

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 19:37:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1819075.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_SRR1819075 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1819075.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 19:37:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1819075.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,050,577
Mapped reads	936,405 / 89.13%
Unmapped reads	114,172 / 10.87%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,002 / 0.38%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	20,244 / 1.93%
Duplication rate	1.68%
Clipped reads	937,330 / 89.22%

2.2. ACGT Content

Number/percentage of A's	13,659,753 / 25.42%
Number/percentage of C's	9,915,846 / 18.45%
Number/percentage of T's	16,498,850 / 30.7%
Number/percentage of G's	13,659,121 / 25.42%
Number/percentage of N's	1,181 / 0%
GC Percentage	43.87%

2.3. Coverage

Mean	0.0174

Standard Deviation	0.1637
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2.4. Mapping Quality

Mean Mapping Quality	44.65
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2.5. Mismatches and indels

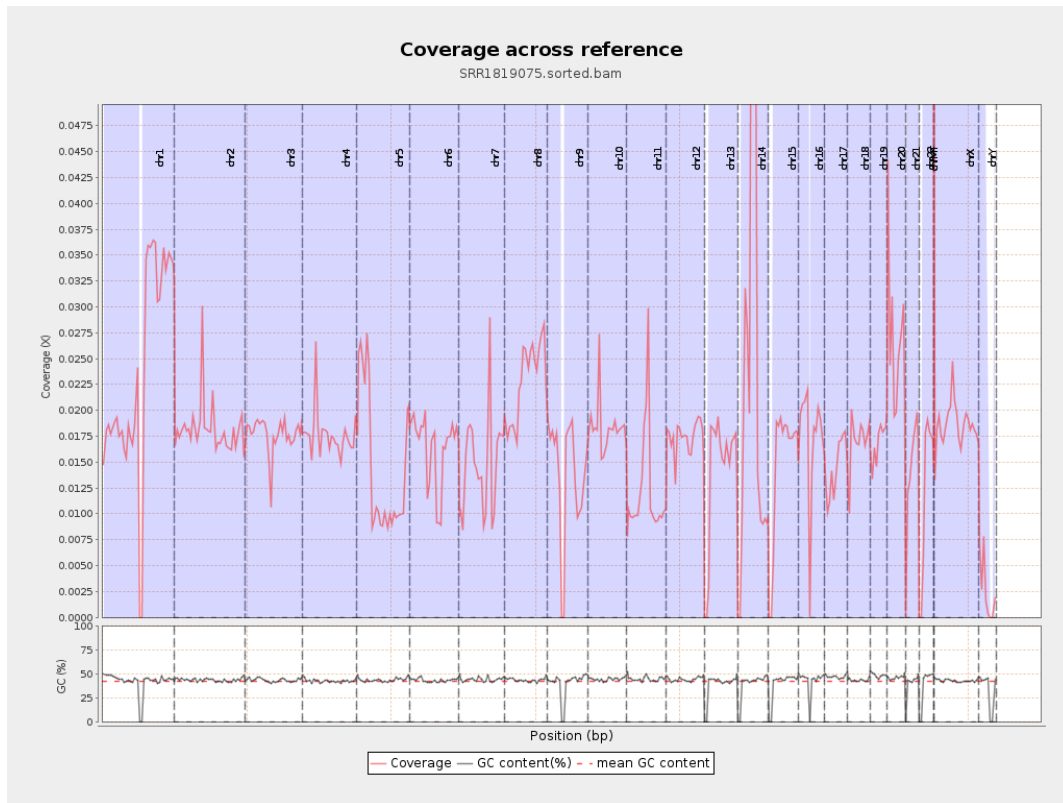
General error rate	0.49%
Mismatches	255,616
Insertions	4,147
Mapped reads with at least one insertion	0.44%
Deletions	8,358
Mapped reads with at least one deletion	0.89%
Homopolymer indels	38.4%

2.6. Chromosome stats

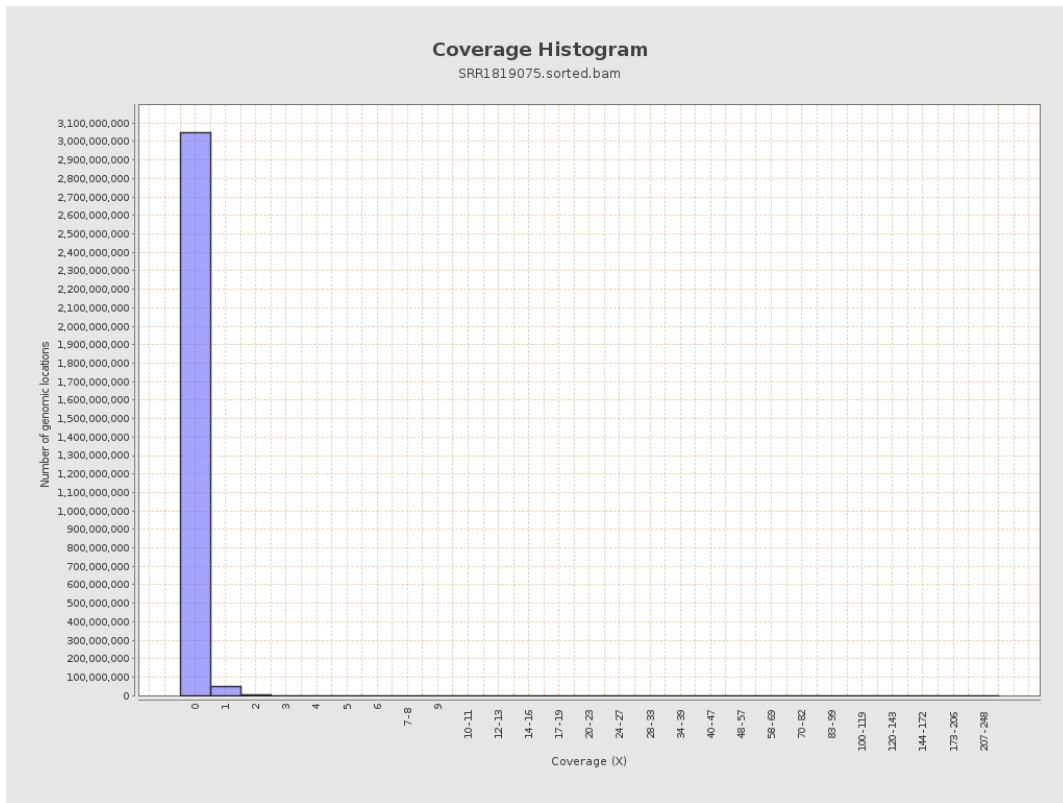
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	5914856	0.0237	0.2351
chr2	243199373	4428255	0.0182	0.1782
chr3	198022430	3498643	0.0177	0.14
chr4	191154276	3367406	0.0176	0.1456
chr5	180915260	2618980	0.0145	0.1281
chr6	171115067	2786271	0.0163	0.1413
chr7	159138663	2360462	0.0148	0.1453

chr8	146364022	3334647	0.0228	0.176
chr9	141213431	1932431	0.0137	0.1546
chr10	135534747	2488859	0.0184	0.1667
chr11	135006516	1673096	0.0124	0.1474
chr12	133851895	2332621	0.0174	0.14
chr13	115169878	1630464	0.0142	0.125
chr14	107349540	2787166	0.026	0.1782
chr15	102531392	1502947	0.0147	0.1273
chr16	90354753	1547830	0.0171	0.1471
chr17	81195210	1171444	0.0144	0.1288
chr18	78077248	1307124	0.0167	0.2977
chr19	59128983	993369	0.0168	0.1728
chr20	63025520	1693203	0.0269	0.1758
chr21	48129895	689934	0.0143	0.1343
chr22	51304566	633763	0.0124	0.1169
chrMT	16571	1179	0.0711	0.2754
chrX	155270560	2905086	0.0187	0.1567
chrY	59373566	148771	0.0025	0.0656

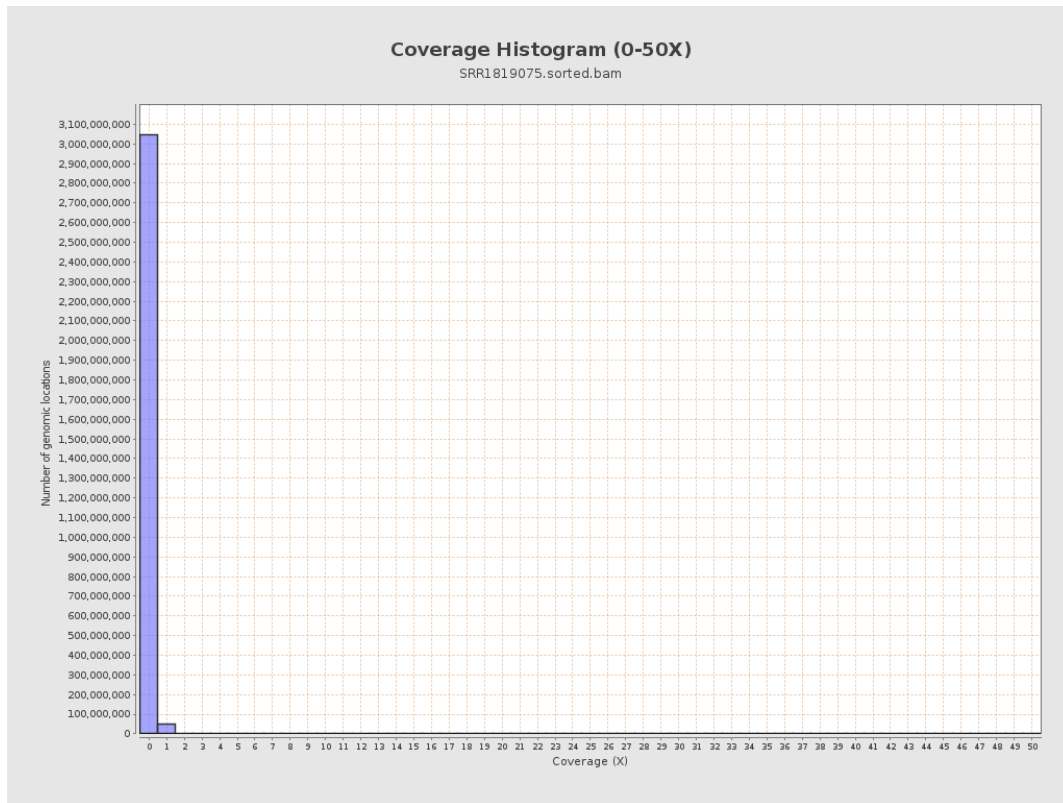
3. Results : Coverage across reference



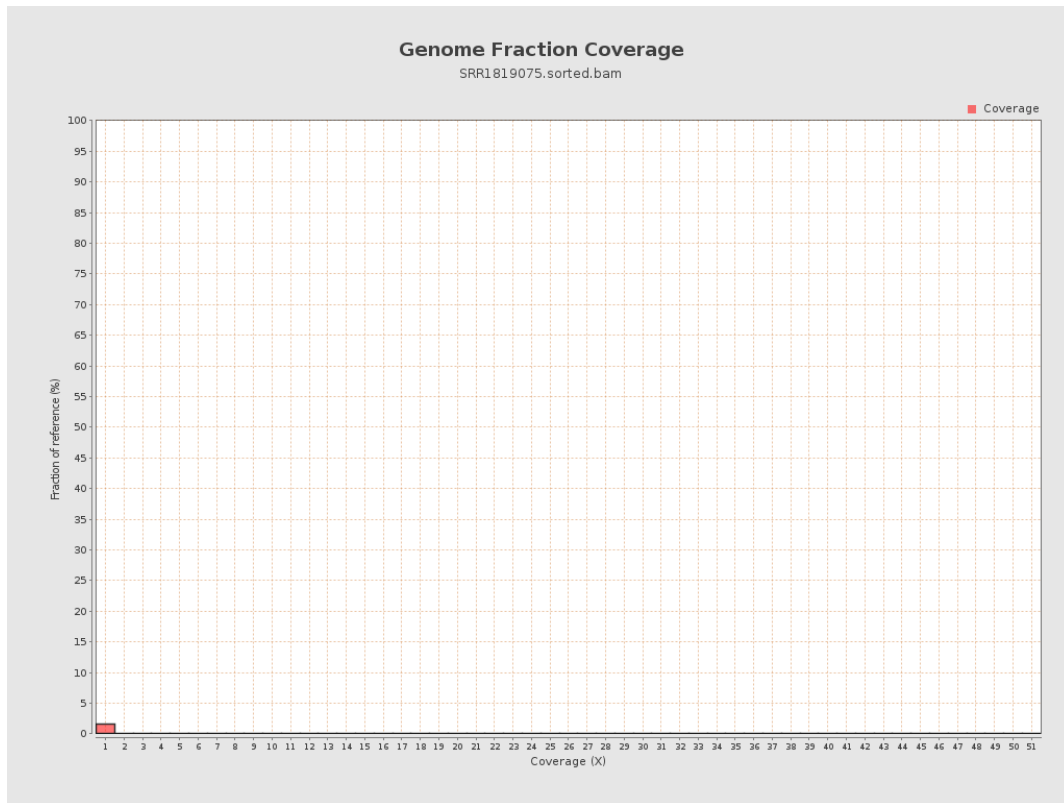
4. Results : Coverage Histogram



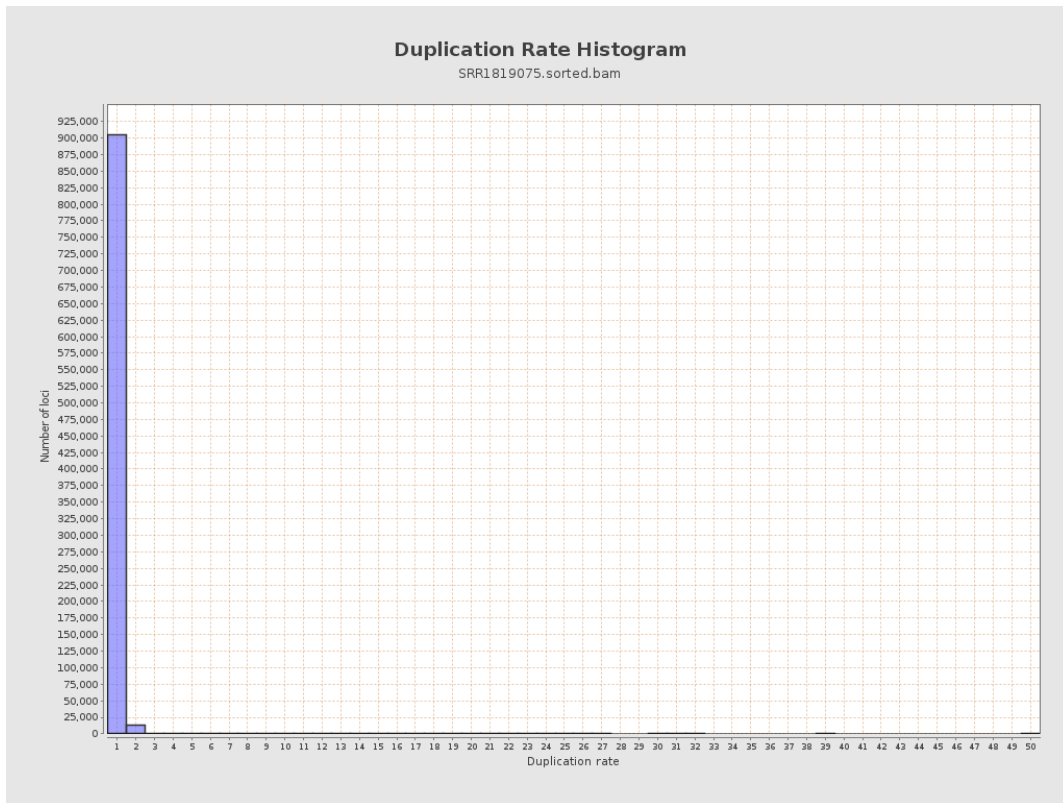
5. Results : Coverage Histogram (0-50X)



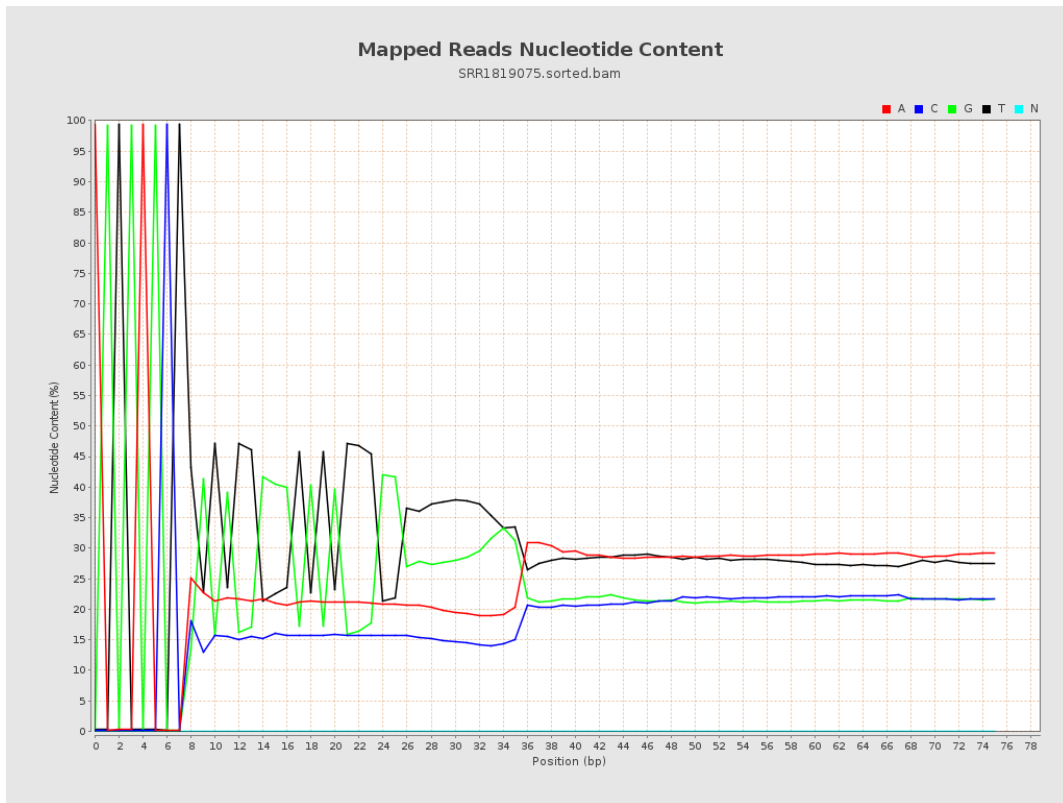
6. Results : Genome Fraction Coverage



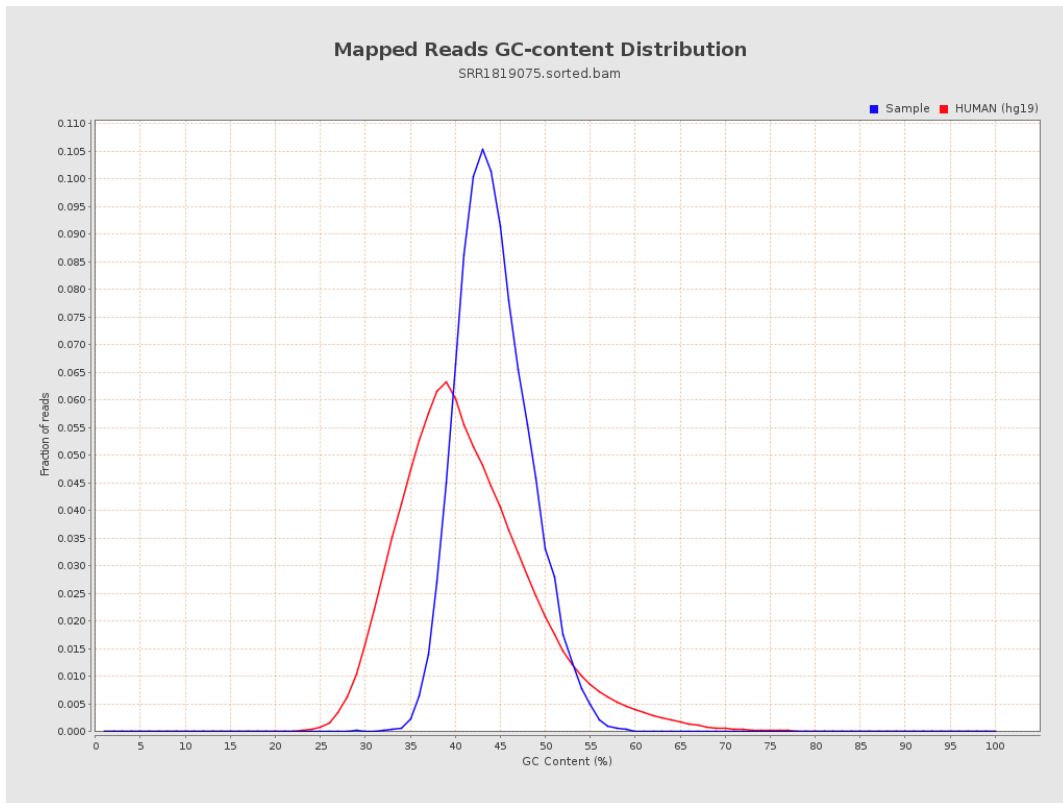
7. Results : Duplication Rate Histogram



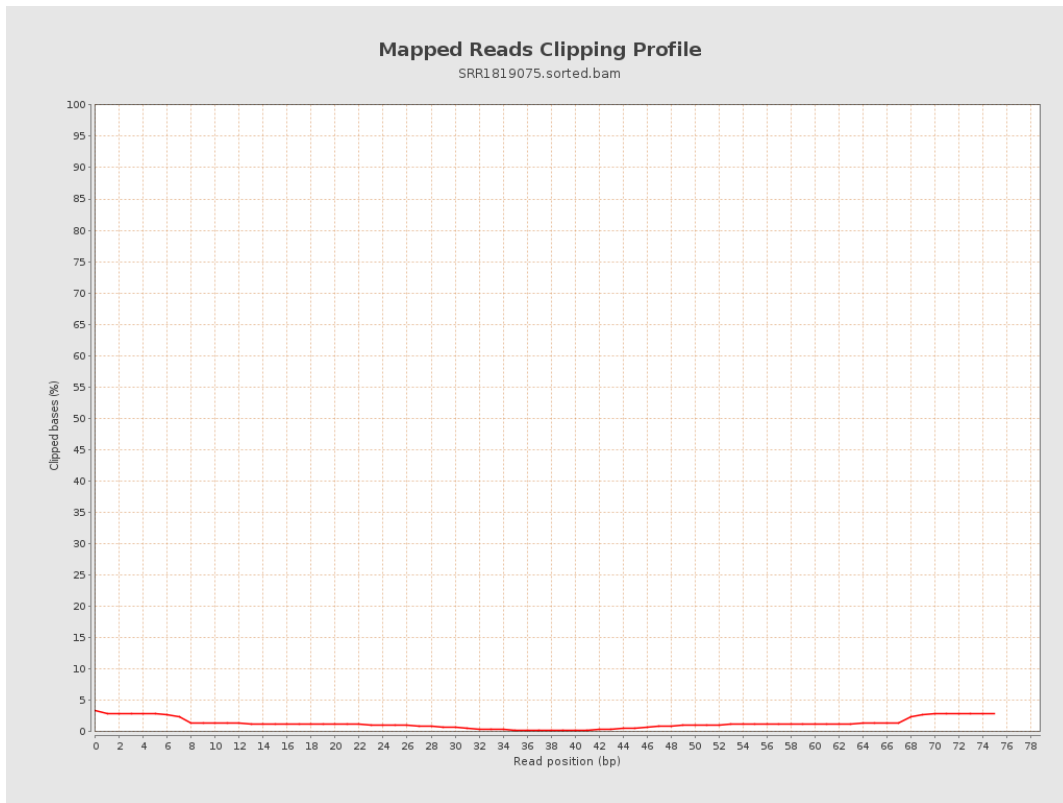
8. Results : Mapped Reads Nucleotide Content



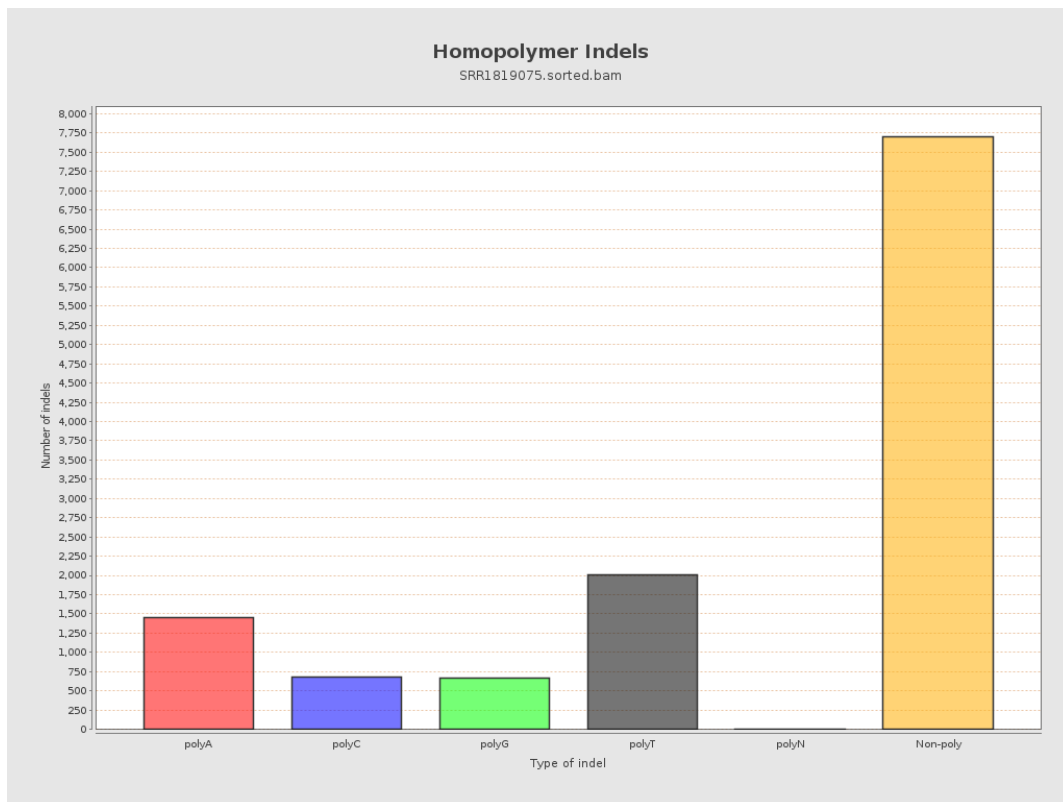
9. Results : Mapped Reads GC-content Distribution



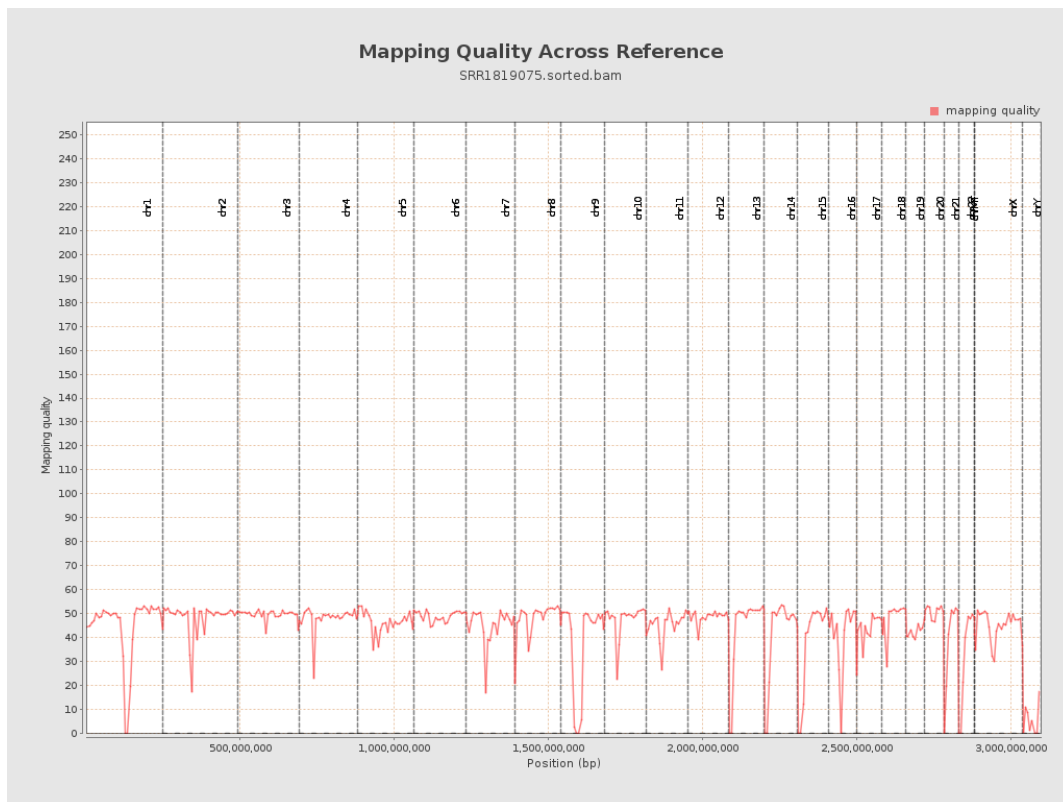
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

