Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 01:08:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1819120.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_SRR1819120 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1819120.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 01:08:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1819120.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,810,377
Mapped reads	1,650,346 / 91.16%
Unmapped reads	160,031 / 8.84%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,680 / 0.31%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	77,945 / 4.31%
Duplication rate	3.56%
Clipped reads	1,651,615 / 91.23%

2.2. ACGT Content

Number/percentage of A's	23,404,633 / 24.49%
Number/percentage of C's	16,988,472 / 17.77%
Number/percentage of T's	31,608,210 / 33.07%
Number/percentage of G's	23,578,289 / 24.67%
Number/percentage of N's	1,362 / 0%
GC Percentage	42.44%

2.3. Coverage

Mean	0.0309

Standard Deviation	0.294

2.4. Mapping Quality

Mean Mapping Quality	44.8

2.5. Mismatches and indels

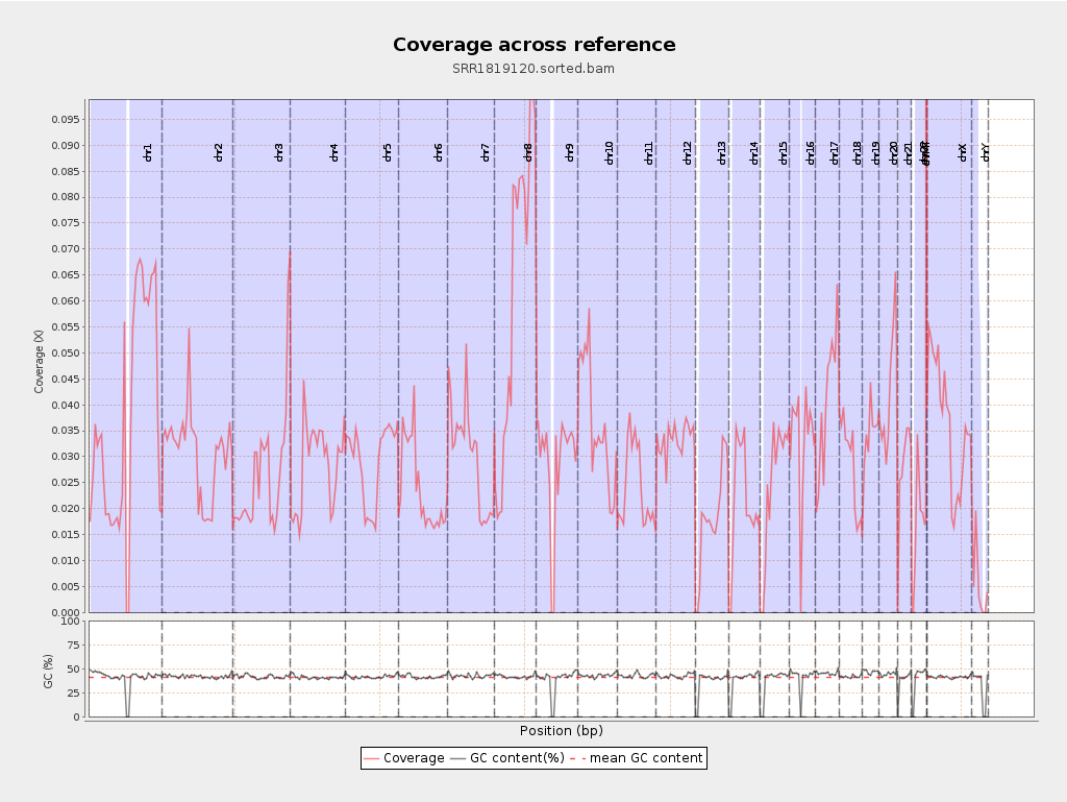
General error rate	0.52%
Mismatches	488,798
Insertions	6,623
Mapped reads with at least one insertion	0.4%
Deletions	17,309
Mapped reads with at least one deletion	1.04%
Homopolymer indels	43.16%

2.6. Chromosome stats

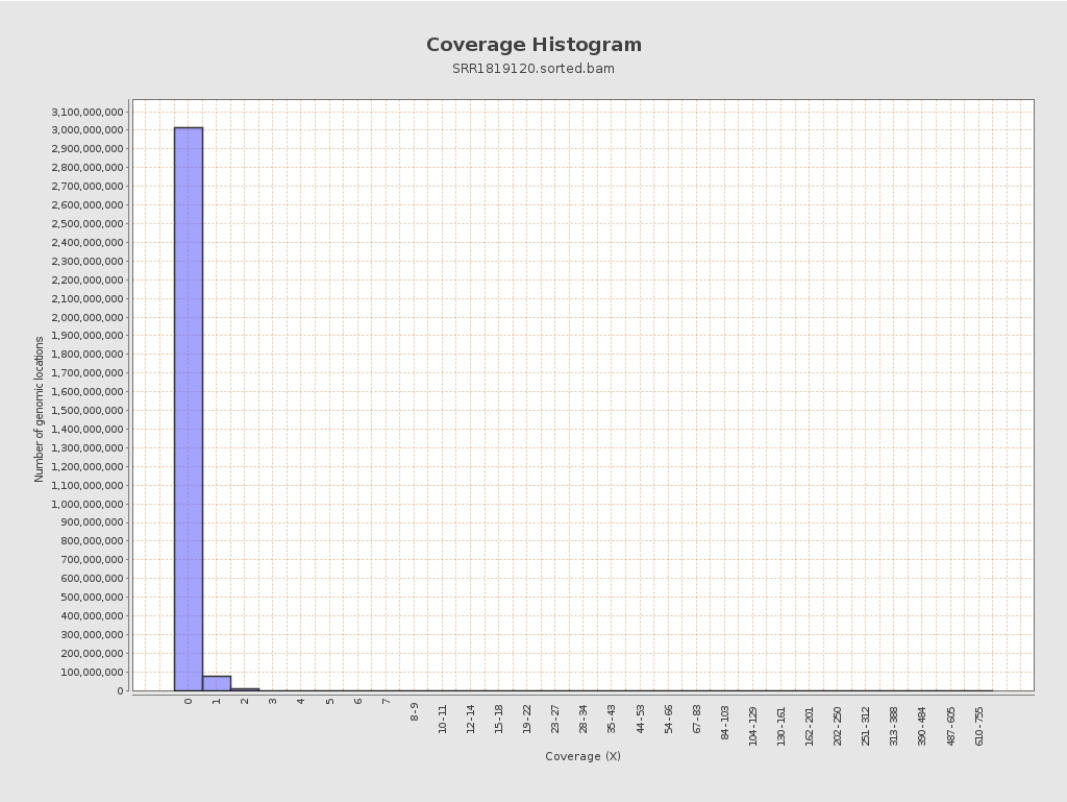
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	9315372	0.0374	0.5618
chr2	243199373	7482159	0.0308	0.3354
chr3	198022430	5132442	0.0259	0.1824
chr4	191154276	5413905	0.0283	0.2179
chr5	180915260	5258064	0.0291	0.1908
chr6	171115067	4062095	0.0237	0.2198
chr7	159138663	4787264	0.0301	0.3548

chr8	146364022	9102507	0.0622	0.3311
chr9	141213431	4034835	0.0286	0.2471
chr10	135534747	4910156	0.0362	0.2941
chr11	135006516	3258925	0.0241	0.2673
chr12	133851895	4473373	0.0334	0.2055
chr13	115169878	2110113	0.0183	0.1513
chr14	107349540	2272658	0.0212	0.1672
chr15	102531392	2516803	0.0245	0.1786
chr16	90354753	2998374	0.0332	0.2194
chr17	81195210	3348996	0.0412	0.2381
chr18	78077248	2245630	0.0288	0.4496
chr19	59128983	2028836	0.0343	0.3826
chr20	63025520	2688734	0.0427	0.2346
chr21	48129895	1341847	0.0279	0.2067
chr22	51304566	822027	0.016	0.1397
chrMT	16571	6611	0.3989	0.7537
chrX	155270560	5673393	0.0365	0.2338
chrY	59373566	324480	0.0055	0.17

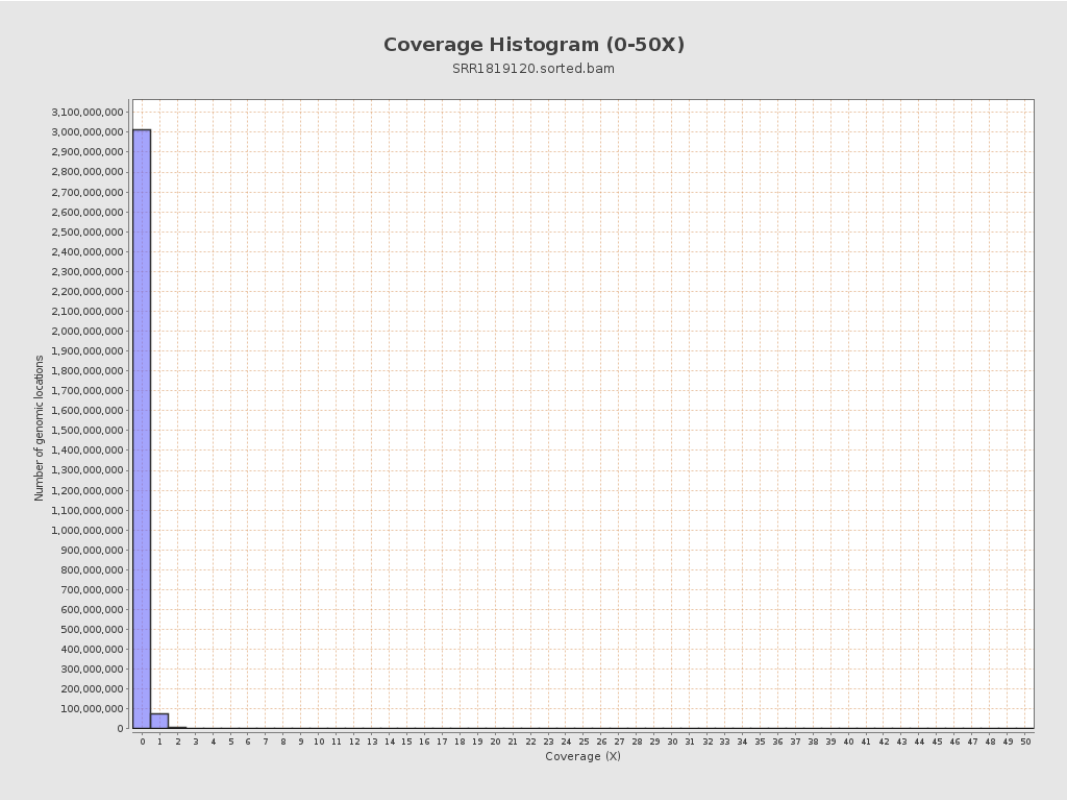
3. Results : Coverage across reference



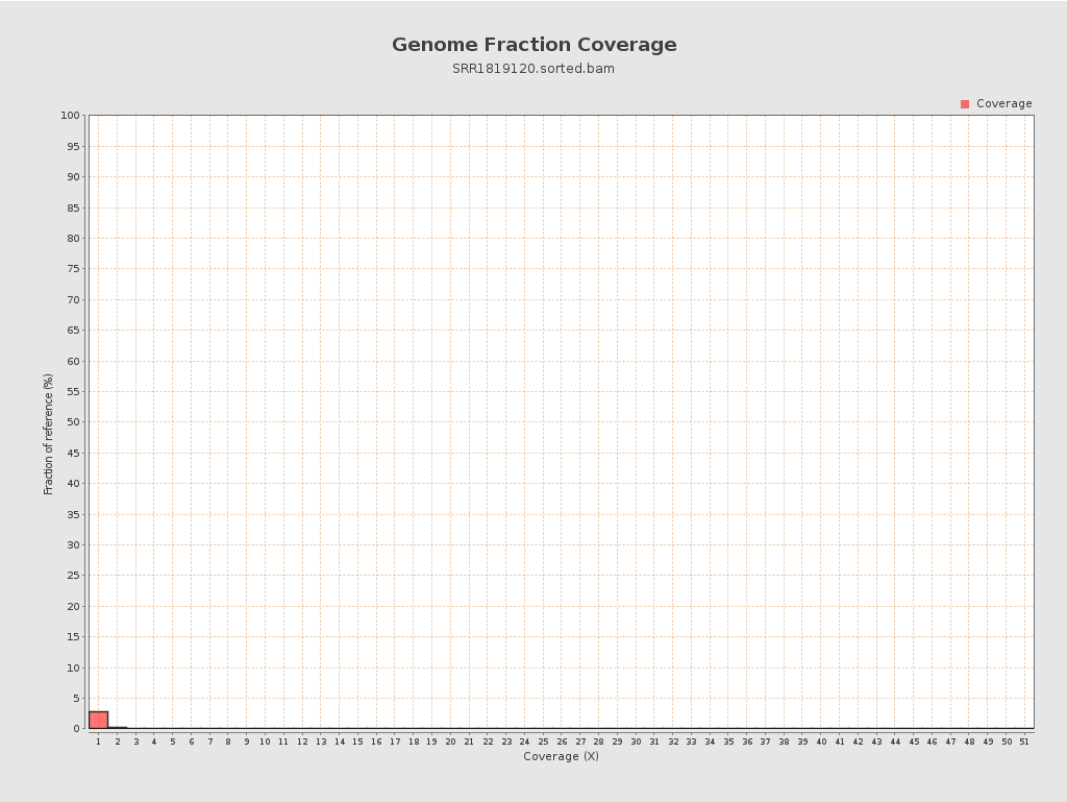
4. Results : Coverage Histogram



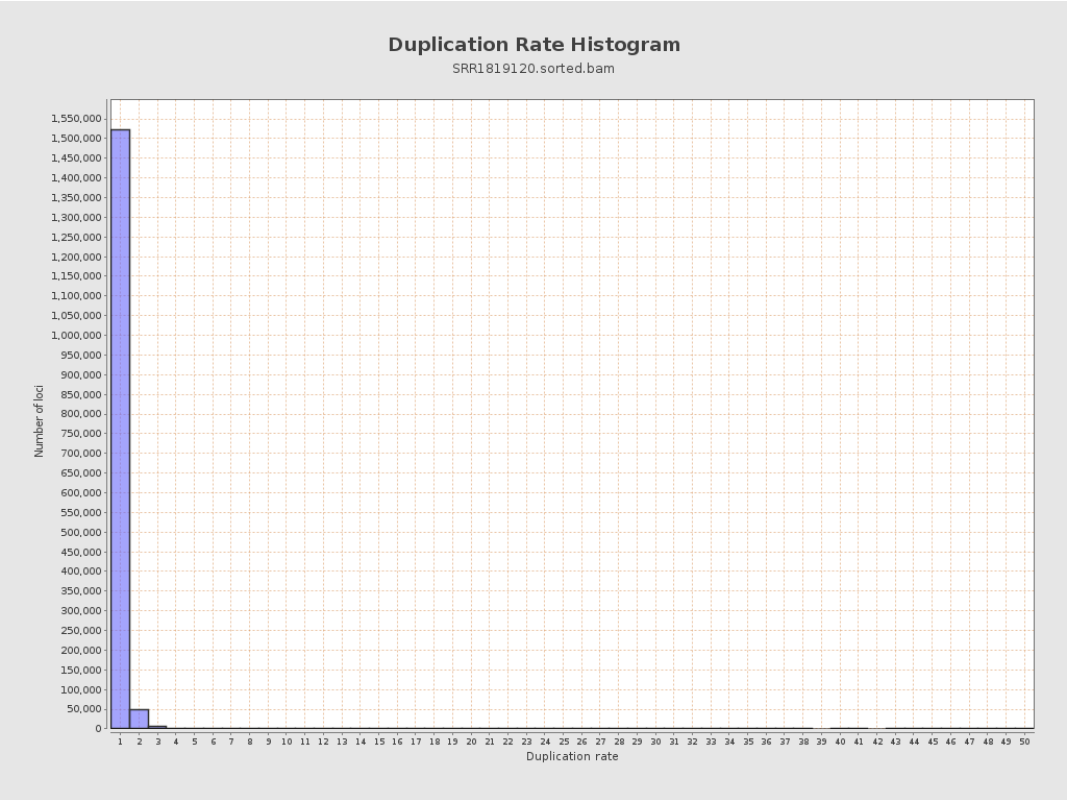
5. Results : Coverage Histogram (0-50X)



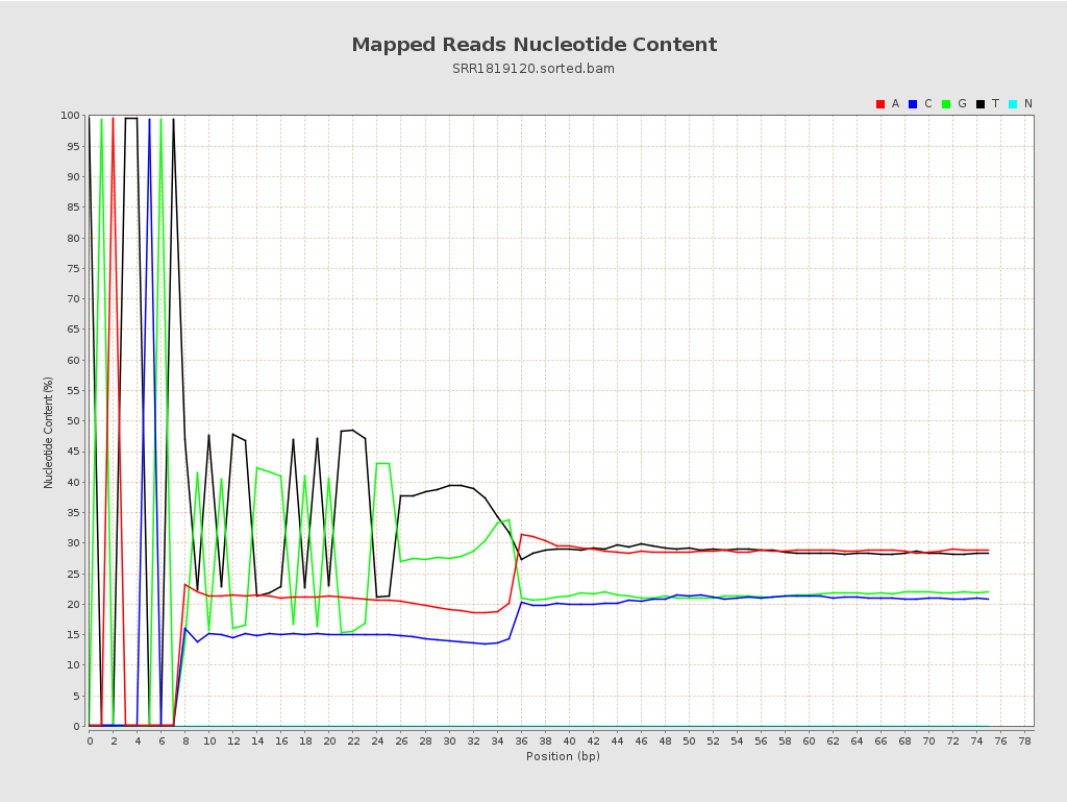
6. Results : Genome Fraction Coverage



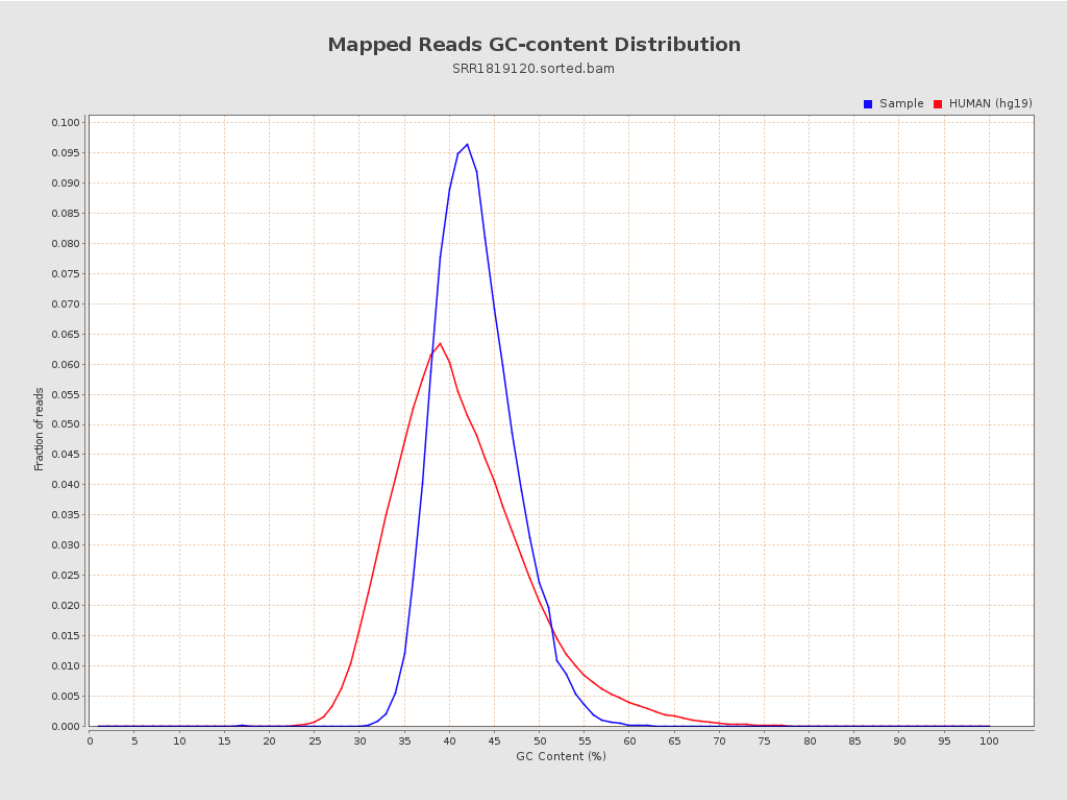
7. Results : Duplication Rate Histogram



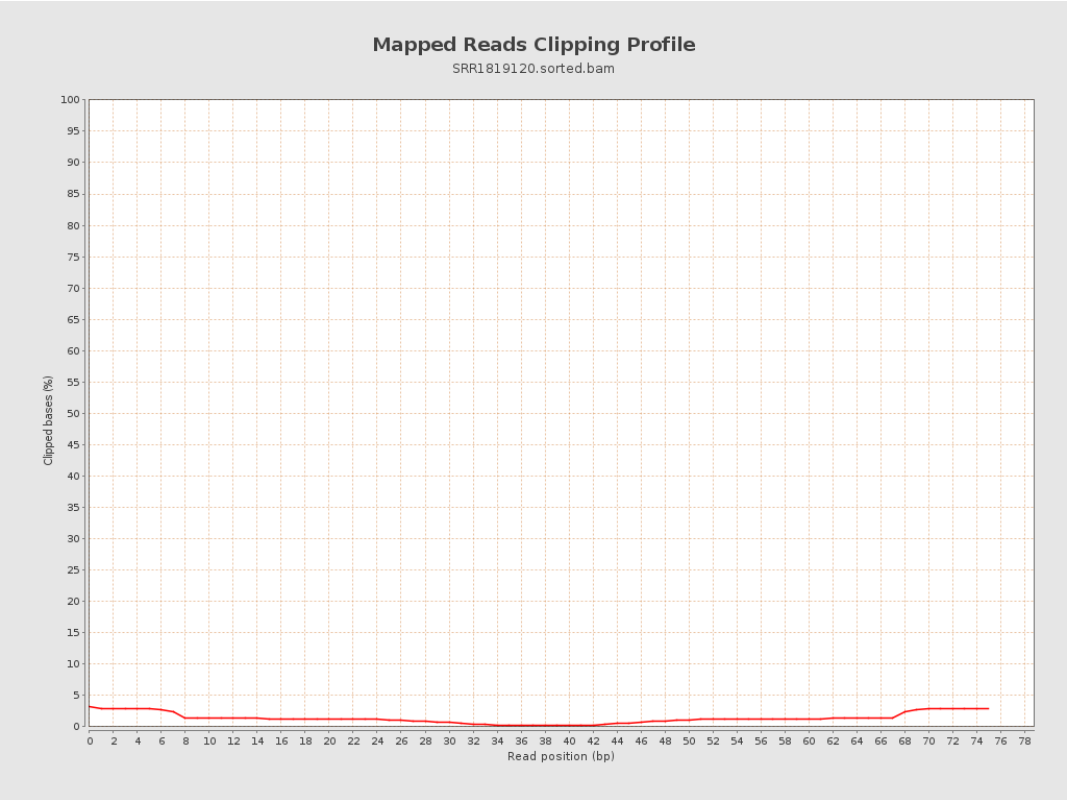
8. Results : Mapped Reads Nucleotide Content



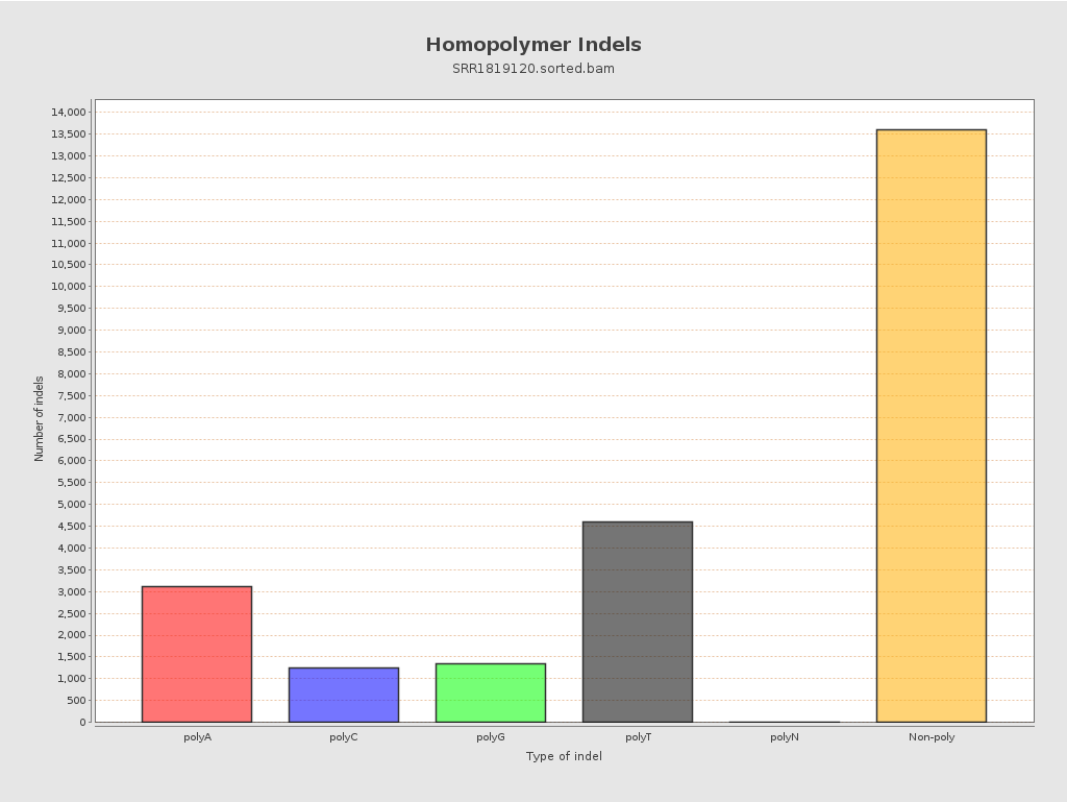
9. Results : Mapped Reads GC-content Distribution



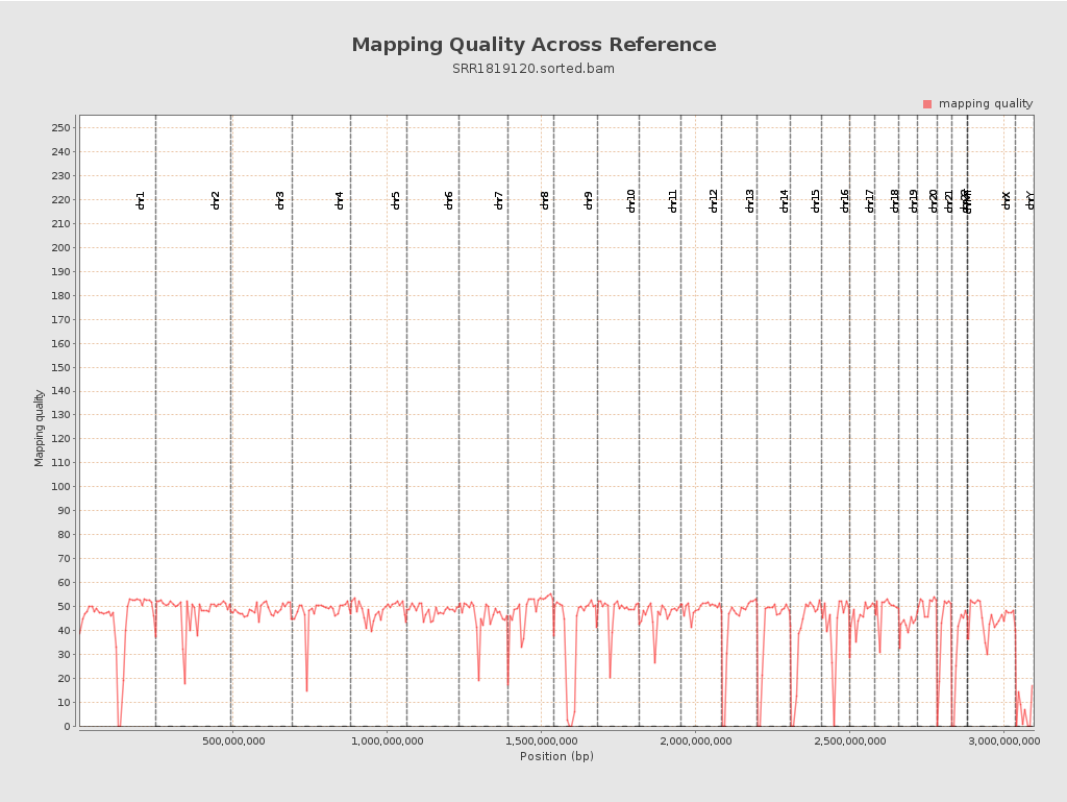
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram