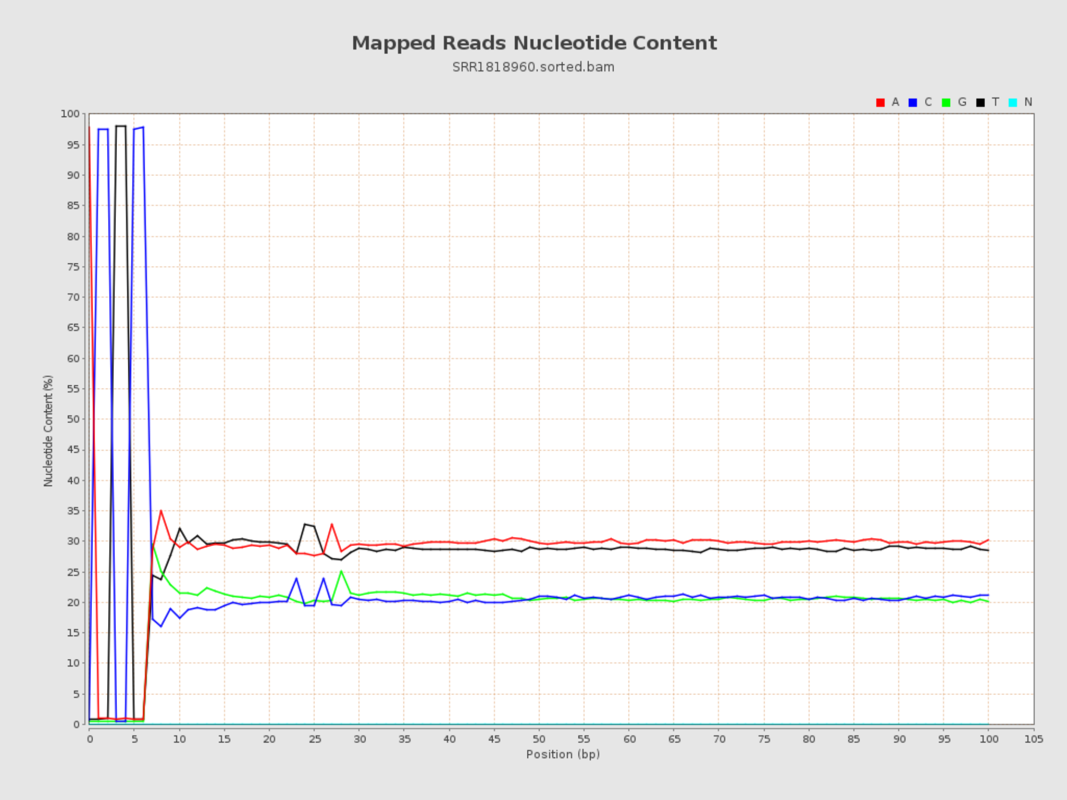
6. Results : Genome Fraction Coverage



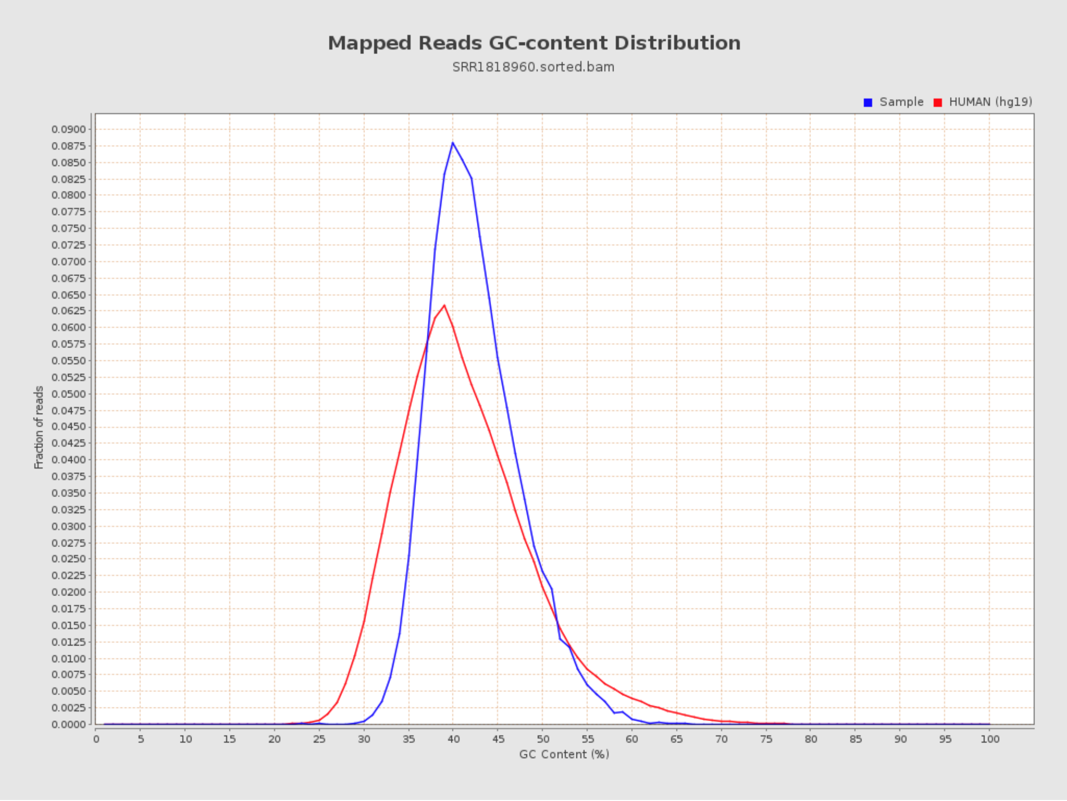
7. Results : Duplication Rate Histogram



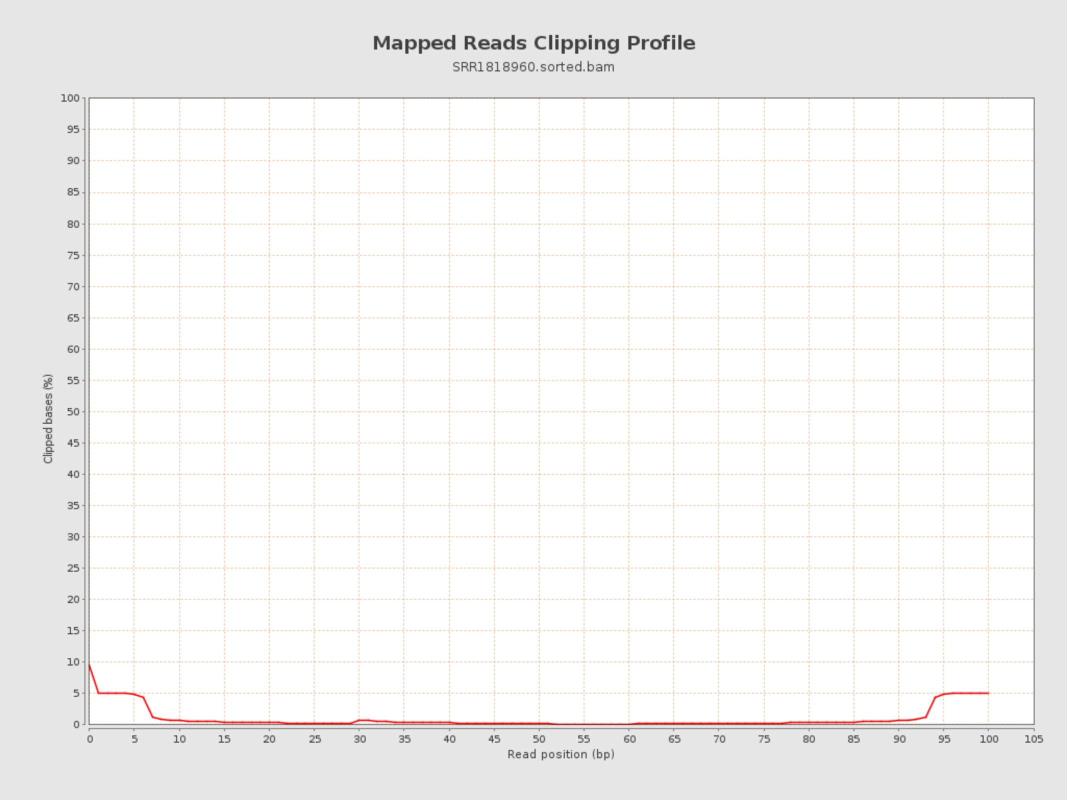
8. Results : Mapped Reads Nucleotide Content



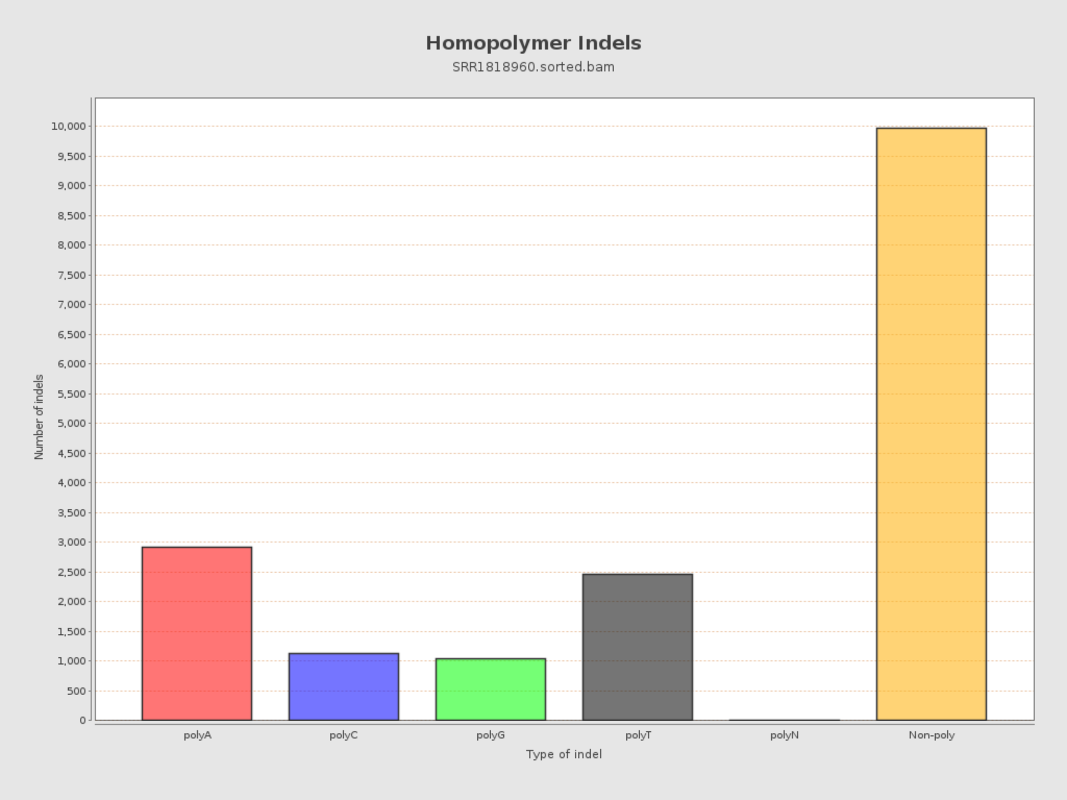
9. Results : Mapped Reads GC-content Distribution



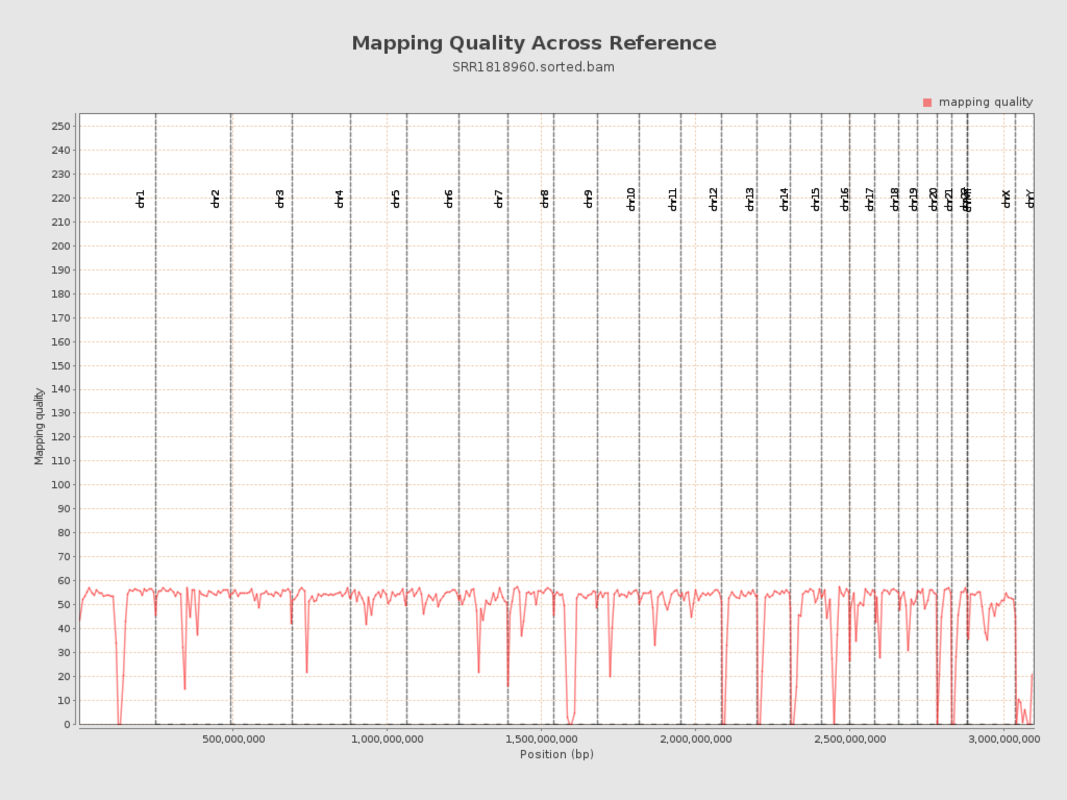
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram