Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 16:18:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818818.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_SRR1818818 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818818.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 16:18:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818818.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,247,182
Mapped reads	3,159,983 / 97.31%
Unmapped reads	87,199 / 2.69%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	27,152 / 0.84%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	2,122,310 / 65.36%
Duplication rate	50.59%
Clipped reads	3,150,052 / 97.01%

2.2. ACGT Content

Number/percentage of A's	63,914,512 / 29.76%
Number/percentage of C's	44,796,779 / 20.86%
Number/percentage of T's	60,115,010 / 27.99%
Number/percentage of G's	45,896,236 / 21.37%
Number/percentage of N's	12,825 / 0.01%
GC Percentage	42.23%

2.3. Coverage

Mean	0.0694

Standard Deviation	0.9392

2.4. Mapping Quality

Mean Mapping Quality	48.14

2.5. Mismatches and indels

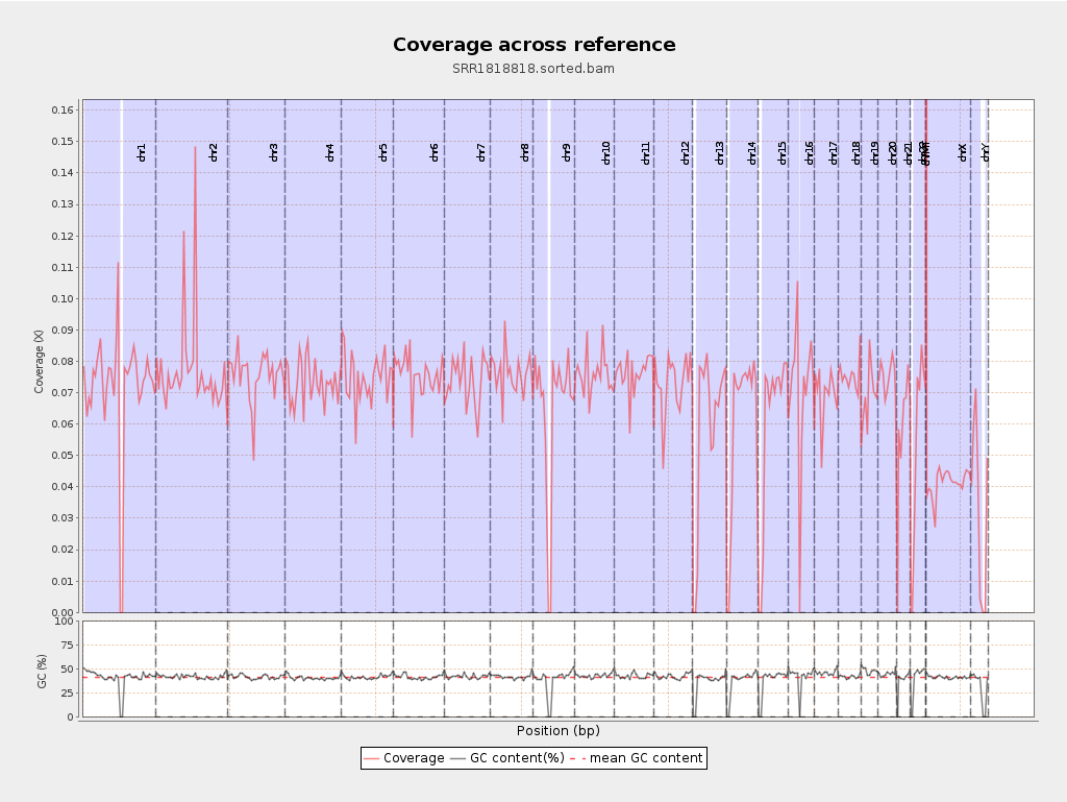
General error rate	0.54%
Mismatches	1,092,767
Insertions	28,340
Mapped reads with at least one insertion	0.89%
Deletions	54,727
Mapped reads with at least one deletion	1.72%
Homopolymer indels	39.95%

2.6. Chromosome stats

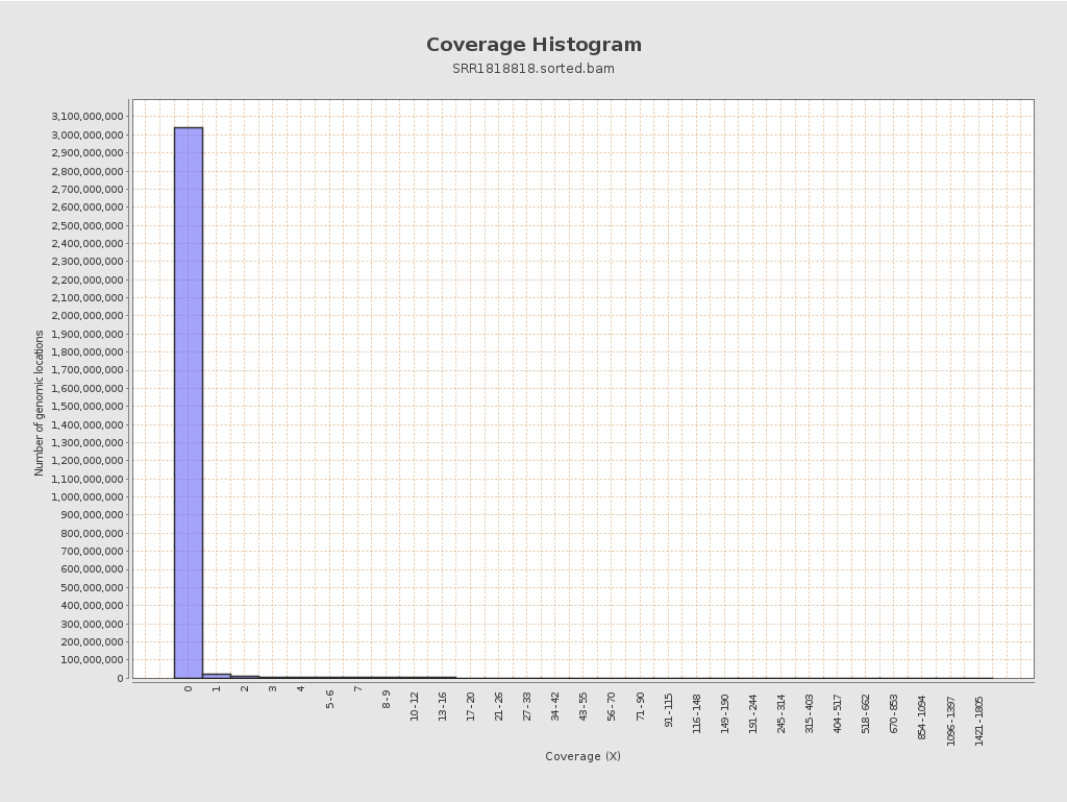
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	17817373	0.0715	1.1705
chr2	243199373	18792134	0.0773	1.4811
chr3	198022430	14922089	0.0754	0.7857
chr4	191154276	14021494	0.0734	0.8331
chr5	180915260	13551533	0.0749	0.8024
chr6	171115067	12978021	0.0758	0.8294
chr7	159138663	11729205	0.0737	0.8657

chr8	146364022	11109511	0.0759	0.8524
chr9	141213431	9159320	0.0649	0.7937
chr10	135534747	10292358	0.0759	0.9639
chr11	135006516	10291282	0.0762	0.8496
chr12	133851895	9825924	0.0734	0.801
chr13	115169878	6795007	0.059	0.6988
chr14	107349540	6656054	0.062	0.7686
chr15	102531392	6084692	0.0593	0.6962
chr16	90354753	6283472	0.0695	0.9748
chr17	81195210	5676869	0.0699	0.7961
chr18	78077248	5859577	0.075	0.9344
chr19	59128983	4105511	0.0694	1.0134
chr20	63025520	4769988	0.0757	0.8383
chr21	48129895	2832002	0.0588	0.7125
chr22	51304566	2731058	0.0532	0.7229
chrMT	16571	151435	9.1386	11.0275
chrX	155270560	6390889	0.0412	0.6021
chrY	59373566	1994477	0.0336	1.5976

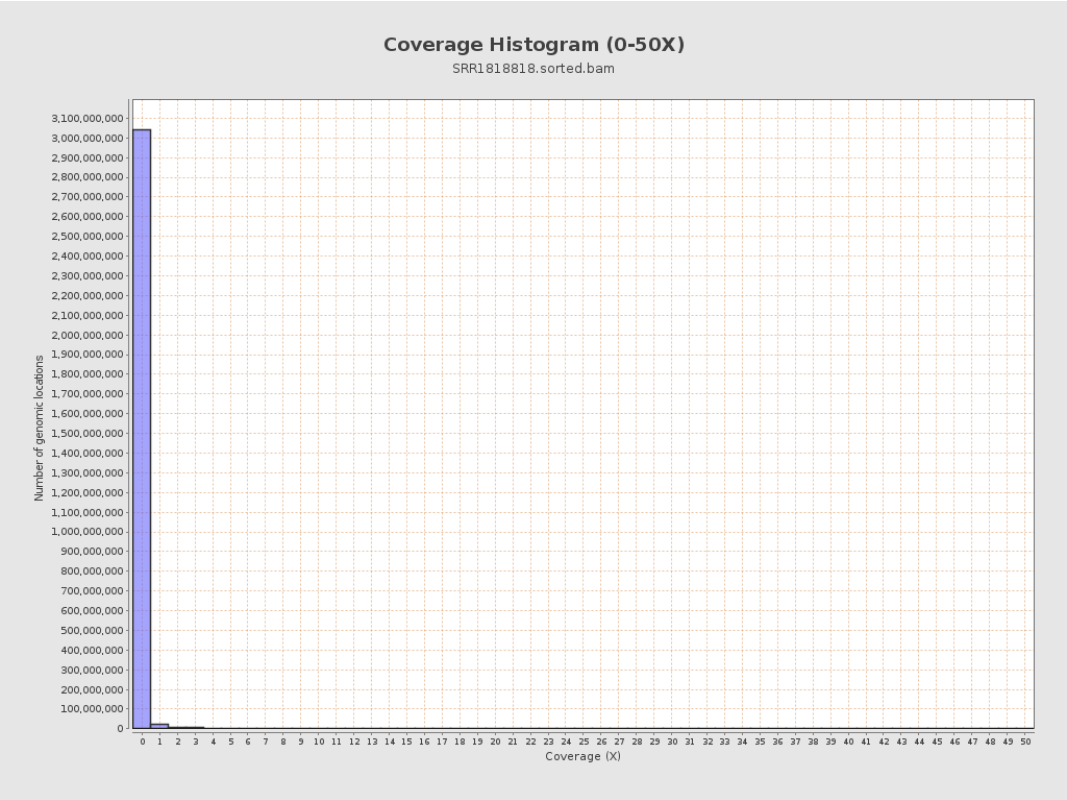
3. Results : Coverage across reference



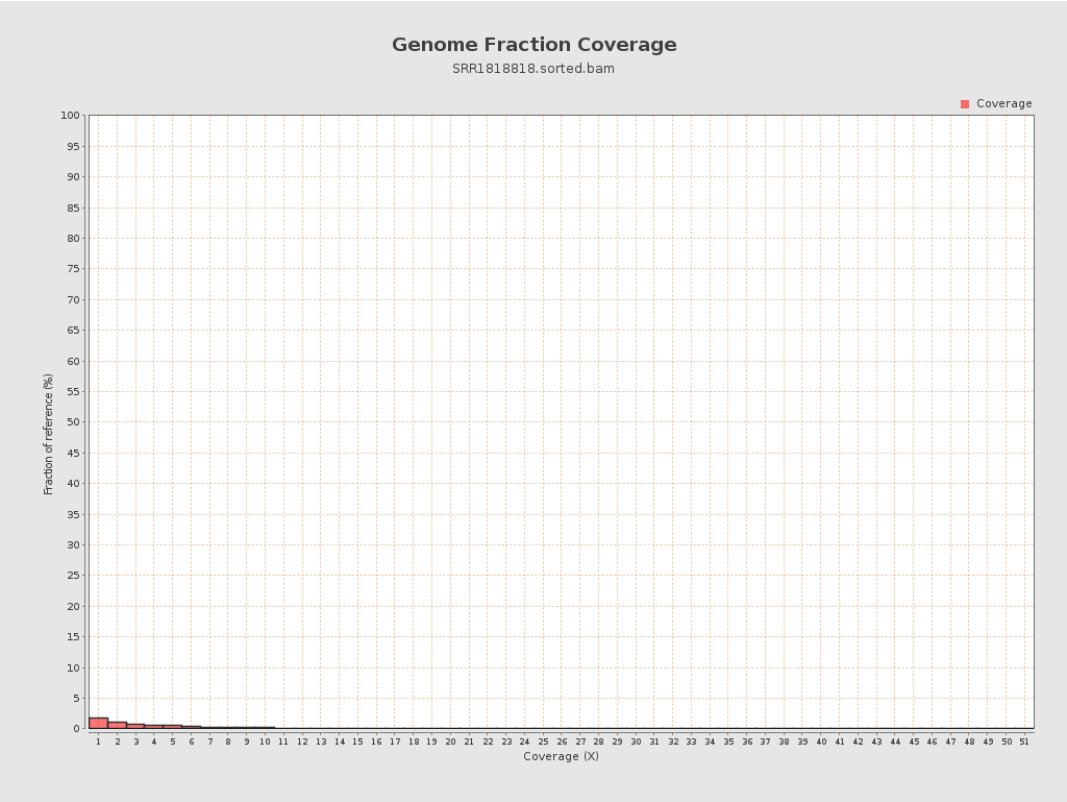
