Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 18:18:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818828.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_SRR1818828 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818828.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 18:18:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818828.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,284,291
Mapped reads	2,229,905 / 97.62%
Unmapped reads	54,386 / 2.38%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,699 / 0.73%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	1,087,873 / 47.62%
Duplication rate	40.56%
Clipped reads	2,227,358 / 97.51%

2.2. ACGT Content

Number/percentage of A's	42,486,328 / 28.02%
Number/percentage of C's	32,158,201 / 21.21%
Number/percentage of T's	43,794,079 / 28.88%
Number/percentage of G's	33,193,002 / 21.89%
Number/percentage of N's	9,084 / 0.01%
GC Percentage	43.1%

2.3. Coverage

Mean	0.049

Standard Deviation	0.6045

2.4. Mapping Quality

Mean Mapping Quality	47.77

2.5. Mismatches and indels

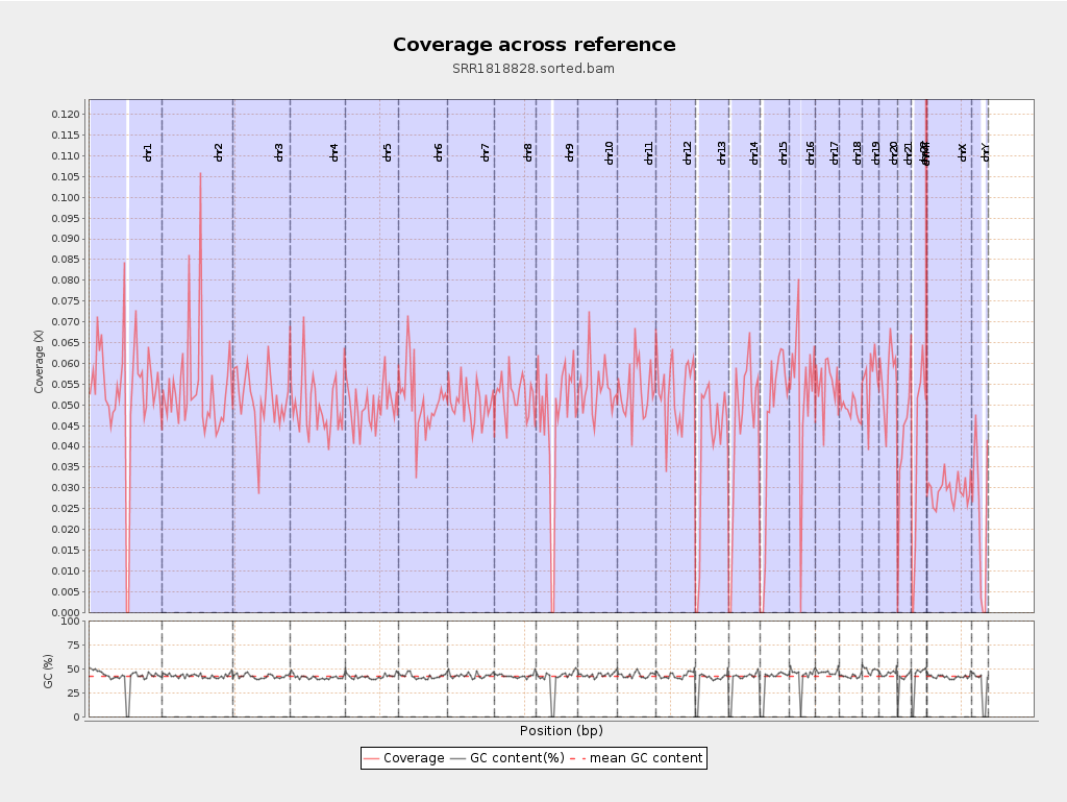
General error rate	0.52%
Mismatches	753,855
Insertions	19,124
Mapped reads with at least one insertion	0.85%
Deletions	37,772
Mapped reads with at least one deletion	1.68%
Homopolymer indels	38.99%

2.6. Chromosome stats

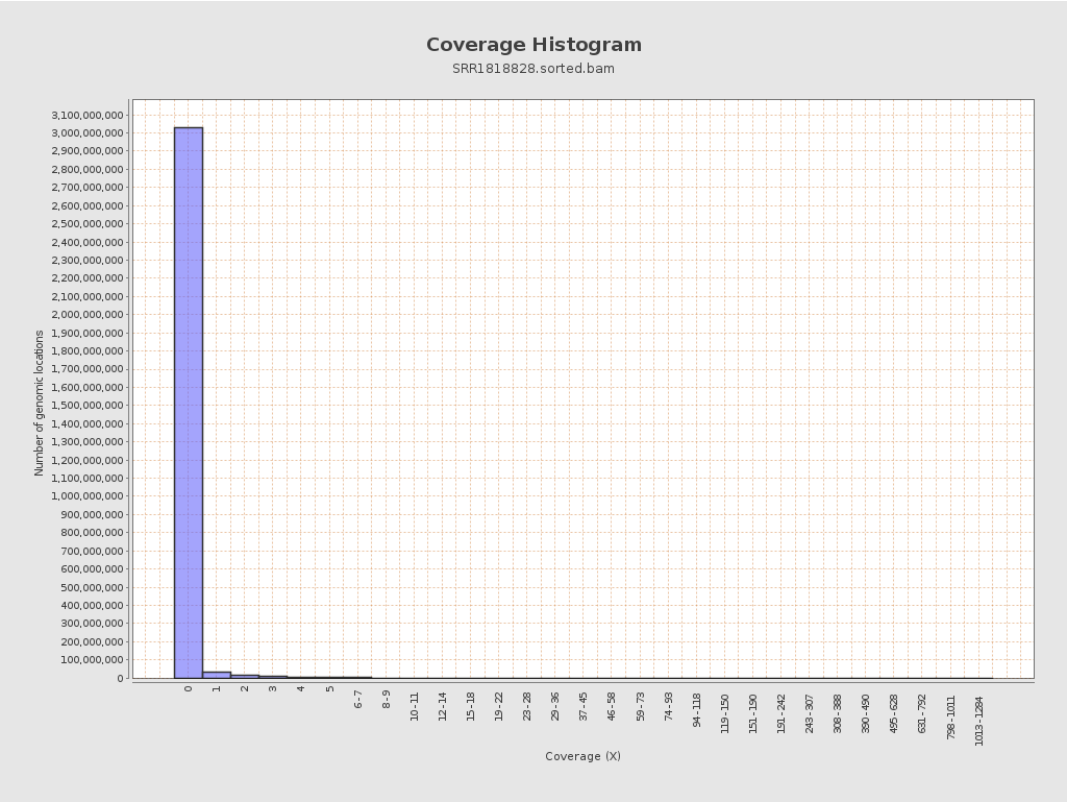
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	13192119	0.0529	0.8923
chr2	243199373	13142929	0.054	0.9935
chr3	198022430	10134869	0.0512	0.4426
chr4	191154276	9511688	0.0498	0.4964
chr5	180915260	8992480	0.0497	0.4452
chr6	171115067	8771537	0.0513	0.4832
chr7	159138663	7987520	0.0502	0.5144

chr8	146364022	7640674	0.0522	0.4966
chr9	141213431	6536992	0.0463	0.5054
chr10	135534747	7299575	0.0539	0.6506
chr11	135006516	7217570	0.0535	0.511
chr12	133851895	7143283	0.0534	0.479
chr13	115169878	4630917	0.0402	0.3957
chr14	107349540	4773856	0.0445	0.4521
chr15	102531392	4592401	0.0448	0.418
chr16	90354753	4914466	0.0544	0.6971
chr17	81195210	4490023	0.0553	0.4917
chr18	78077248	3843600	0.0492	0.6373
chr19	59128983	3333083	0.0564	0.7696
chr20	63025520	3554242	0.0564	0.5143
chr21	48129895	1999588	0.0415	0.4229
chr22	51304566	1971879	0.0384	0.417
chrMT	16571	131906	7.9601	7.9997
chrX	155270560	4556507	0.0293	0.384
chrY	59373566	1339546	0.0226	0.8795

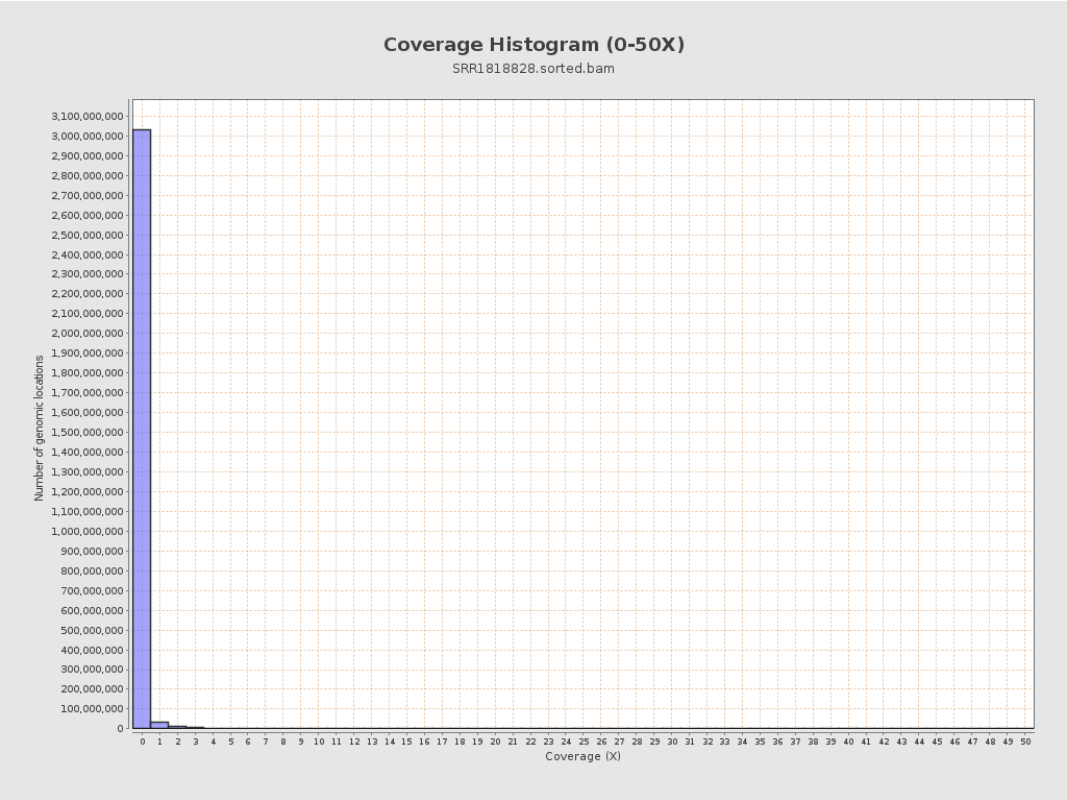
3. Results : Coverage across reference



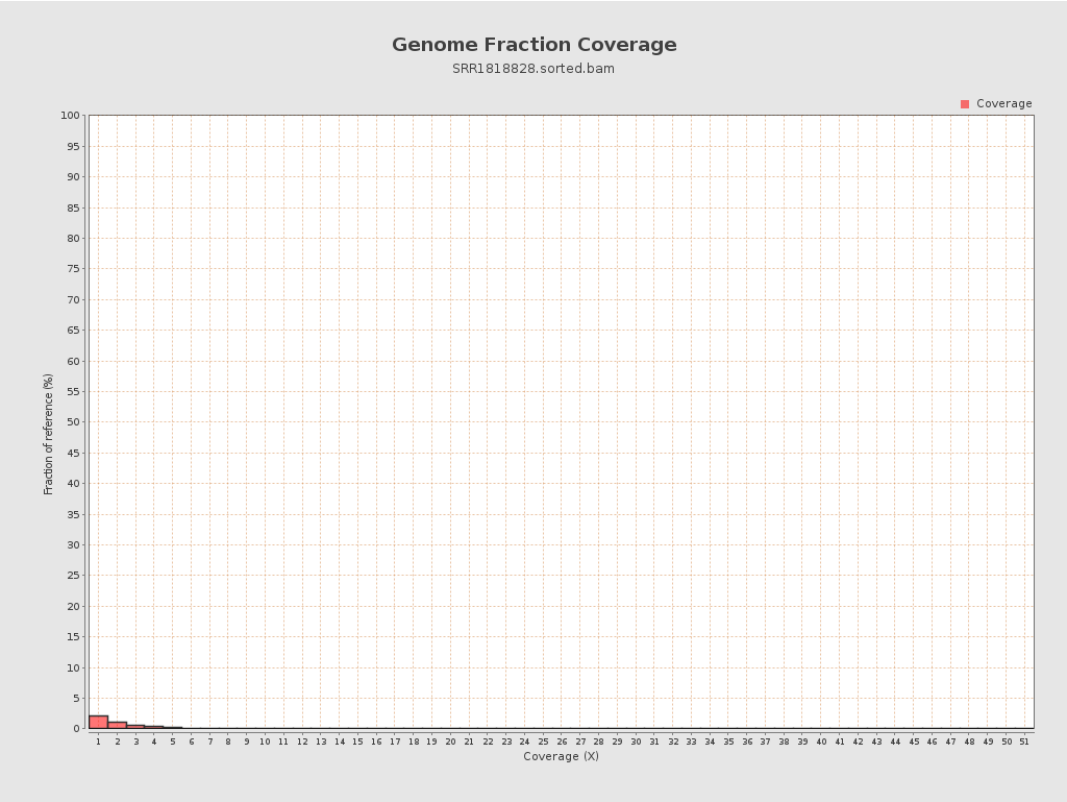
4. Results : Coverage Histogram



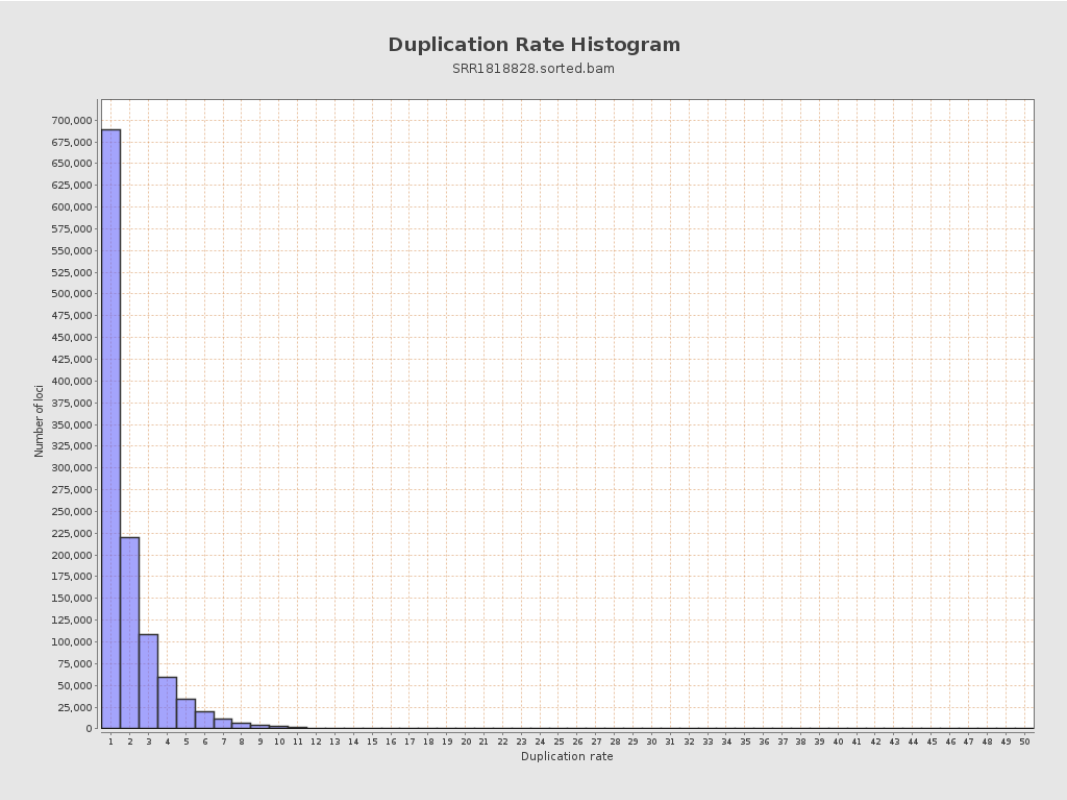
5. Results : Coverage Histogram (0-50X)



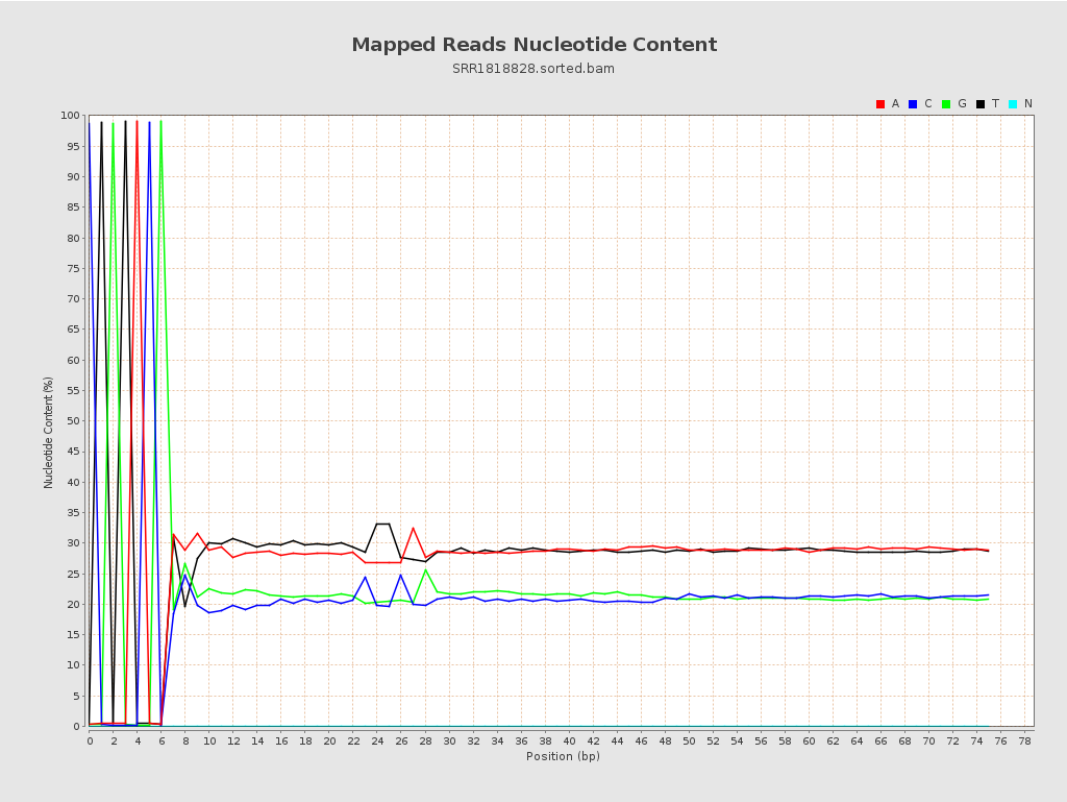
6. Results : Genome Fraction Coverage



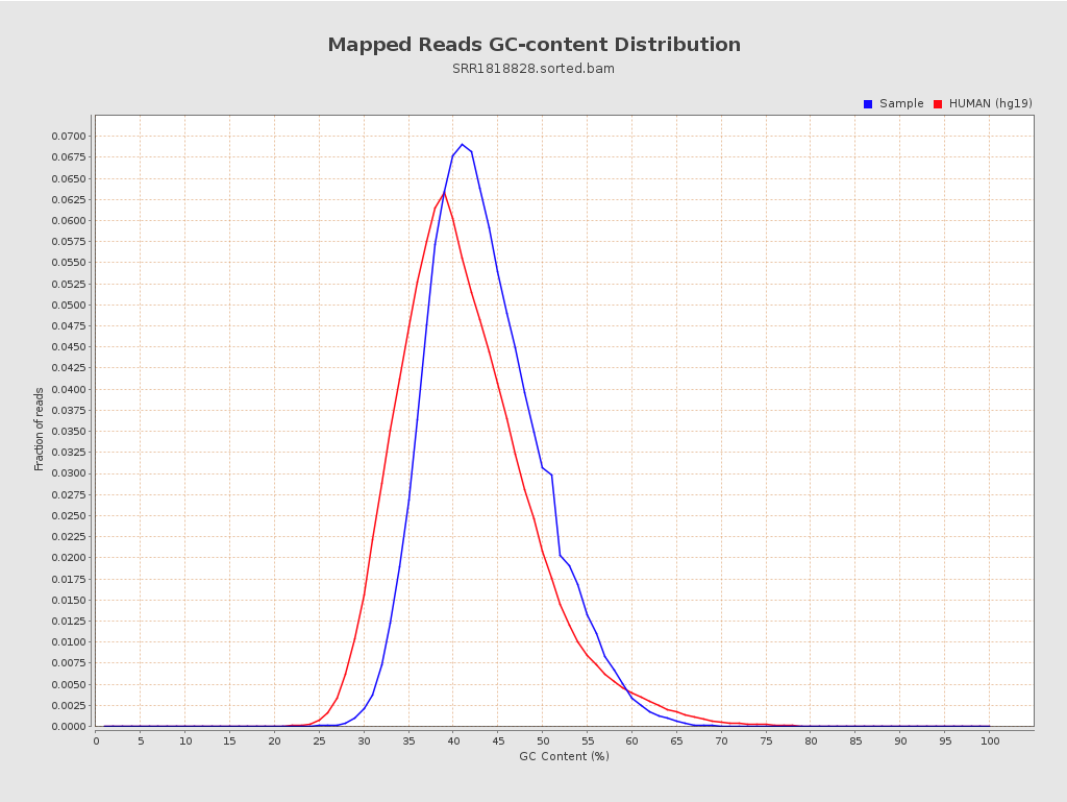
7. Results : Duplication Rate Histogram



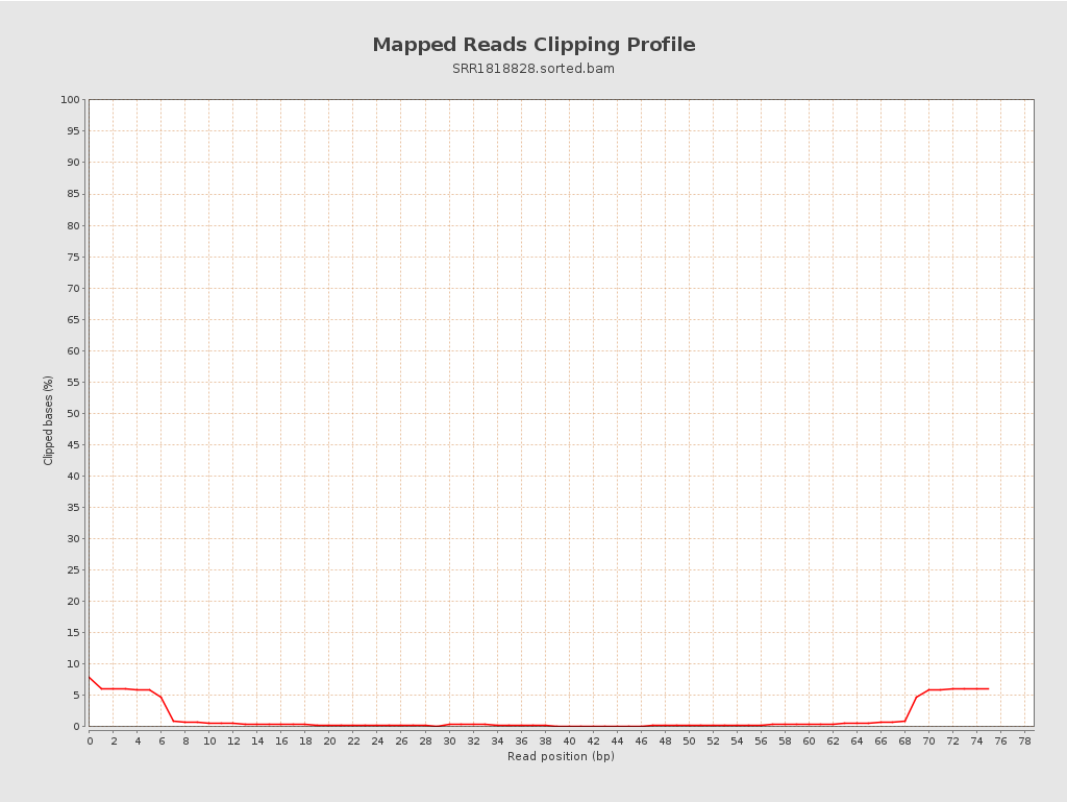
8. Results : Mapped Reads Nucleotide Content



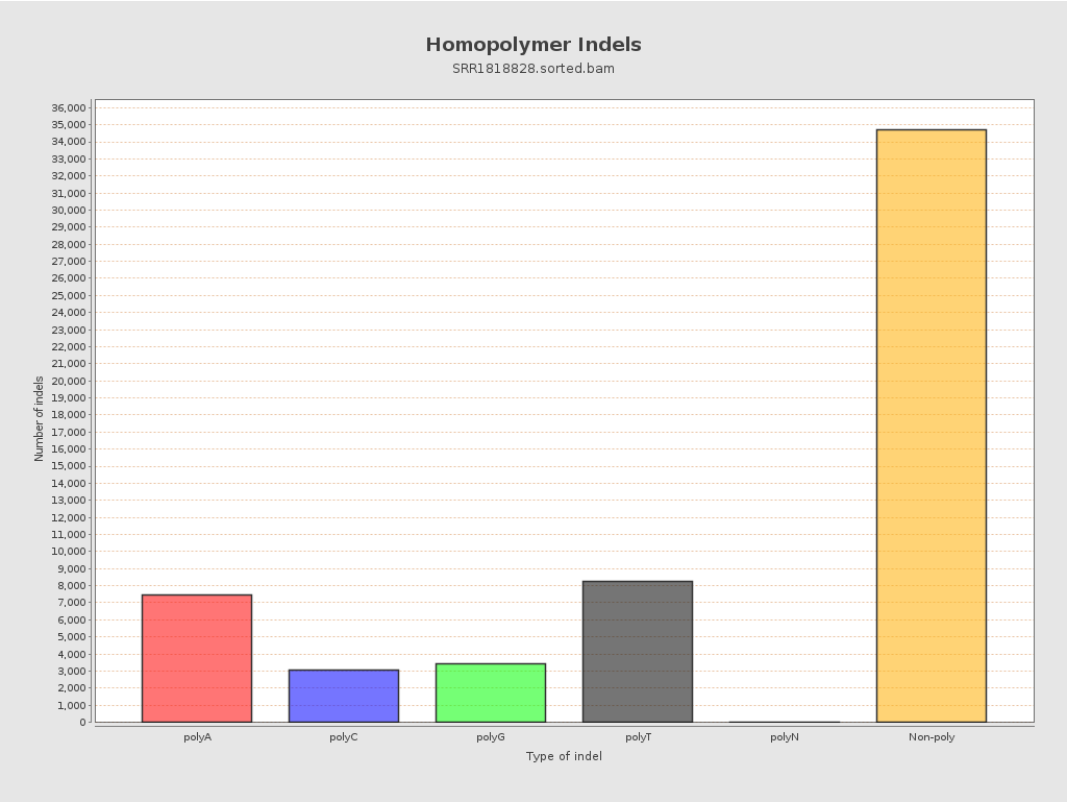
9. Results : Mapped Reads GC-content Distribution



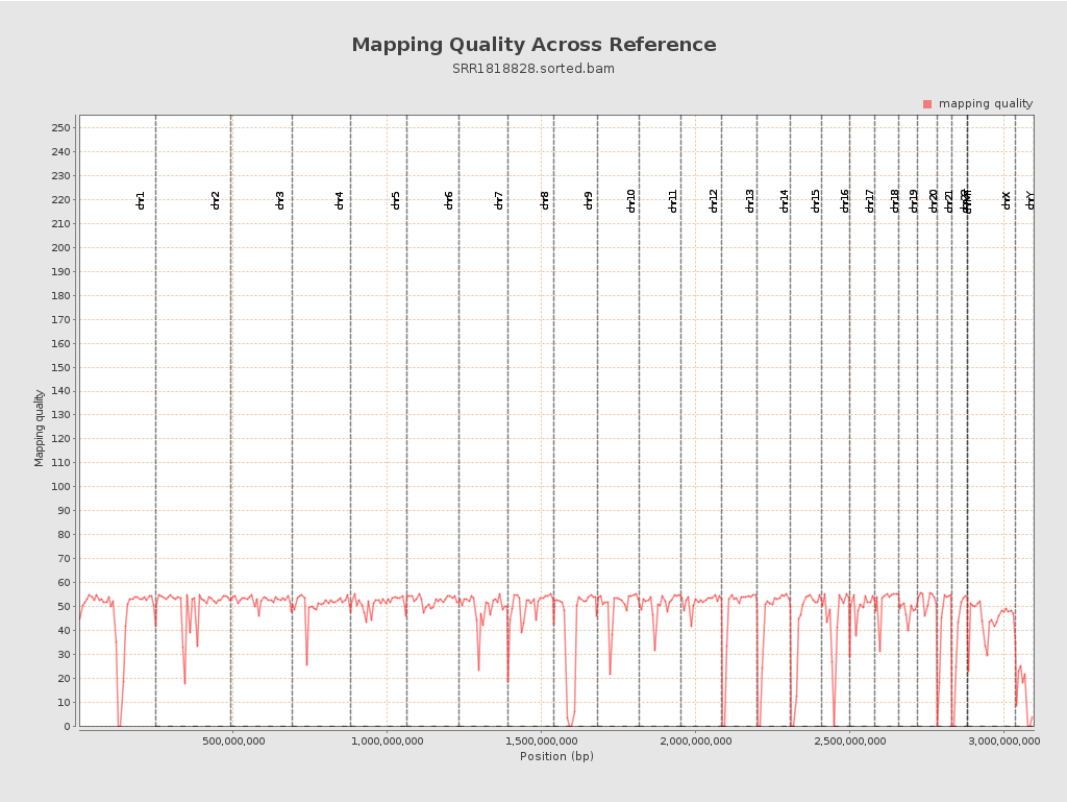
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram