

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 23:22:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524858.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_SRR10524858 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524858.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 23:22:15 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524858.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,137,510
Mapped reads	1,048,566 / 92.18%
Unmapped reads	88,944 / 7.82%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,764 / 0.59%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	24,925 / 2.19%
Duplication rate	1.6%
Clipped reads	1,053,386 / 92.6%

2.2. ACGT Content

Number/percentage of A's	15,185,044 / 24.73%
Number/percentage of C's	11,374,765 / 18.52%
Number/percentage of T's	19,671,085 / 32.04%
Number/percentage of G's	15,165,522 / 24.7%
Number/percentage of N's	8,267 / 0.01%
GC Percentage	43.22%

2.3. Coverage

Mean	0.0198

Standard Deviation	0.2133
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2.4. Mapping Quality

Mean Mapping Quality	44.4
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2.5. Mismatches and indels

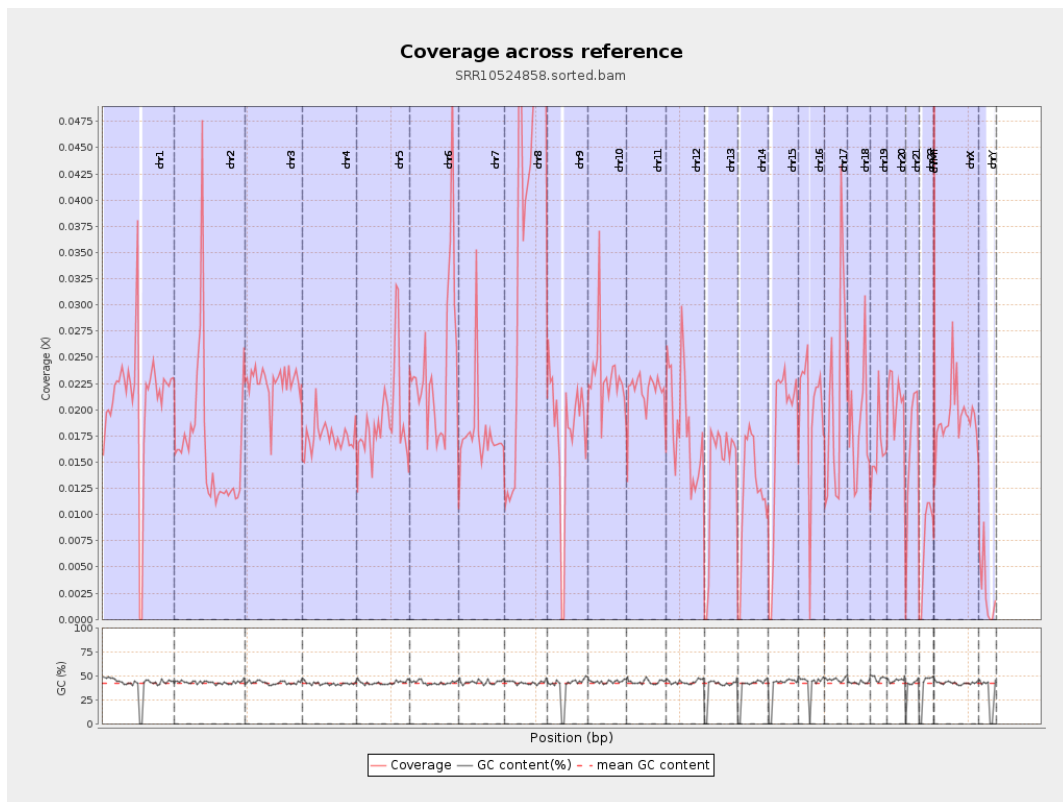
General error rate	0.48%
Mismatches	290,180
Insertions	4,034
Mapped reads with at least one insertion	0.38%
Deletions	11,364
Mapped reads with at least one deletion	1.08%
Homopolymer indels	44.18%

2.6. Chromosome stats

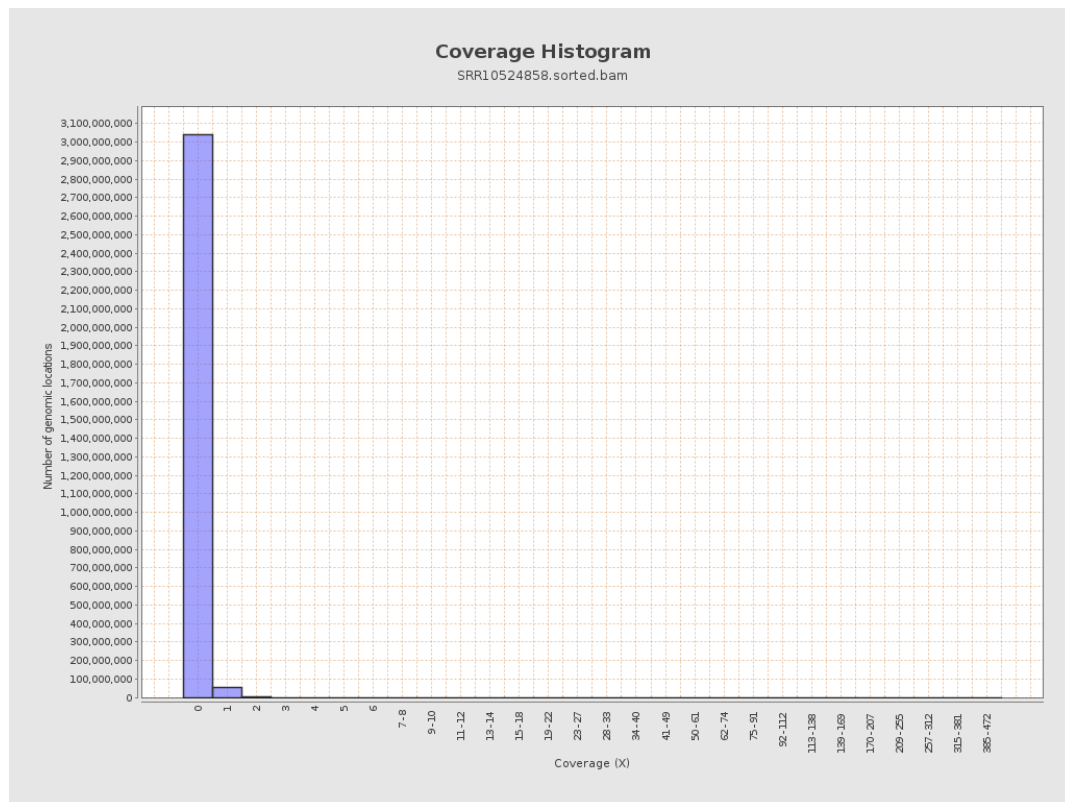
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	5213860	0.0209	0.395
chr2	243199373	3976814	0.0164	0.2105
chr3	198022430	4482008	0.0226	0.1575
chr4	191154276	3328809	0.0174	0.1452
chr5	180915260	3475440	0.0192	0.1454
chr6	171115067	4043585	0.0236	0.1733
chr7	159138663	2834395	0.0178	0.2794

chr8	146364022	6597795	0.0451	0.2887
chr9	141213431	2523071	0.0179	0.1833
chr10	135534747	3147002	0.0232	0.2106
chr11	135006516	2958525	0.0219	0.1904
chr12	133851895	2466544	0.0184	0.1446
chr13	115169878	1600247	0.0139	0.1227
chr14	107349540	1310177	0.0122	0.1248
chr15	102531392	1825756	0.0178	0.1421
chr16	90354753	1791208	0.0198	0.1569
chr17	81195210	1755583	0.0216	0.1699
chr18	78077248	1467039	0.0188	0.3212
chr19	59128983	960642	0.0162	0.2838
chr20	63025520	1318556	0.0209	0.1535
chr21	48129895	788358	0.0164	0.1409
chr22	51304566	379755	0.0074	0.0894
chrMT	16571	1469	0.0886	0.3162
chrX	155270560	3016308	0.0194	0.1616
chrY	59373566	159546	0.0027	0.0773

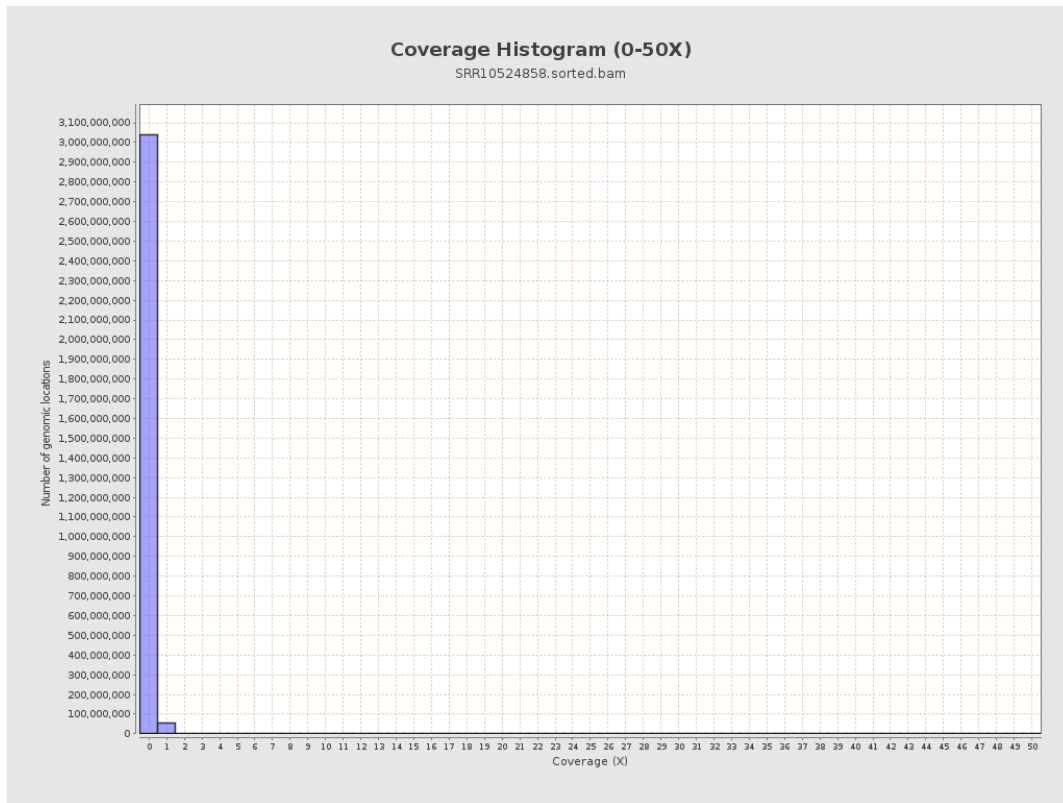
3. Results : Coverage across reference



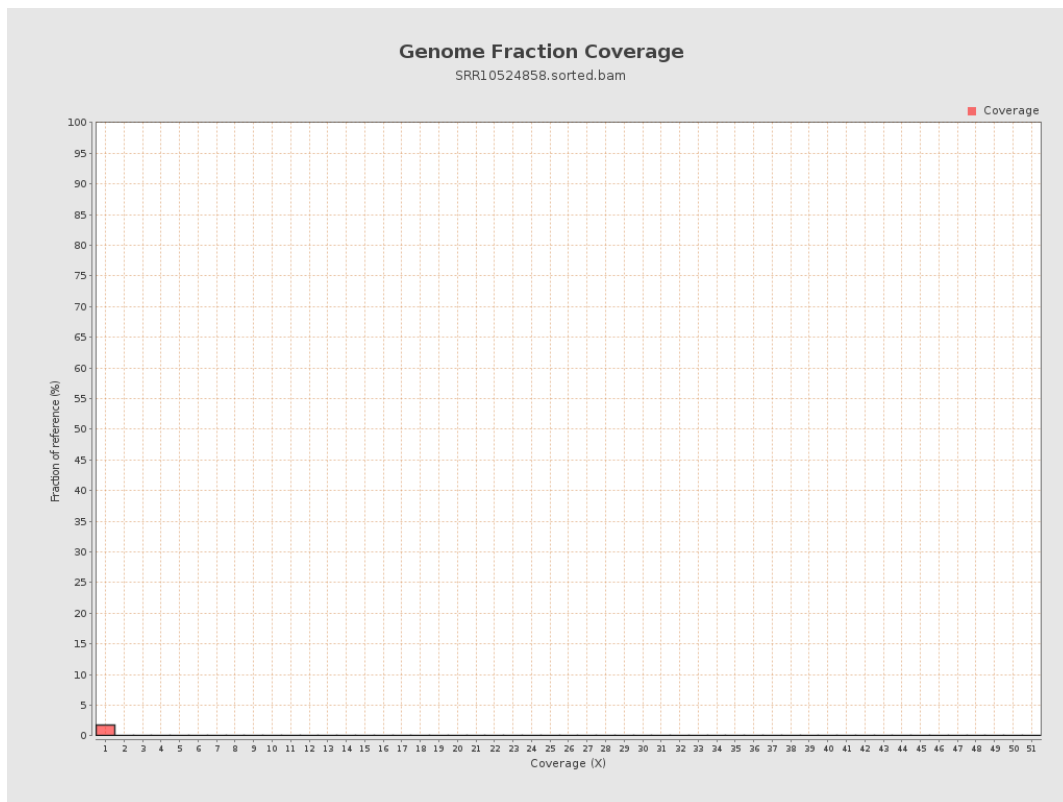
4. Results : Coverage Histogram



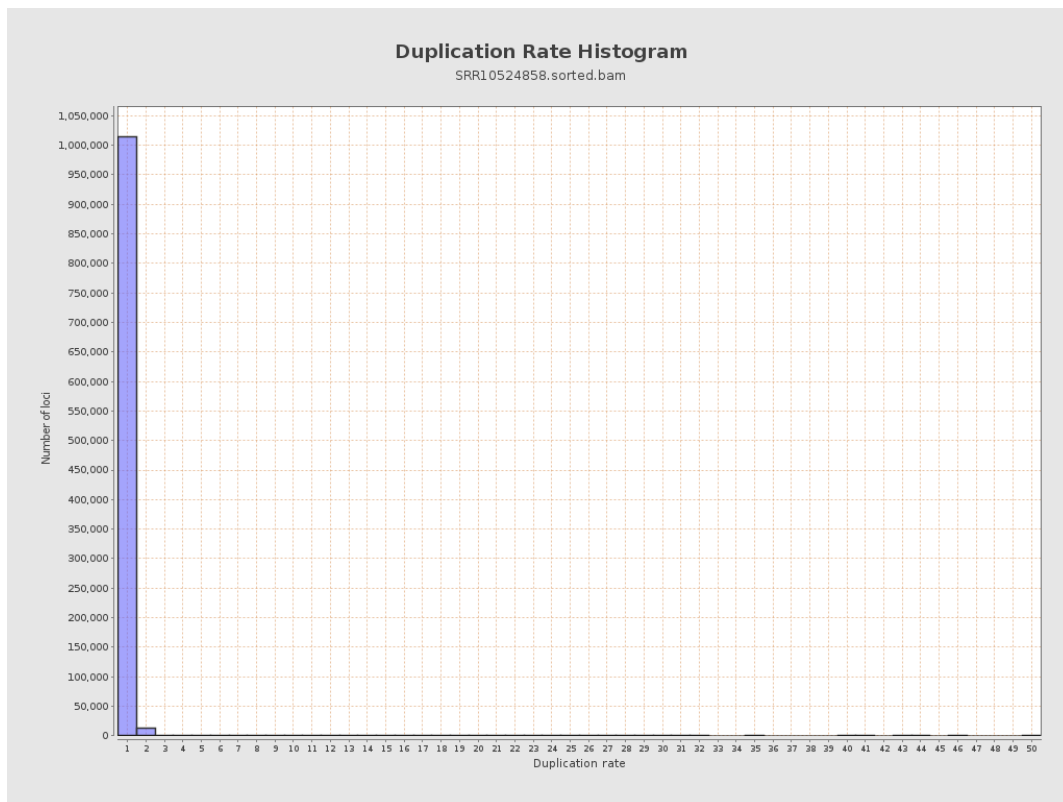
5. Results : Coverage Histogram (0-50X)



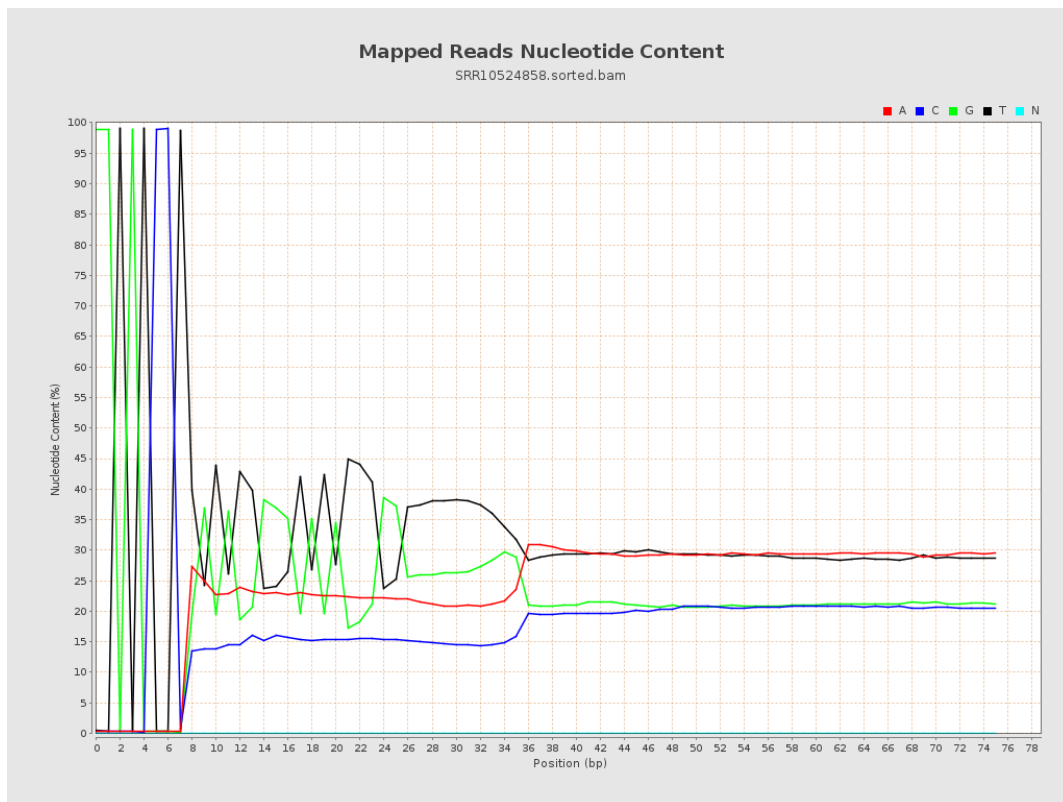
6. Results : Genome Fraction Coverage



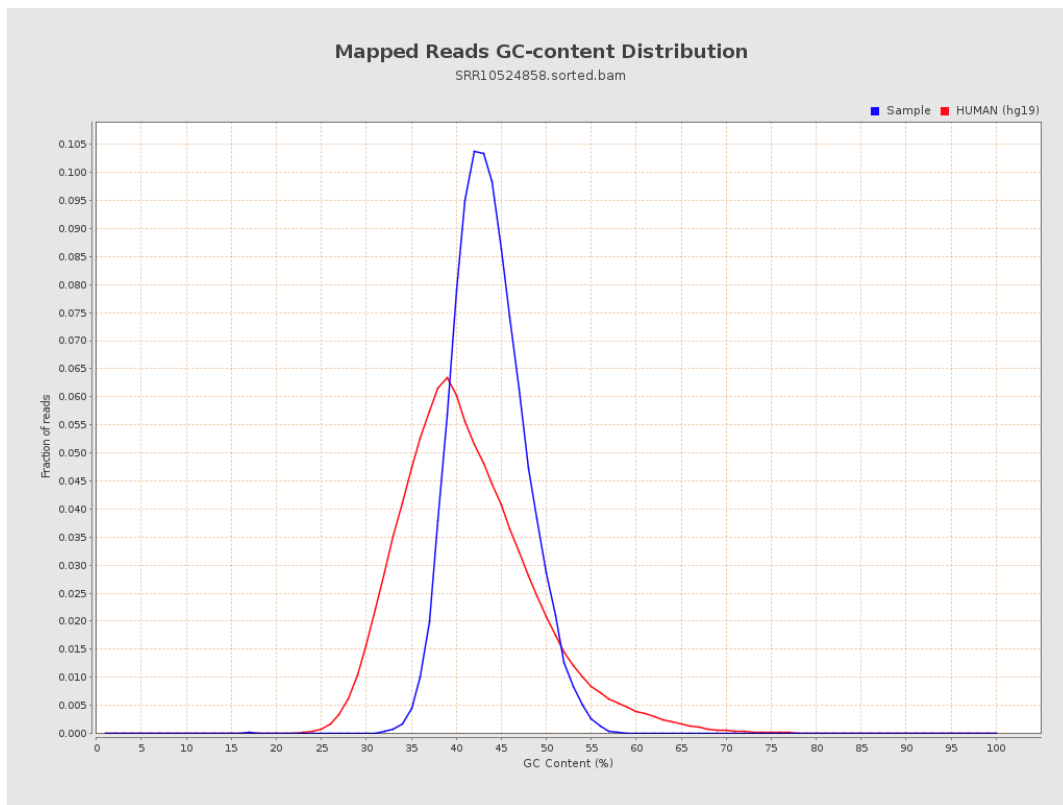
7. Results : Duplication Rate Histogram



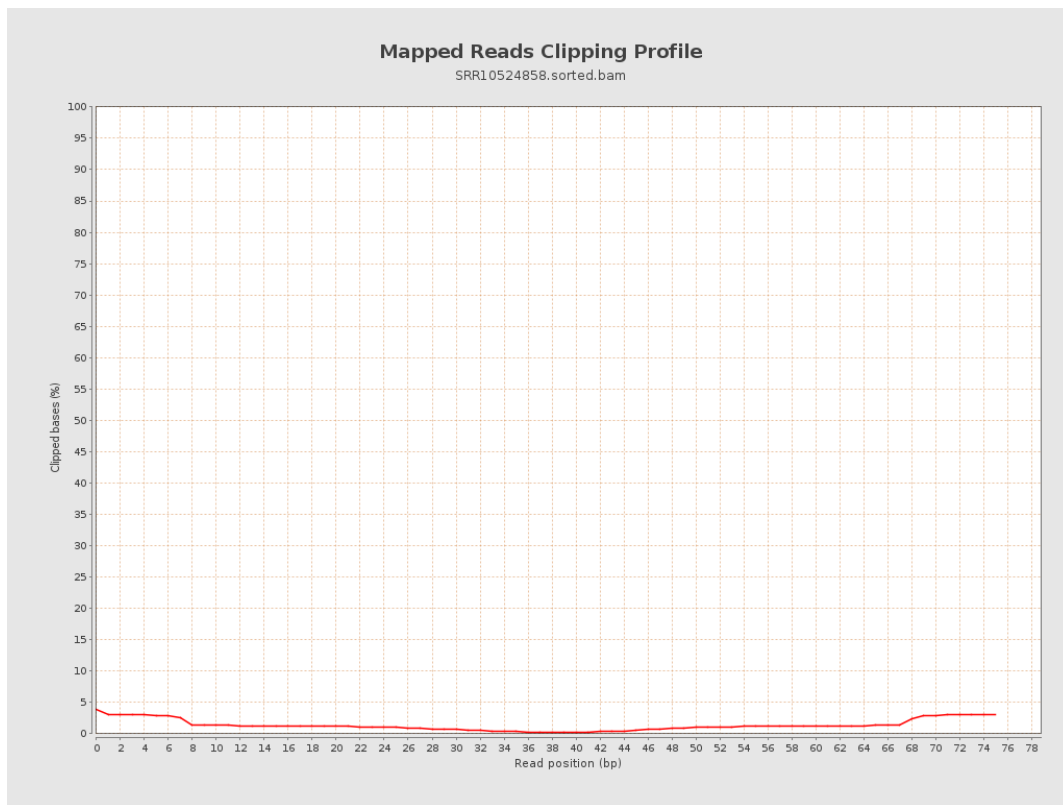
8. Results : Mapped Reads Nucleotide Content



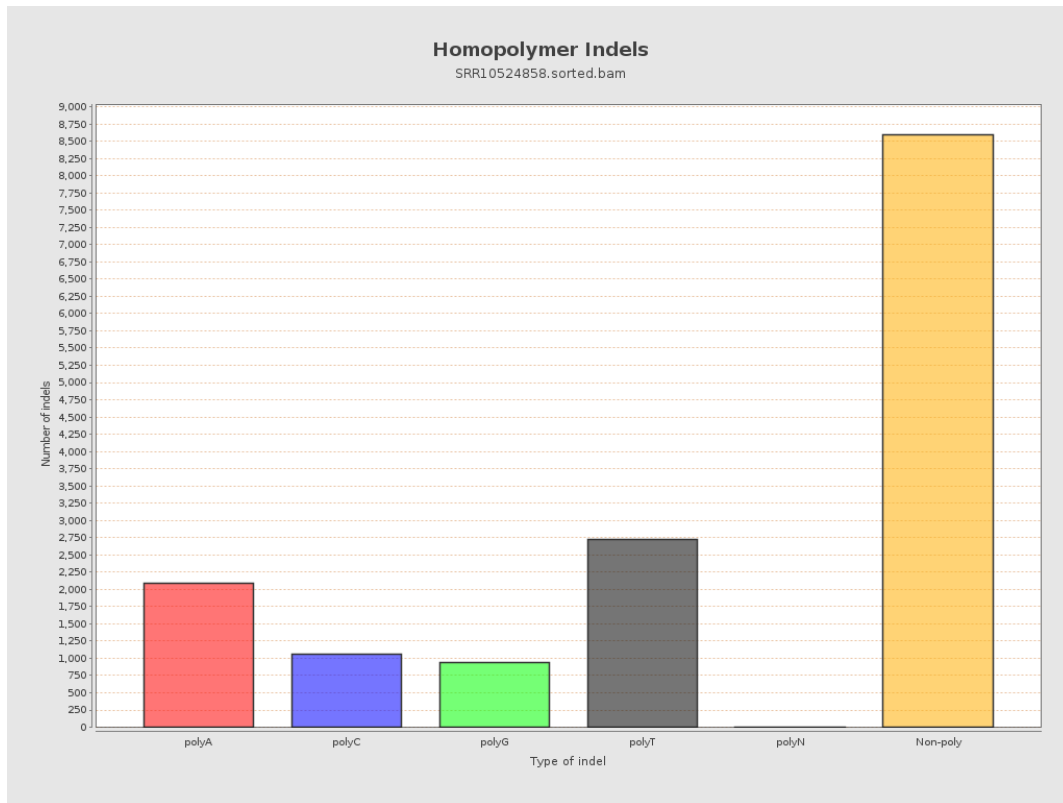
9. Results : Mapped Reads GC-content Distribution



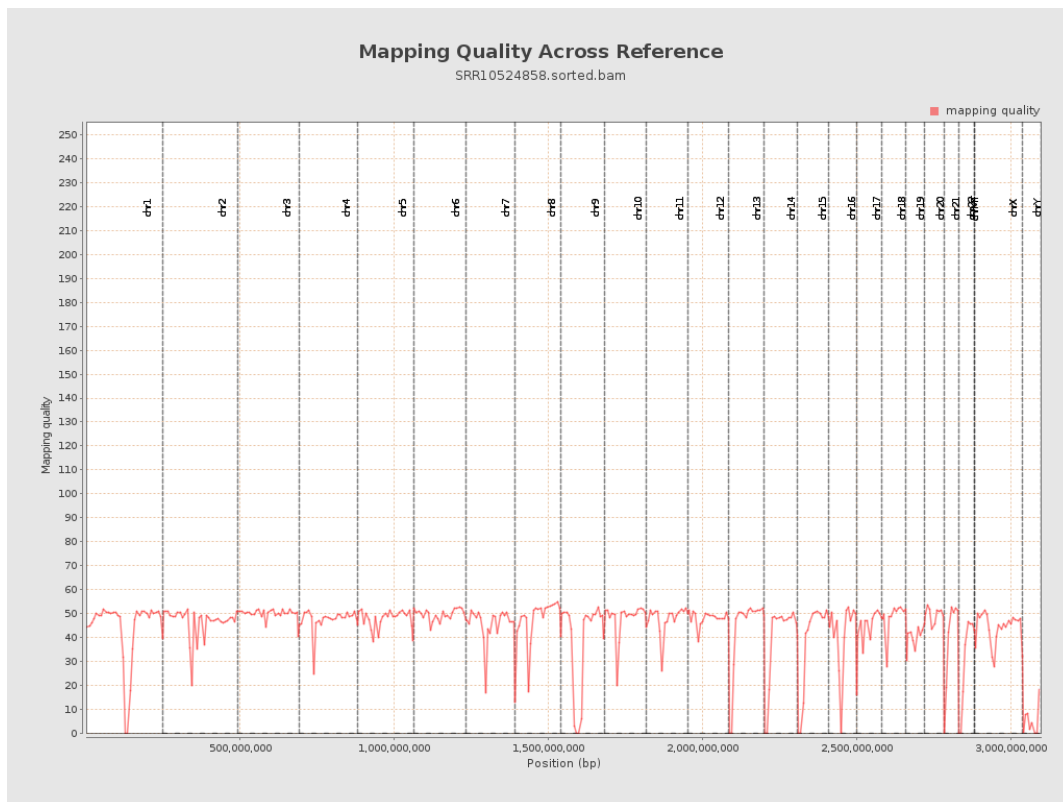
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

