

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 22:00:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524821.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_SRR10524821 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524821.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 22:00:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524821.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,727,985
Mapped reads	1,555,297 / 90.01%
Unmapped reads	172,688 / 9.99%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,798 / 0.28%
Read min/max/mean length	30 / 76 / 76.09
Duplicated reads (estimated)	63,756 / 3.69%
Duplication rate	3.18%
Clipped reads	1,556,481 / 90.07%

2.2. ACGT Content

Number/percentage of A's	22,388,758 / 25.41%
Number/percentage of C's	15,438,972 / 17.52%
Number/percentage of T's	27,843,545 / 31.6%
Number/percentage of G's	22,419,656 / 25.45%
Number/percentage of N's	10,345 / 0.01%
GC Percentage	42.97%

2.3. Coverage

Mean	0.0285

Standard Deviation	0.2461
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2.4. Mapping Quality

Mean Mapping Quality	44.63
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2.5. Mismatches and indels

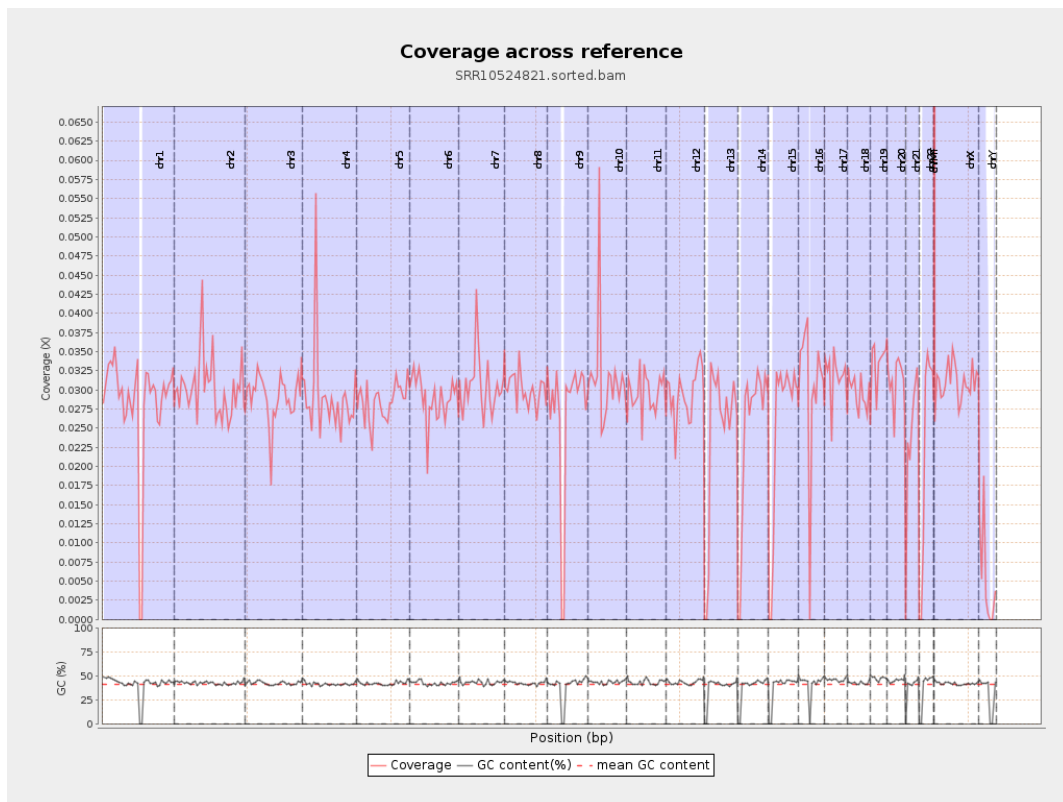
General error rate	0.52%
Mismatches	448,761
Insertions	6,155
Mapped reads with at least one insertion	0.39%
Deletions	16,692
Mapped reads with at least one deletion	1.06%
Homopolymer indels	42.19%

2.6. Chromosome stats

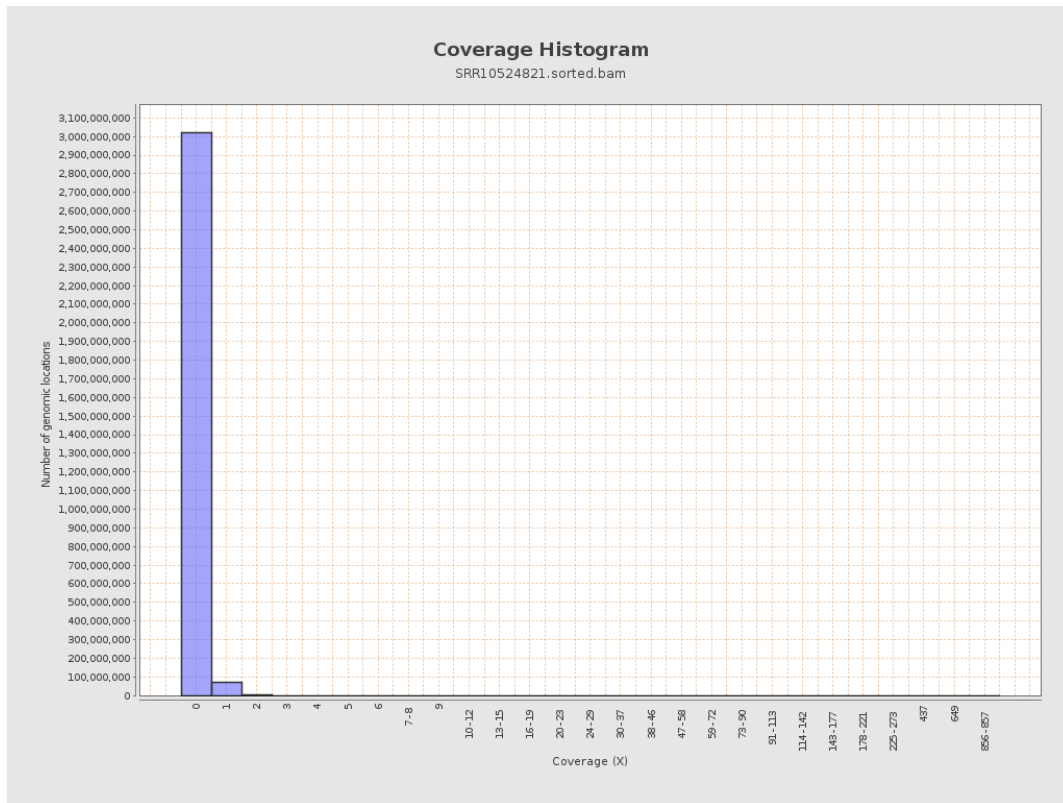
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	7056691	0.0283	0.2741
chr2	243199373	7354935	0.0302	0.4181
chr3	198022430	5752995	0.0291	0.1937
chr4	191154276	5557377	0.0291	0.2221
chr5	180915260	5171174	0.0286	0.1884
chr6	171115067	4950813	0.0289	0.2105
chr7	159138663	4858739	0.0305	0.288

chr8	146364022	4386402	0.03	0.2163
chr9	141213431	3761794	0.0266	0.2137
chr10	135534747	4292757	0.0317	0.3065
chr11	135006516	4013548	0.0297	0.2318
chr12	133851895	3948055	0.0295	0.1937
chr13	115169878	2784071	0.0242	0.1732
chr14	107349540	2663444	0.0248	0.1785
chr15	102531392	2561509	0.025	0.1799
chr16	90354753	2731678	0.0302	0.2157
chr17	81195210	2576475	0.0317	0.2084
chr18	78077248	2310460	0.0296	0.3108
chr19	59128983	1976855	0.0334	0.2571
chr20	63025520	1953970	0.031	0.208
chr21	48129895	1167043	0.0242	0.1944
chr22	51304566	1160383	0.0226	0.1714
chrMT	16571	10826	0.6533	0.9822
chrX	155270560	4815510	0.031	0.2147
chrY	59373566	310456	0.0052	0.1486

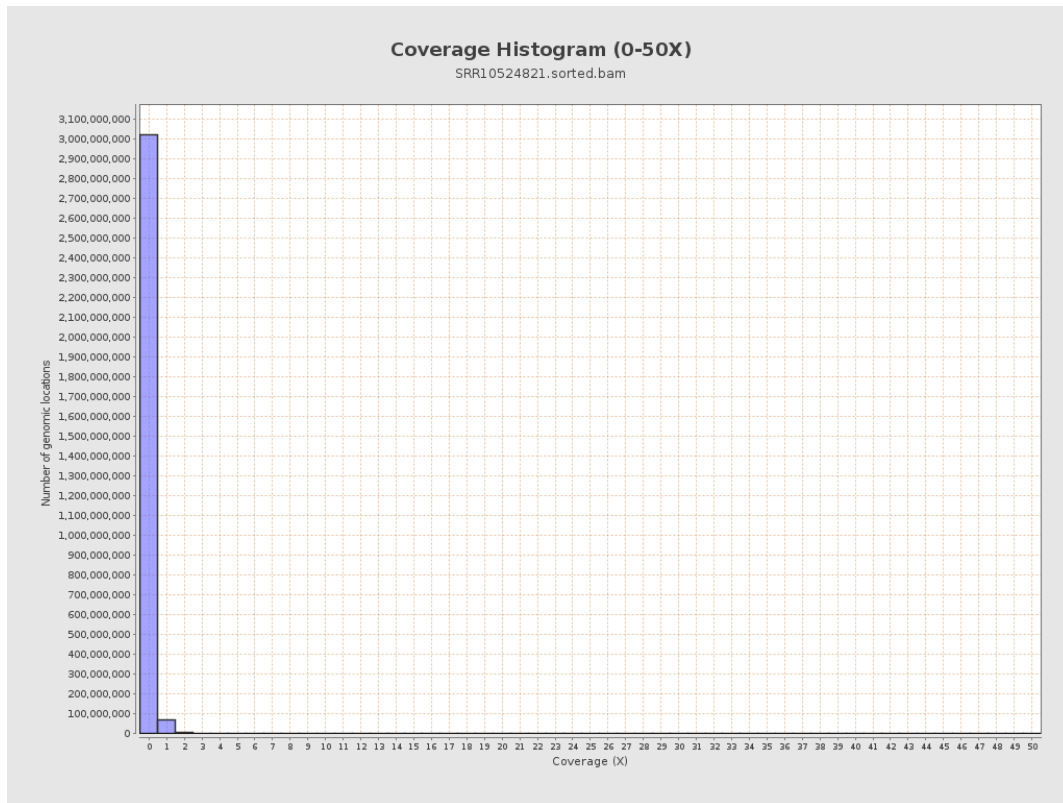
3. Results : Coverage across reference



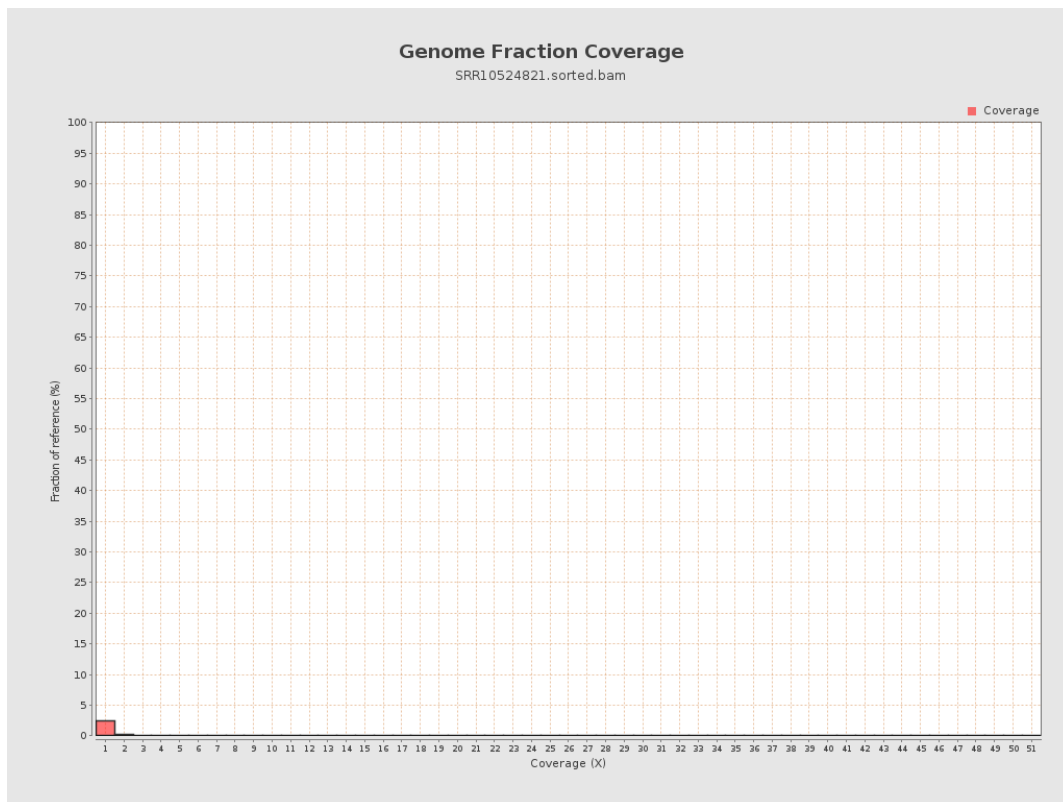
4. Results : Coverage Histogram



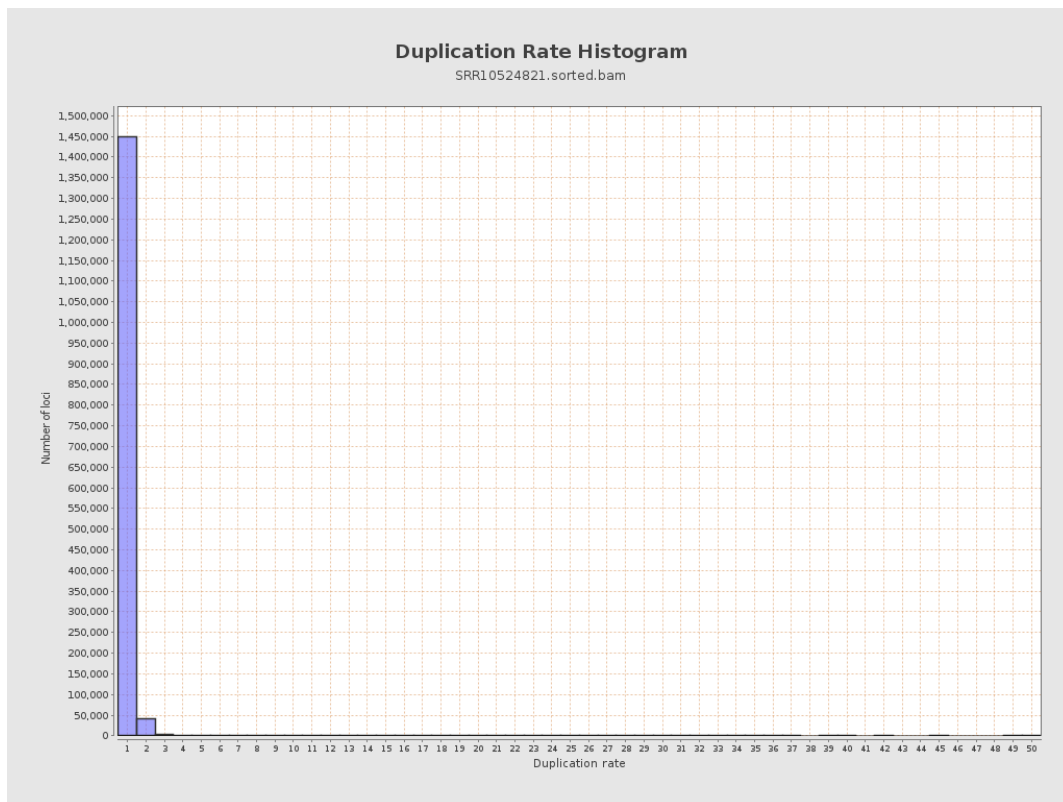
5. Results : Coverage Histogram (0-50X)



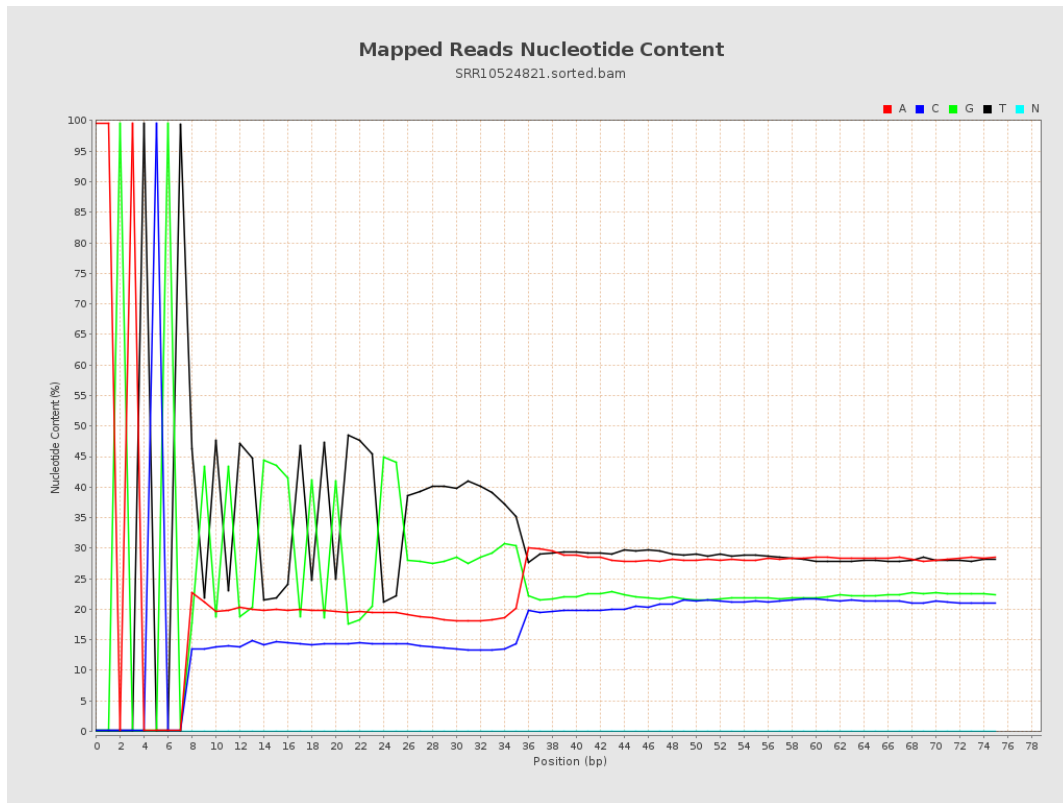
6. Results : Genome Fraction Coverage



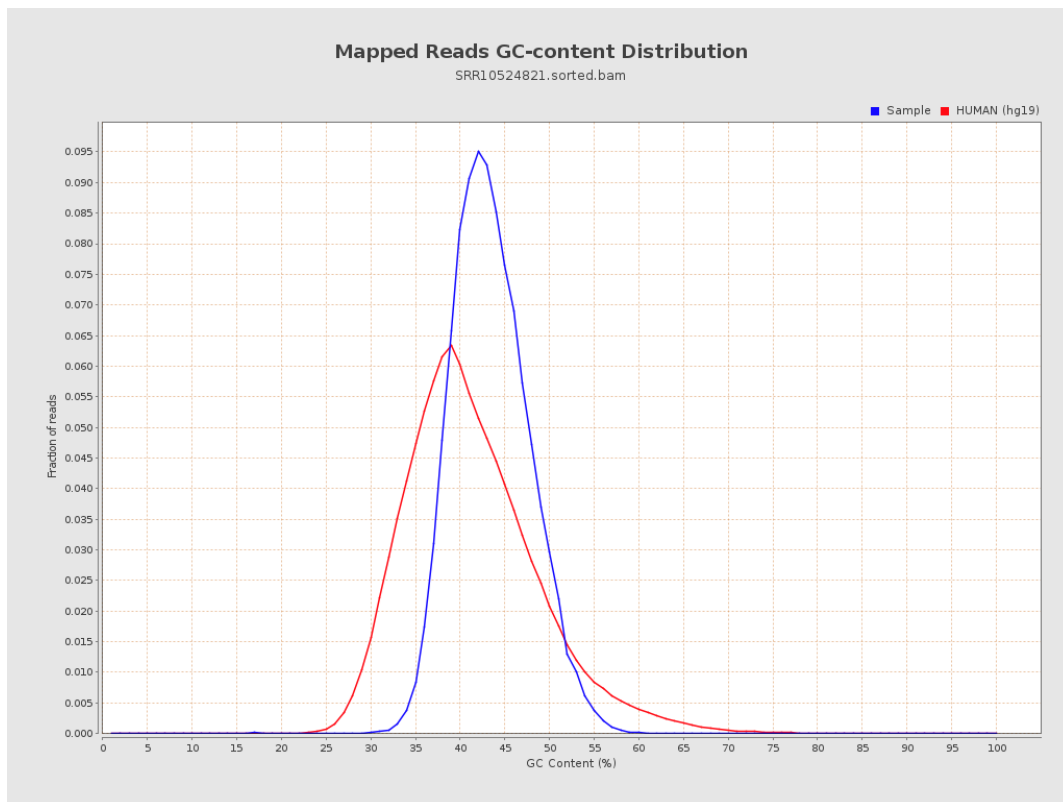
7. Results : Duplication Rate Histogram



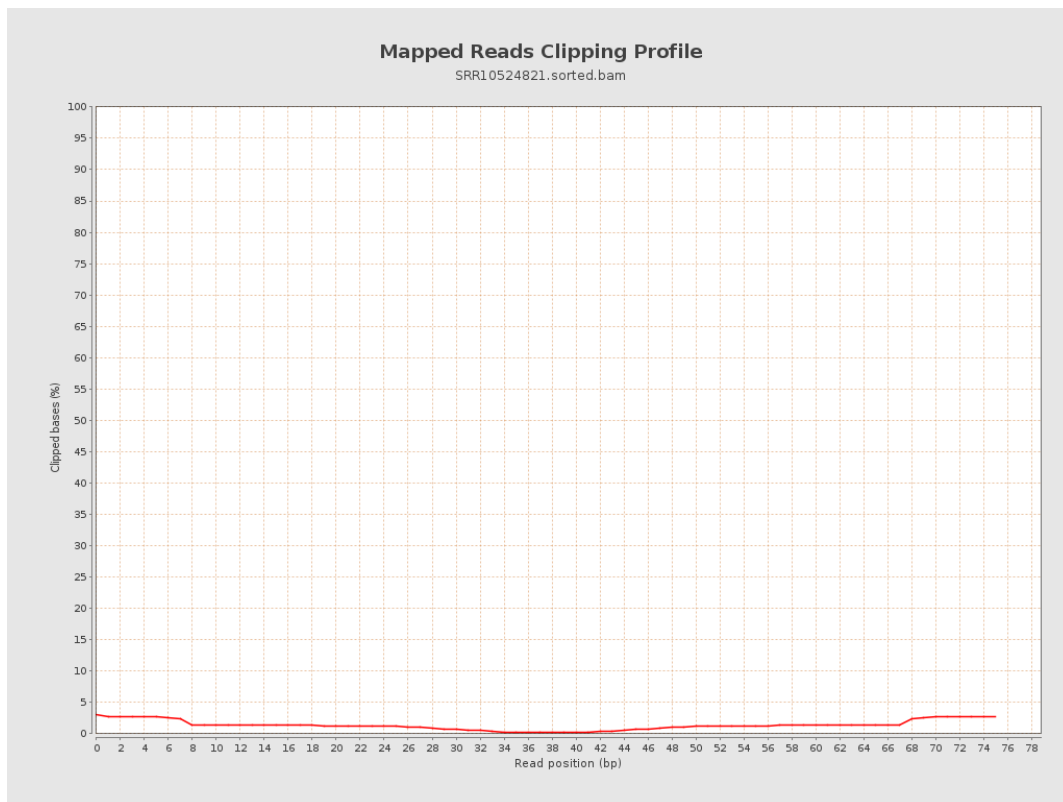
8. Results : Mapped Reads Nucleotide Content



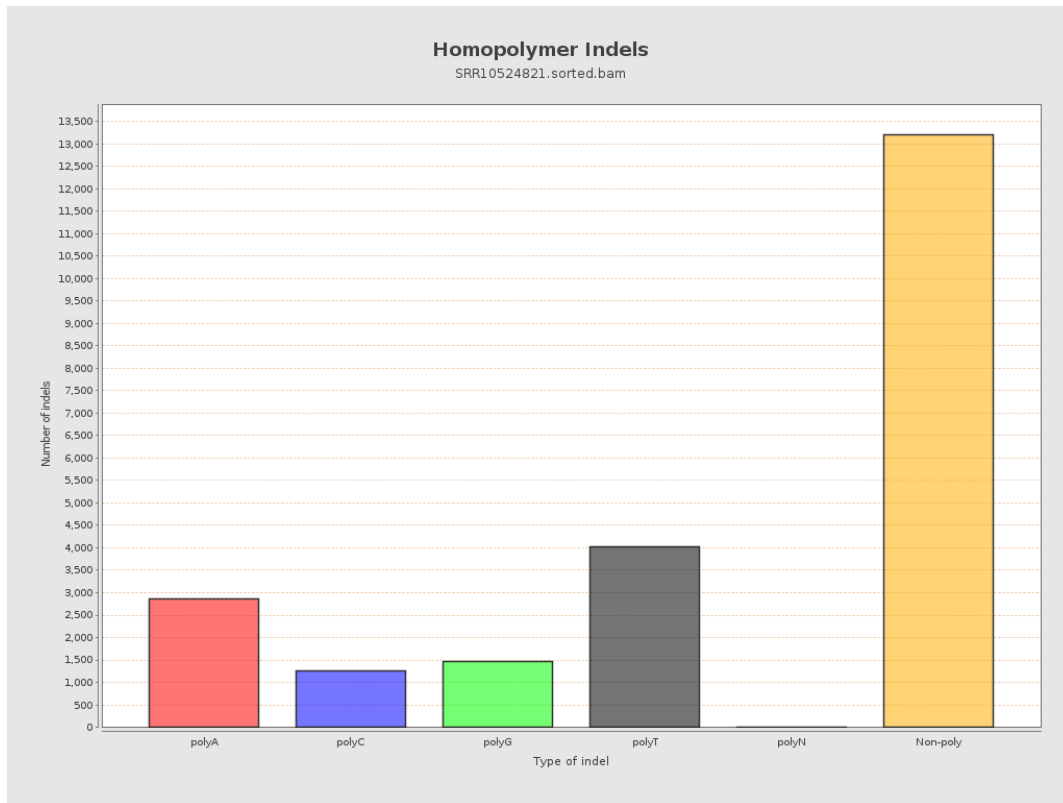
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