4. Results : Coverage Histogram



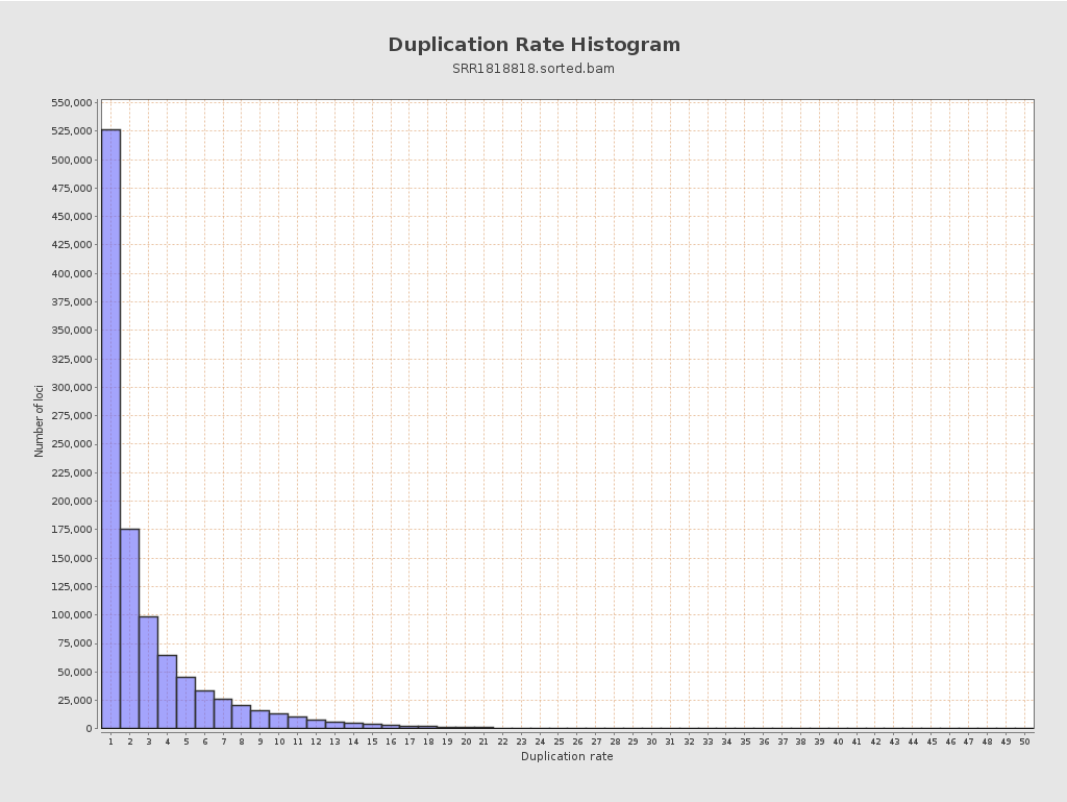
5. Results : Coverage Histogram (0-50X)



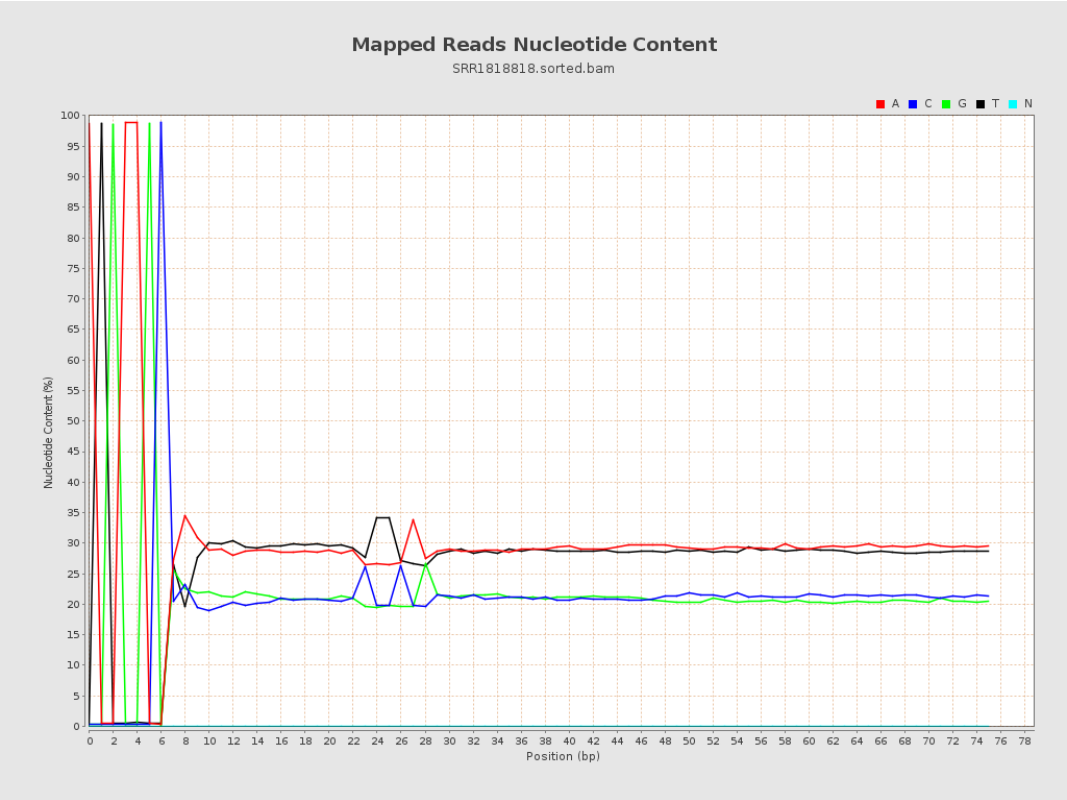
6. Results : Genome Fraction Coverage



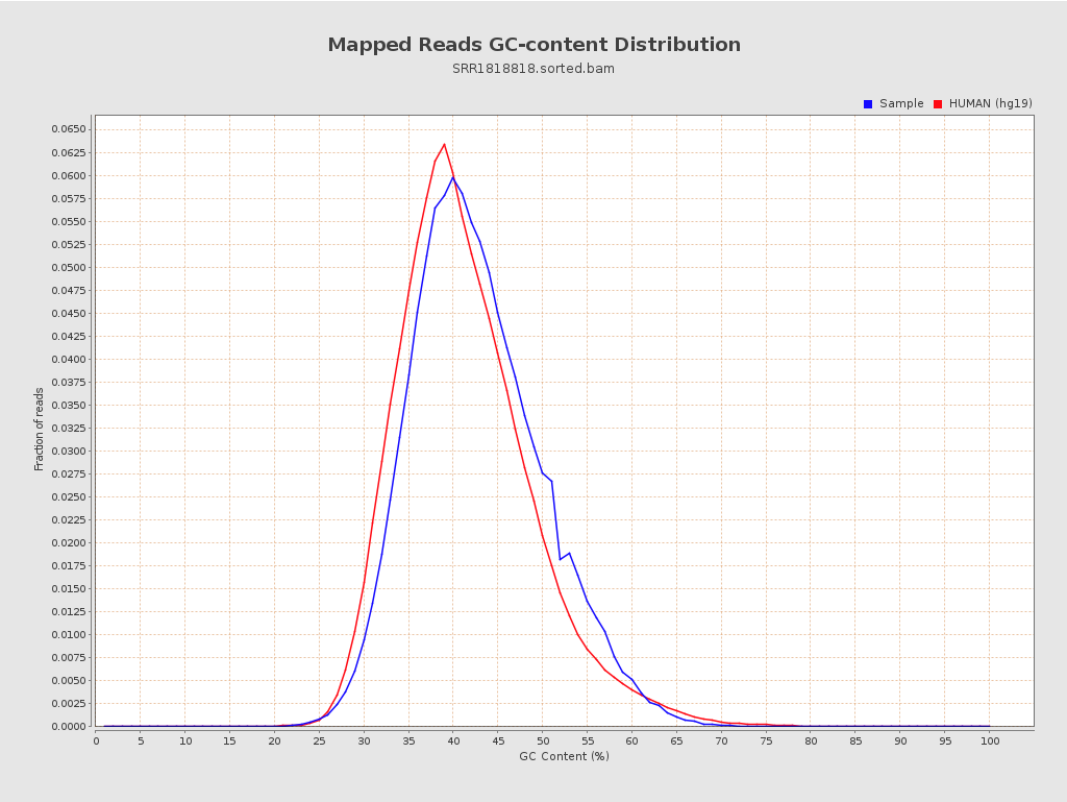
7. Results : Duplication Rate Histogram



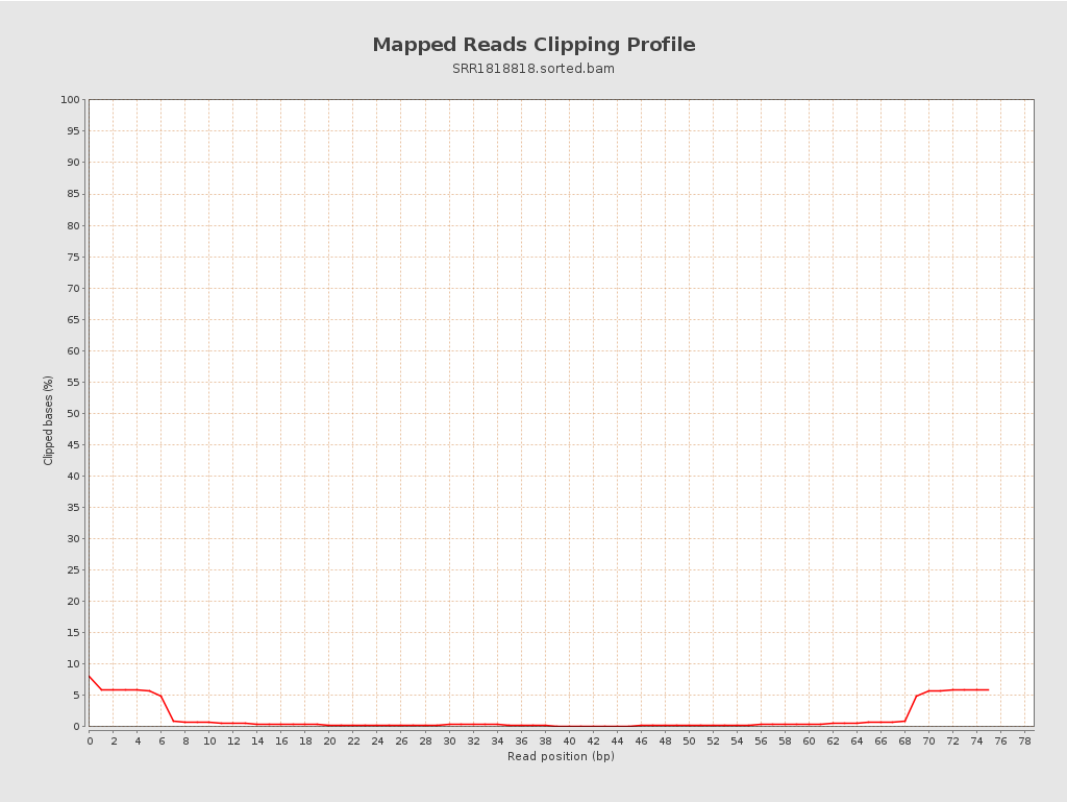
8. Results : Mapped Reads Nucleotide Content



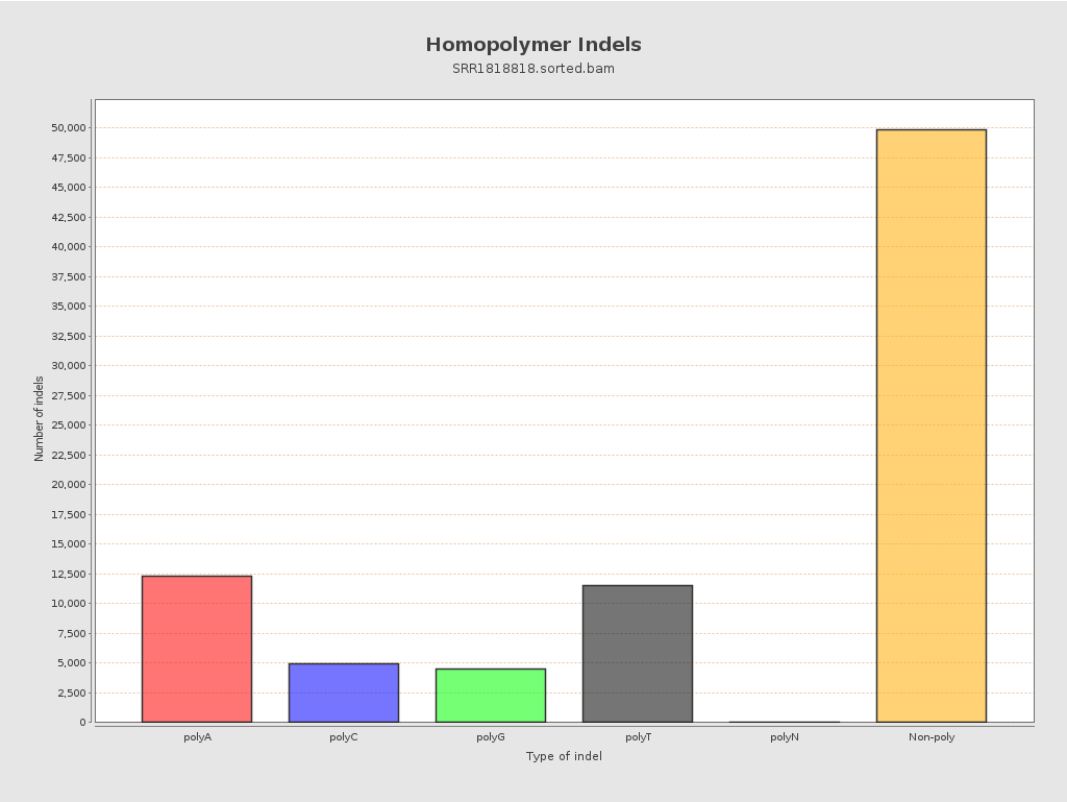
9. Results : Mapped Reads GC-content Distribution



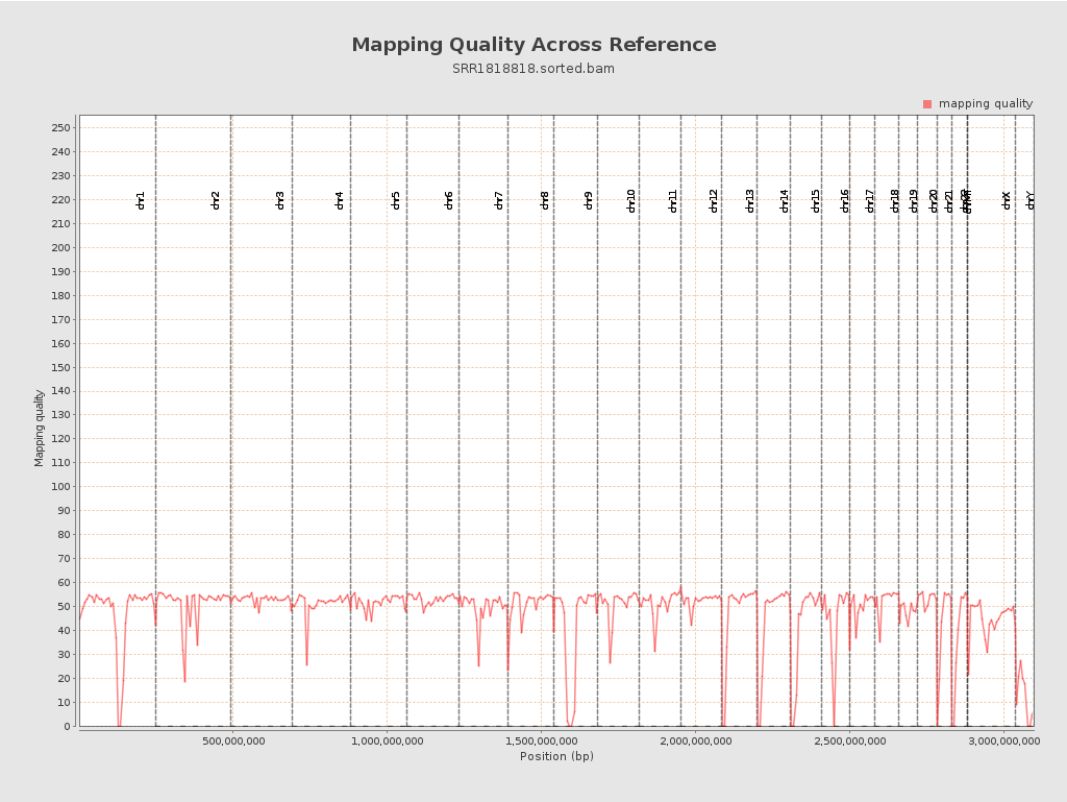
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram