

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 04:27:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524921.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_SRR10524921 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524921.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 04:27:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524921.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,302,342
Mapped reads	1,202,694 / 92.35%
Unmapped reads	99,648 / 7.65%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,793 / 0.37%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	50,930 / 3.91%
Duplication rate	3.37%
Clipped reads	1,203,916 / 92.44%

2.2. ACGT Content

Number/percentage of A's	17,664,685 / 25.32%
Number/percentage of C's	12,997,989 / 18.63%
Number/percentage of T's	22,559,147 / 32.34%
Number/percentage of G's	16,543,630 / 23.71%
Number/percentage of N's	562 / 0%
GC Percentage	42.34%

2.3. Coverage

Mean	0.0225

Standard Deviation	0.2164
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2.4. Mapping Quality

Mean Mapping Quality	44.66
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2.5. Mismatches and indels

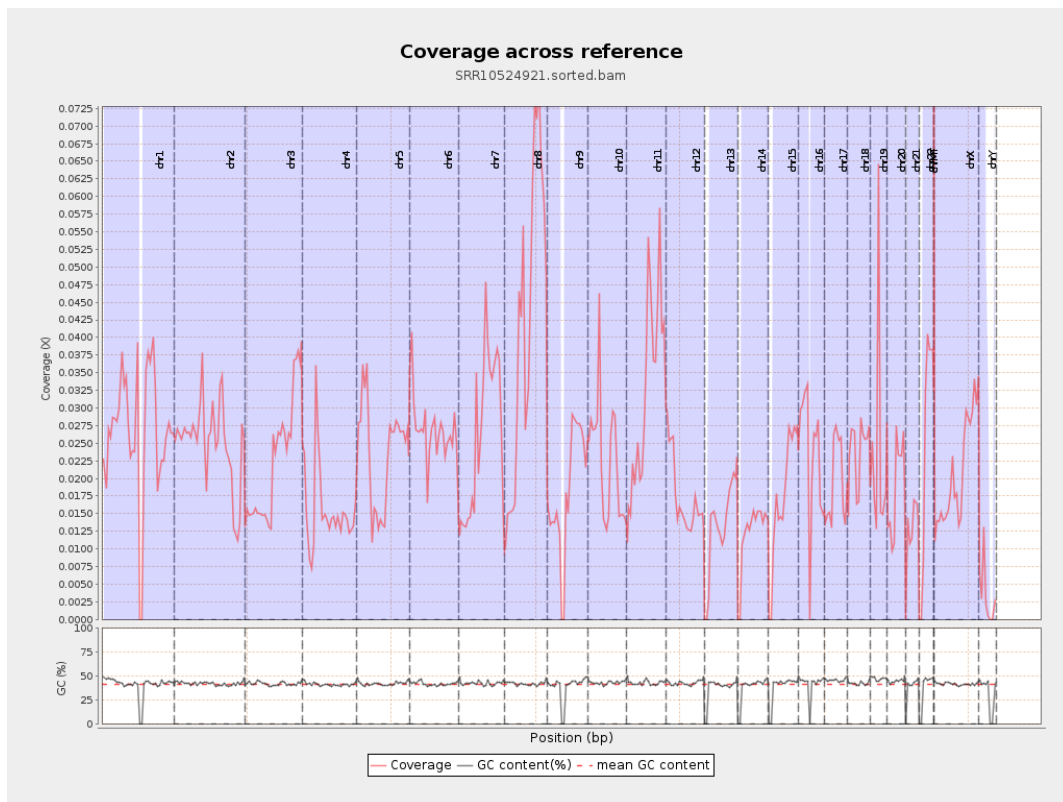
General error rate	0.52%
Mismatches	351,590
Insertions	4,563
Mapped reads with at least one insertion	0.38%
Deletions	13,019
Mapped reads with at least one deletion	1.08%
Homopolymer indels	41.93%

2.6. Chromosome stats

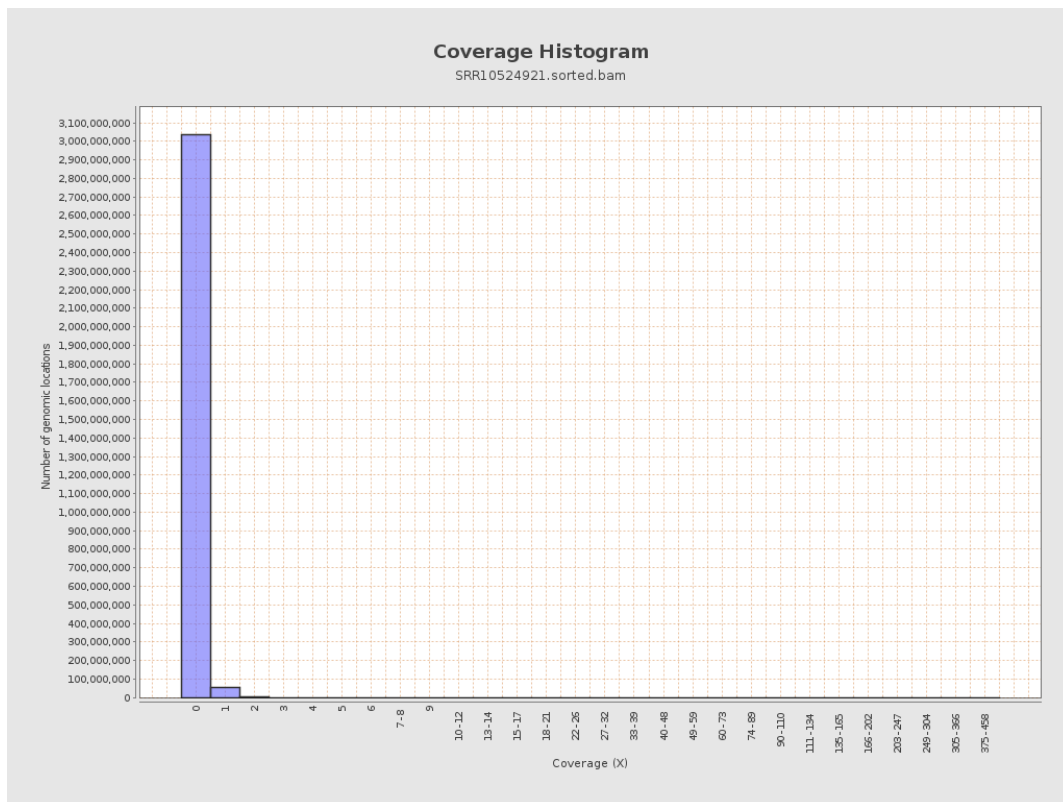
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	6603813	0.0265	0.3665
chr2	243199373	6086863	0.025	0.2763
chr3	198022430	4418355	0.0223	0.1645
chr4	191154276	3022763	0.0158	0.1611
chr5	180915260	4299891	0.0238	0.1686
chr6	171115067	4585258	0.0268	0.1865
chr7	159138663	4142932	0.026	0.2586

chr8	146364022	6225163	0.0425	0.2726
chr9	141213431	2558548	0.0181	0.1725
chr10	135534747	3099624	0.0229	0.2334
chr11	135006516	4405279	0.0326	0.2174
chr12	133851895	2331380	0.0174	0.1463
chr13	115169878	1500234	0.013	0.1259
chr14	107349540	1304973	0.0122	0.1229
chr15	102531392	1769455	0.0173	0.1447
chr16	90354753	2111086	0.0234	0.1737
chr17	81195210	1553307	0.0191	0.1555
chr18	78077248	1860478	0.0238	0.2552
chr19	59128983	1409226	0.0238	0.2732
chr20	63025520	1178047	0.0187	0.1537
chr21	48129895	612515	0.0127	0.1438
chr22	51304566	1286492	0.0251	0.1748
chrMT	16571	1423	0.0859	0.326
chrX	155270560	3218747	0.0207	0.1682
chrY	59373566	201935	0.0034	0.1134

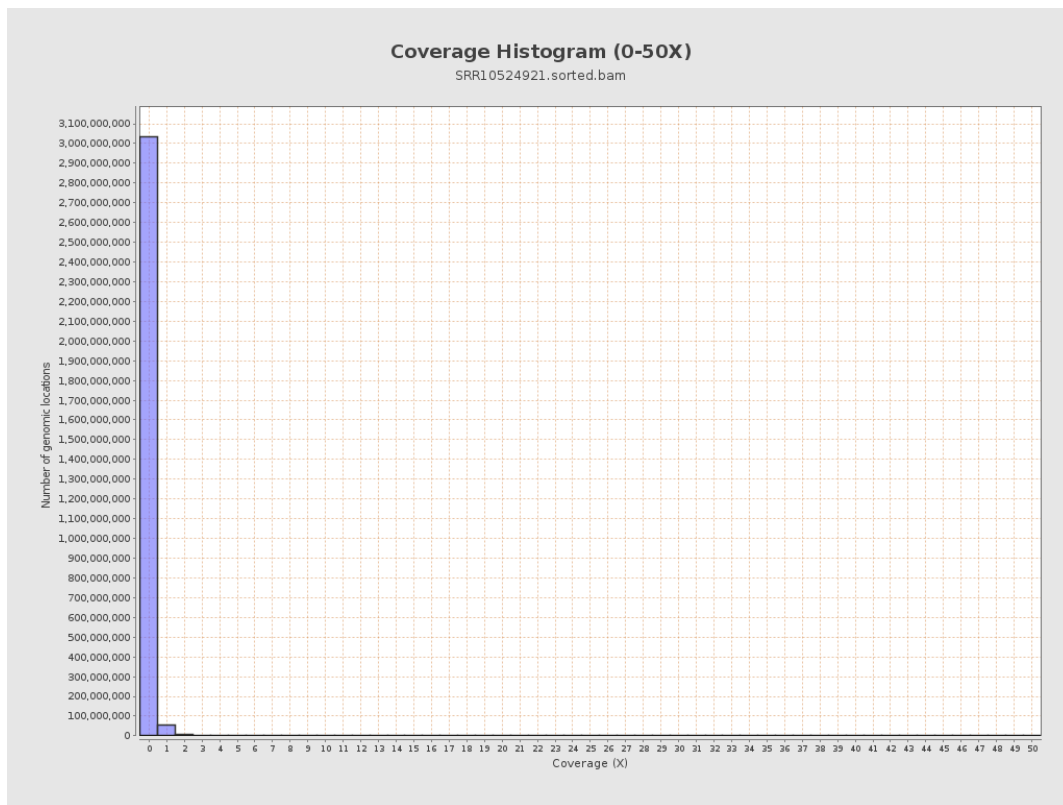
3. Results : Coverage across reference



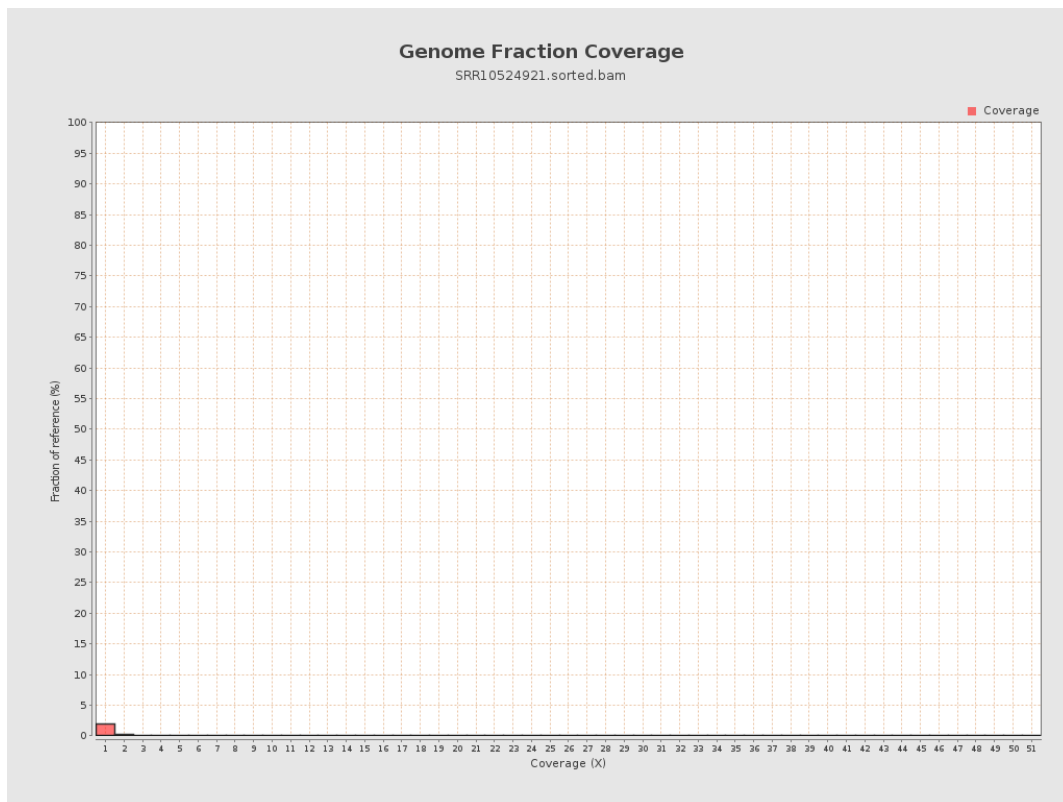
4. Results : Coverage Histogram



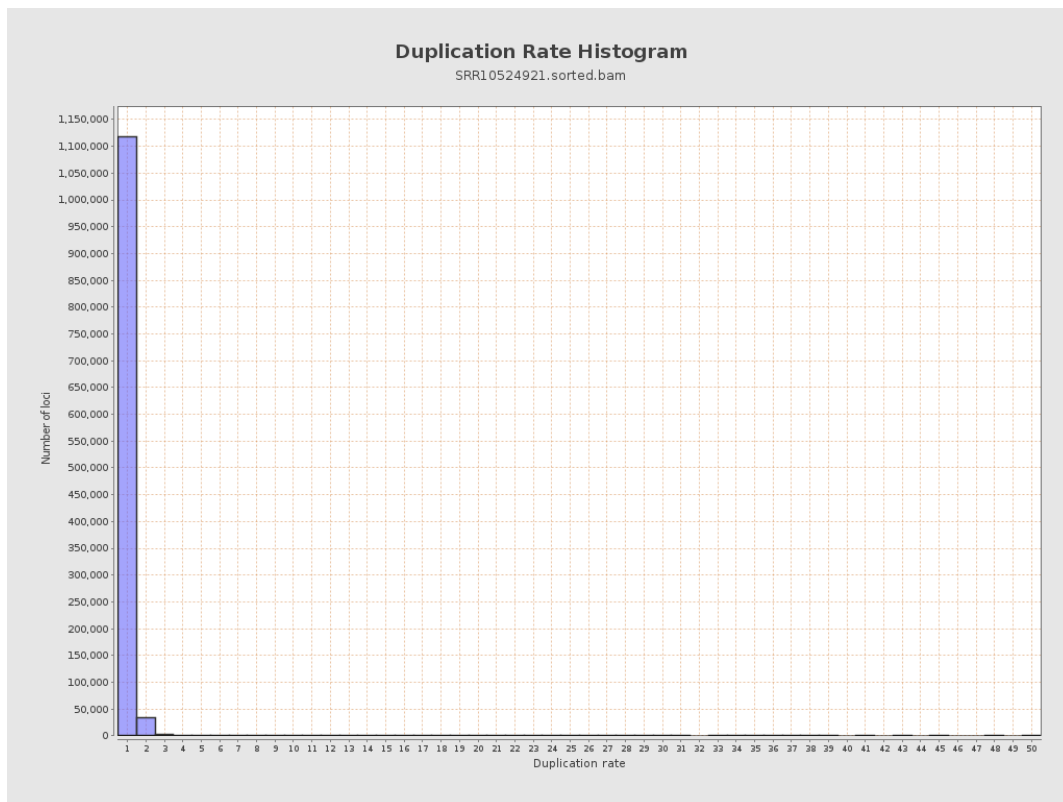
5. Results : Coverage Histogram (0-50X)



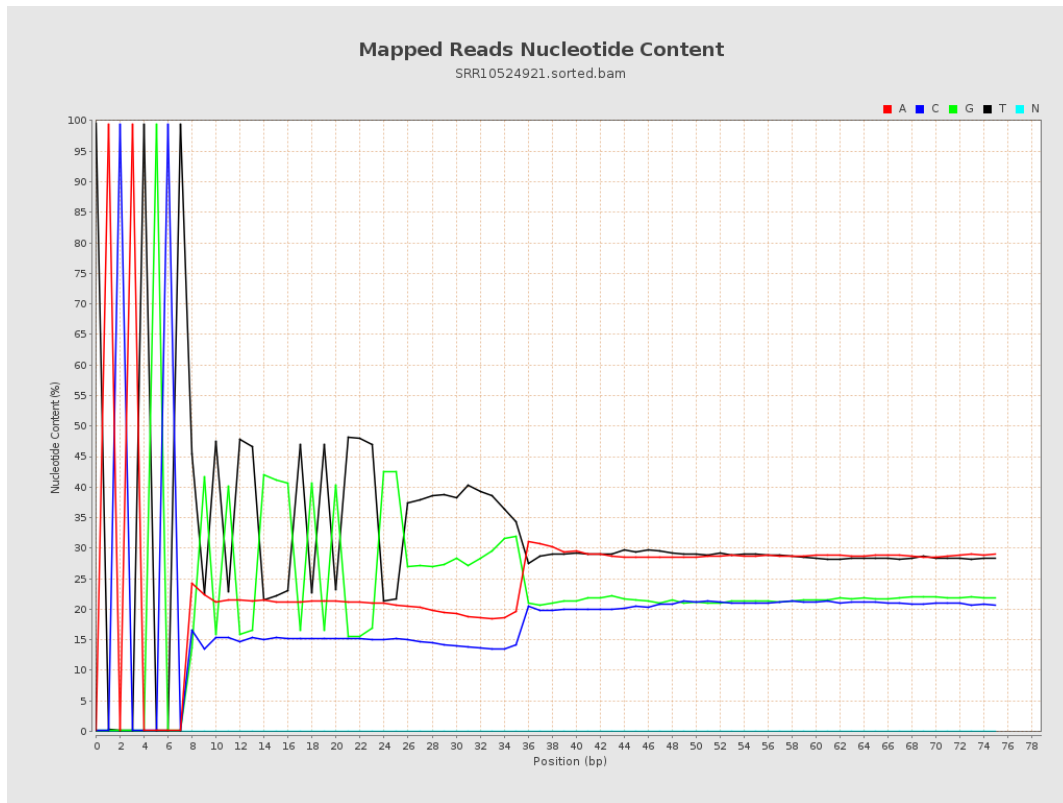
6. Results : Genome Fraction Coverage



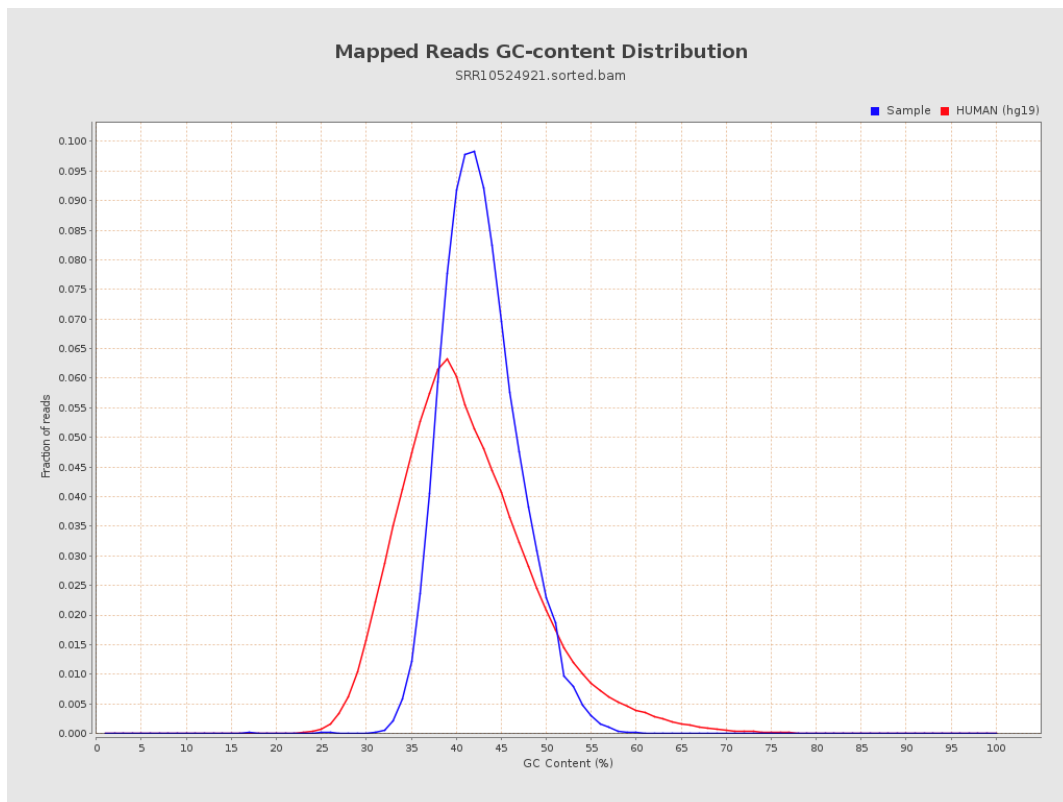
7. Results : Duplication Rate Histogram



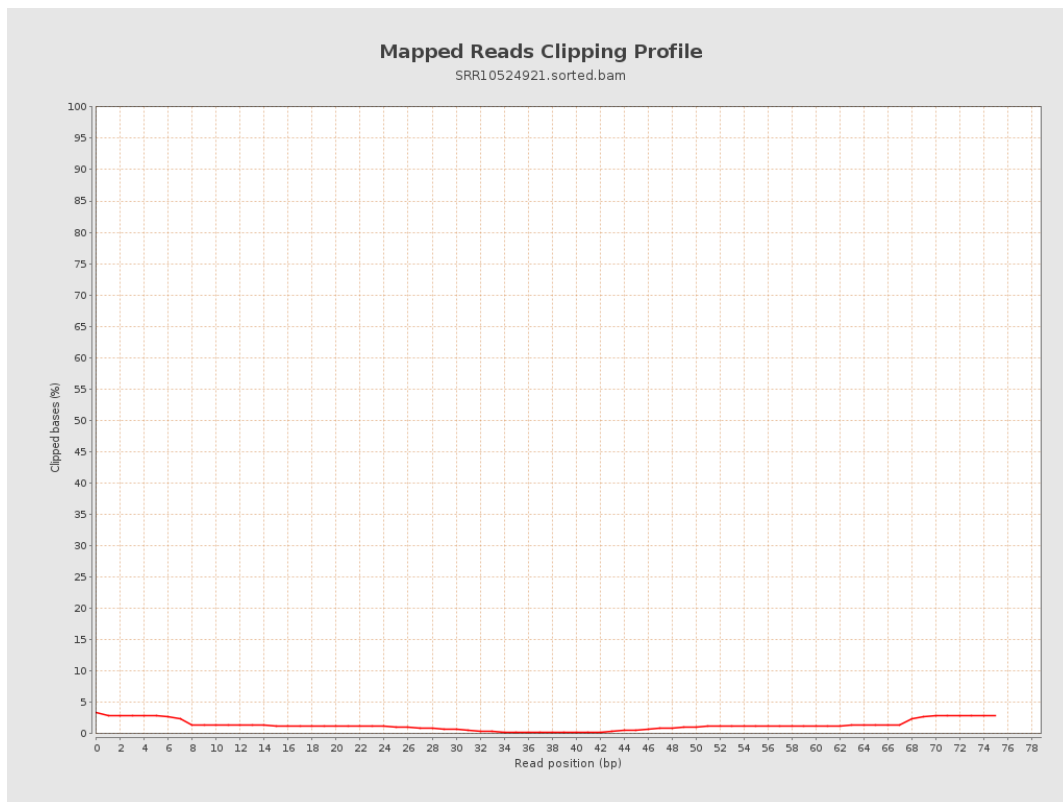
8. Results : Mapped Reads Nucleotide Content



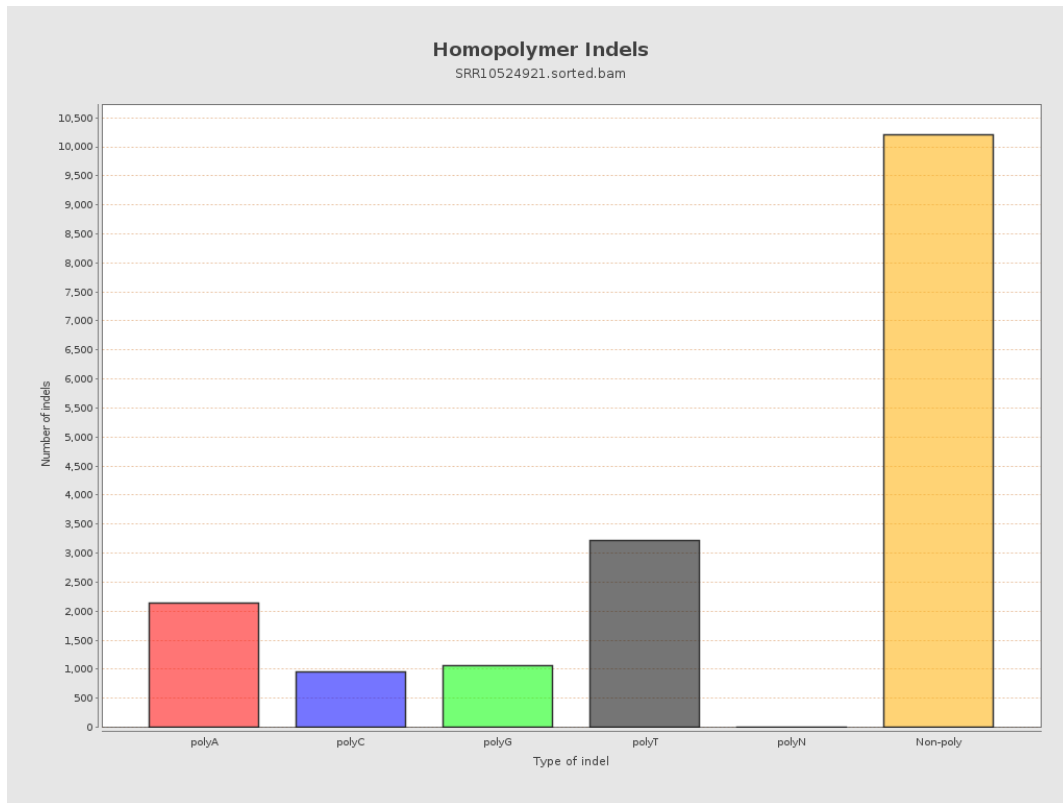
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

