

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 12:34:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084762.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_SRR3084762 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084762.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 12:34:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084762.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,454,452
Mapped reads	1,296,817 / 89.16%
Unmapped reads	157,635 / 10.84%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,298 / 0.91%
Read min/max/mean length	30 / 76 / 76.32
Duplicated reads (estimated)	45,691 / 3.14%
Duplication rate	2.91%
Clipped reads	527,021 / 36.24%

2.2. ACGT Content

Number/percentage of A's	24,463,389 / 27.87%
Number/percentage of C's	16,553,839 / 18.86%
Number/percentage of T's	27,331,978 / 31.13%
Number/percentage of G's	19,405,657 / 22.1%
Number/percentage of N's	35,177 / 0.04%
GC Percentage	40.96%

2.3. Coverage

Mean	0.0284

Standard Deviation	0.2452
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2.4. Mapping Quality

Mean Mapping Quality	47.02
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2.5. Mismatches and indels

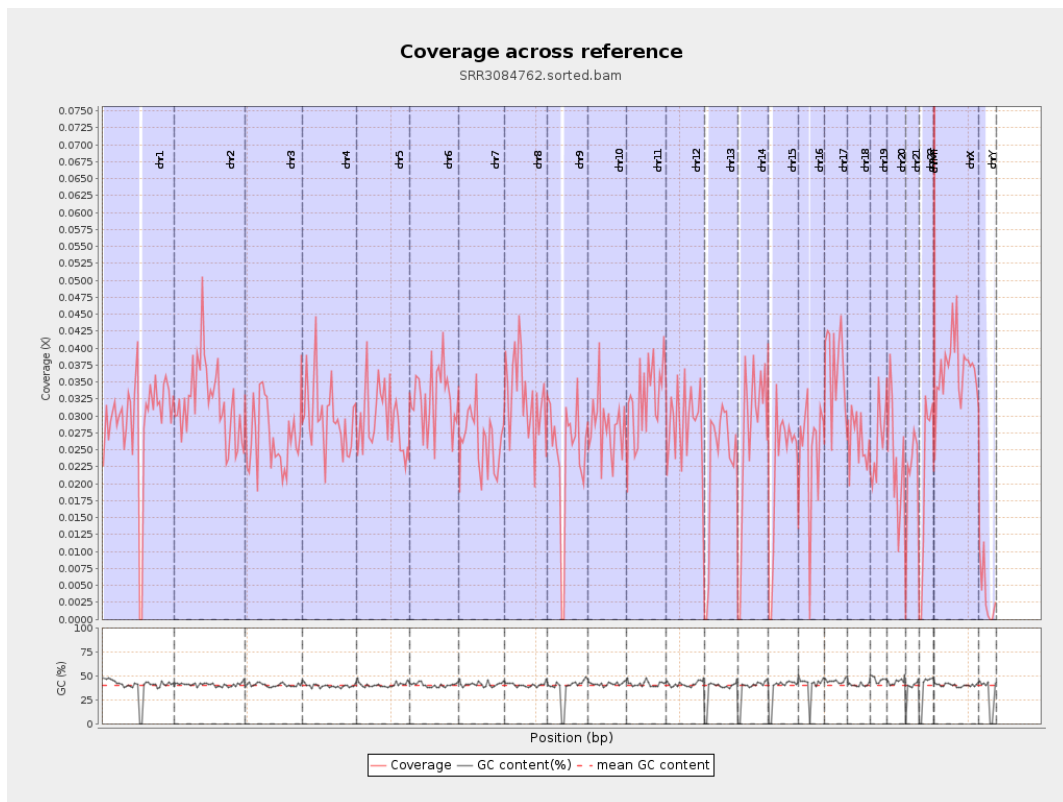
General error rate	0.85%
Mismatches	731,498
Insertions	6,700
Mapped reads with at least one insertion	0.51%
Deletions	20,776
Mapped reads with at least one deletion	1.59%
Homopolymer indels	46.97%

2.6. Chromosome stats

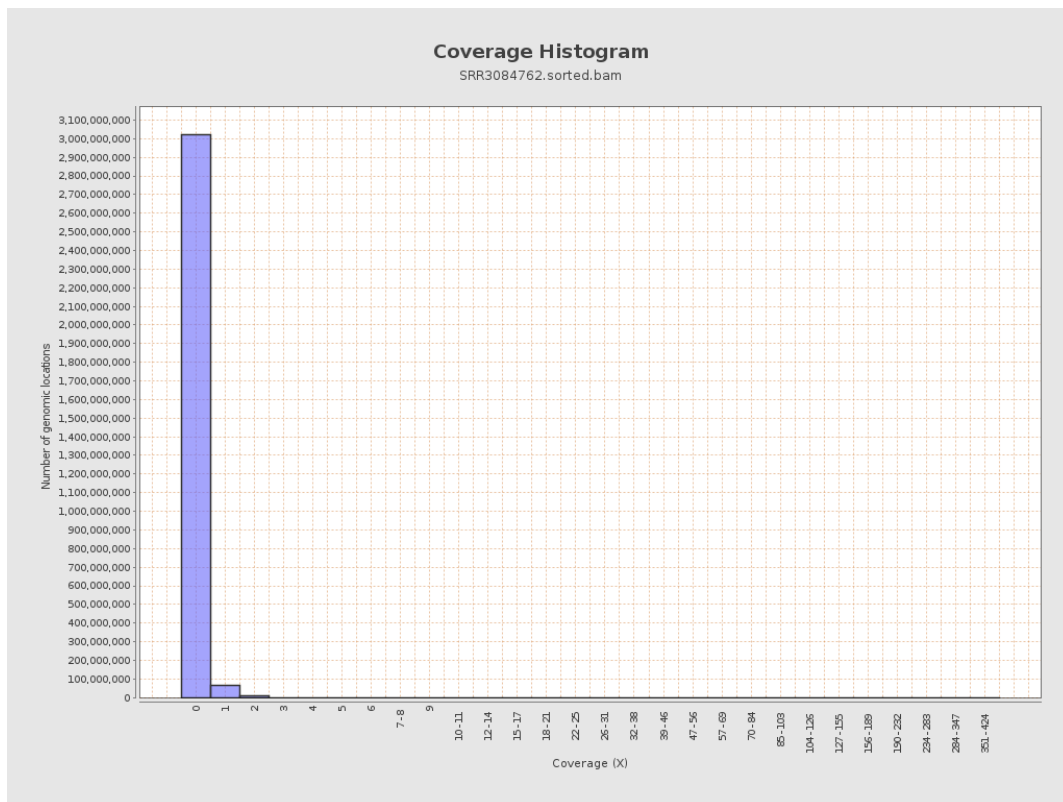
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	7258571	0.0291	0.3966
chr2	243199373	7792866	0.032	0.2894
chr3	198022430	5280501	0.0267	0.1822
chr4	191154276	5708956	0.0299	0.2042
chr5	180915260	5360999	0.0296	0.1921
chr6	171115067	5560128	0.0325	0.2146
chr7	159138663	4225226	0.0266	0.255

chr8	146364022	4804383	0.0328	0.2745
chr9	141213431	3420943	0.0242	0.2232
chr10	135534747	3847839	0.0284	0.2481
chr11	135006516	4427333	0.0328	0.2349
chr12	133851895	3834584	0.0286	0.19
chr13	115169878	2631883	0.0229	0.1692
chr14	107349540	2925630	0.0273	0.1897
chr15	102531392	2292814	0.0224	0.1694
chr16	90354753	2219728	0.0246	0.1823
chr17	81195210	3030022	0.0373	0.2233
chr18	78077248	2046108	0.0262	0.3945
chr19	59128983	1565547	0.0265	0.3153
chr20	63025520	1507855	0.0239	0.1765
chr21	48129895	1013262	0.0211	0.1723
chr22	51304566	1090567	0.0213	0.1606
chrMT	16571	5139	0.3101	0.5746
chrX	155270560	5758175	0.0371	0.2272
chrY	59373566	215536	0.0036	0.0893

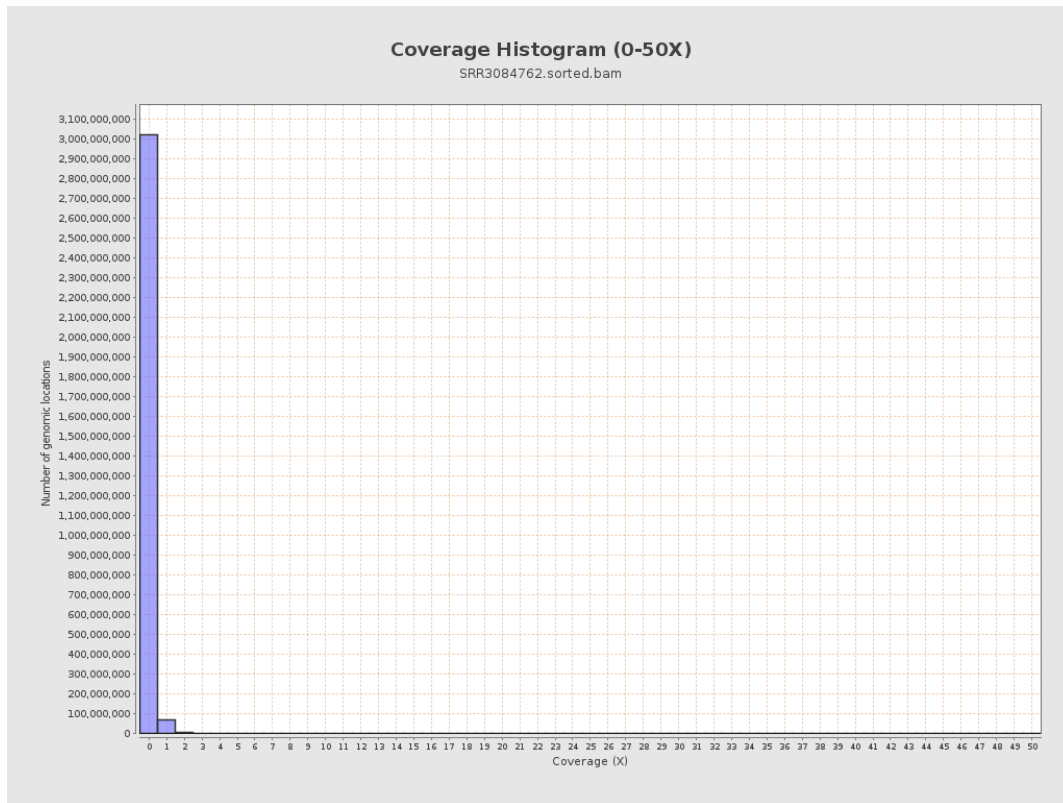
3. Results : Coverage across reference



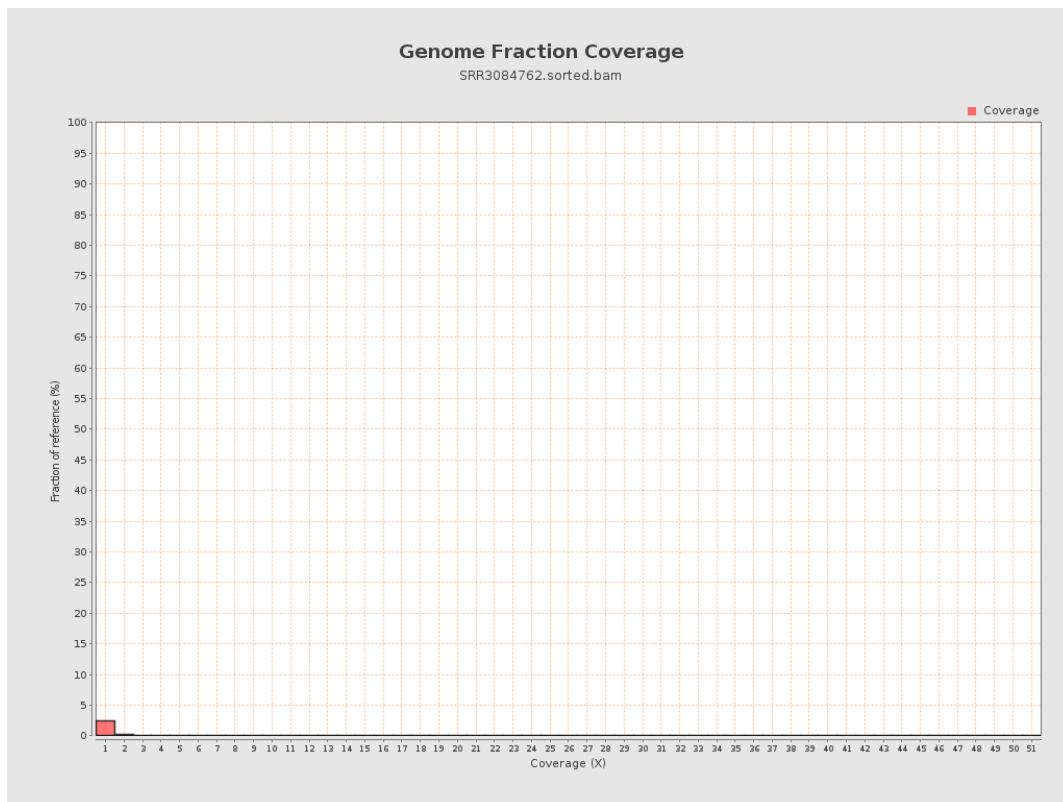
4. Results : Coverage Histogram



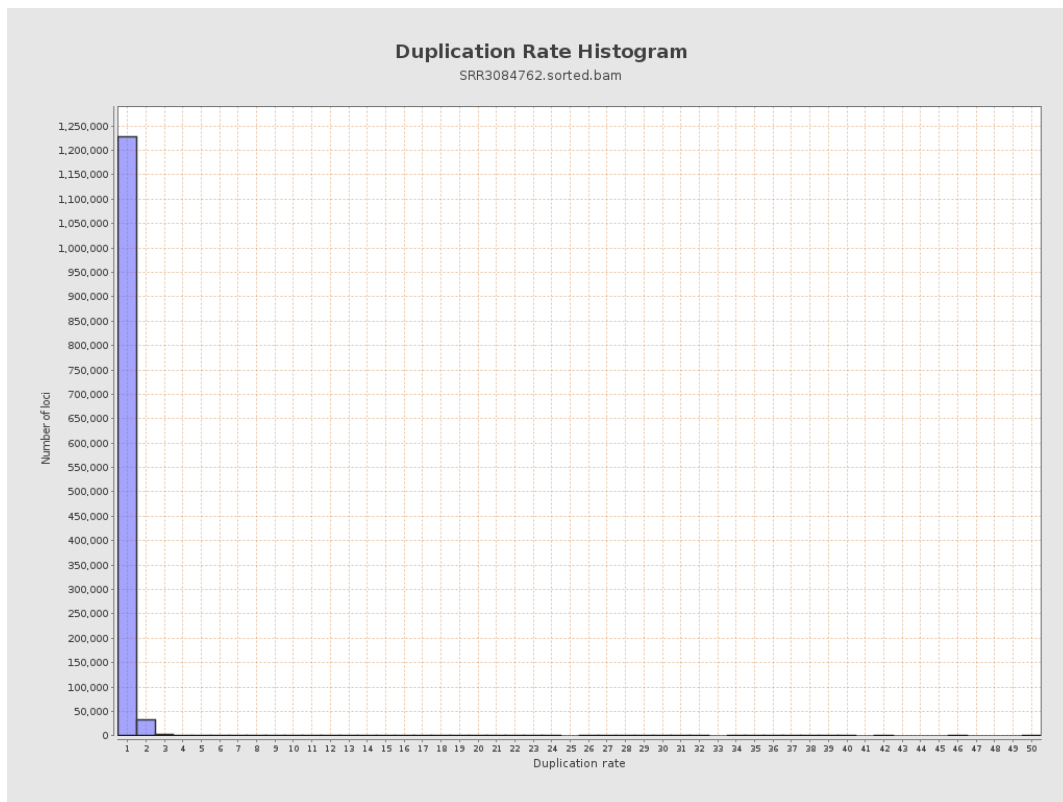
5. Results : Coverage Histogram (0-50X)



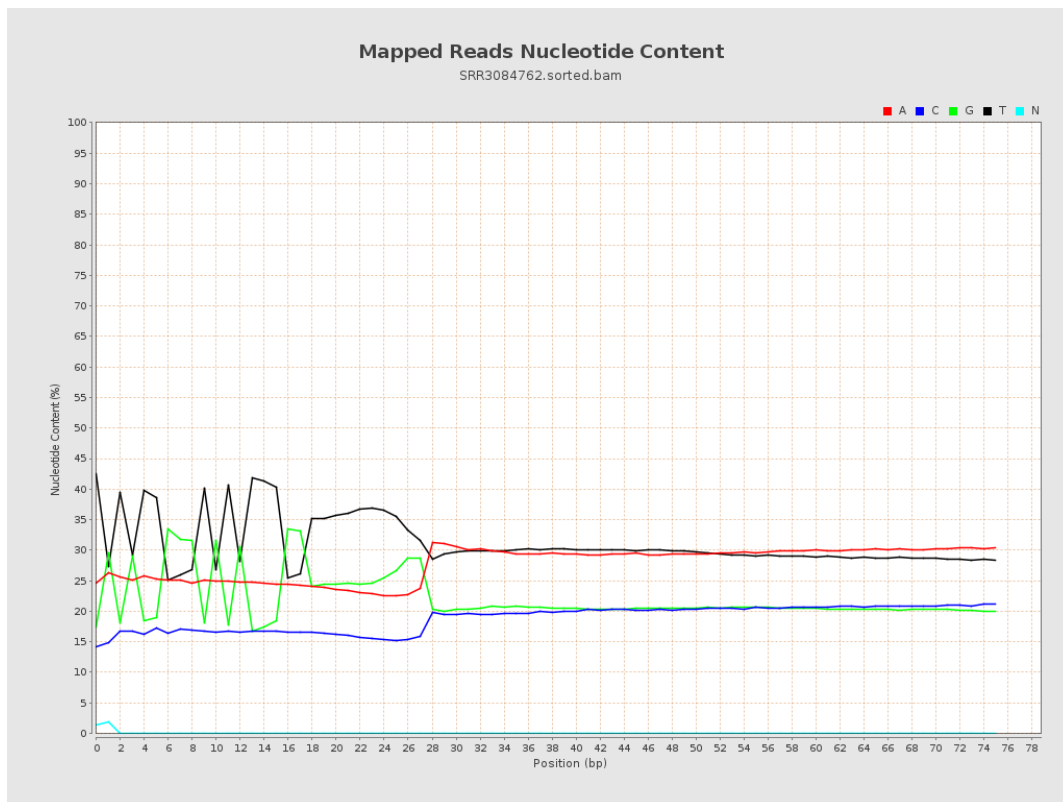
6. Results : Genome Fraction Coverage



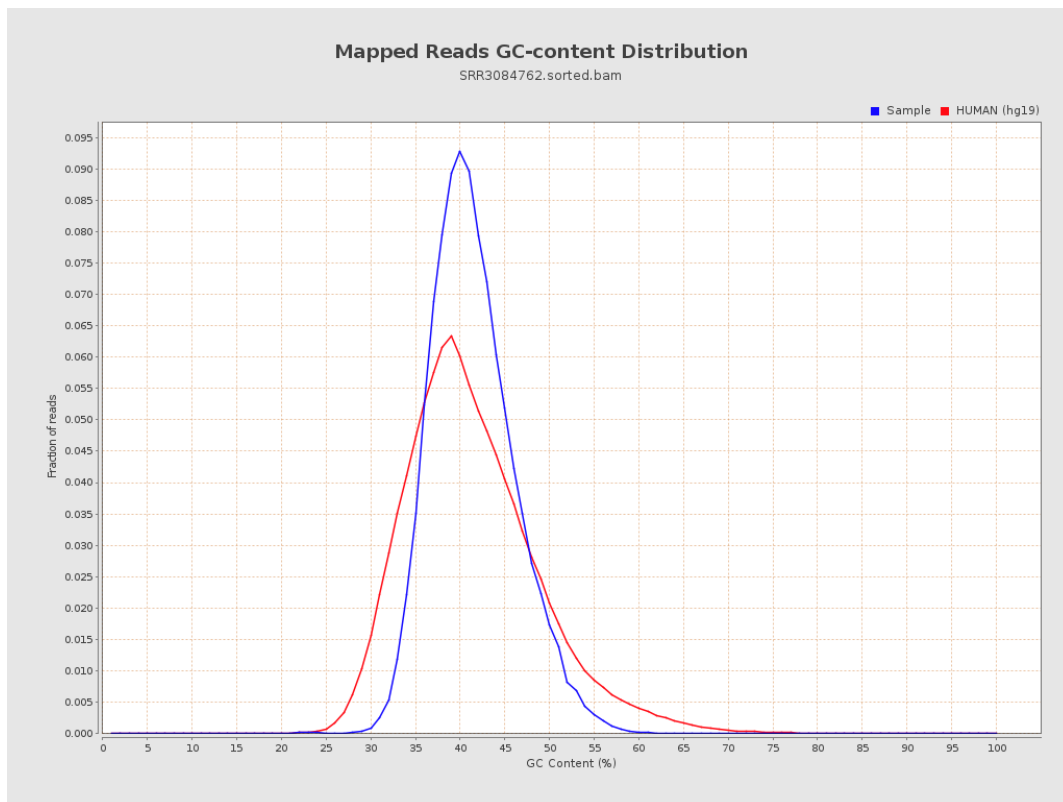
7. Results : Duplication Rate Histogram



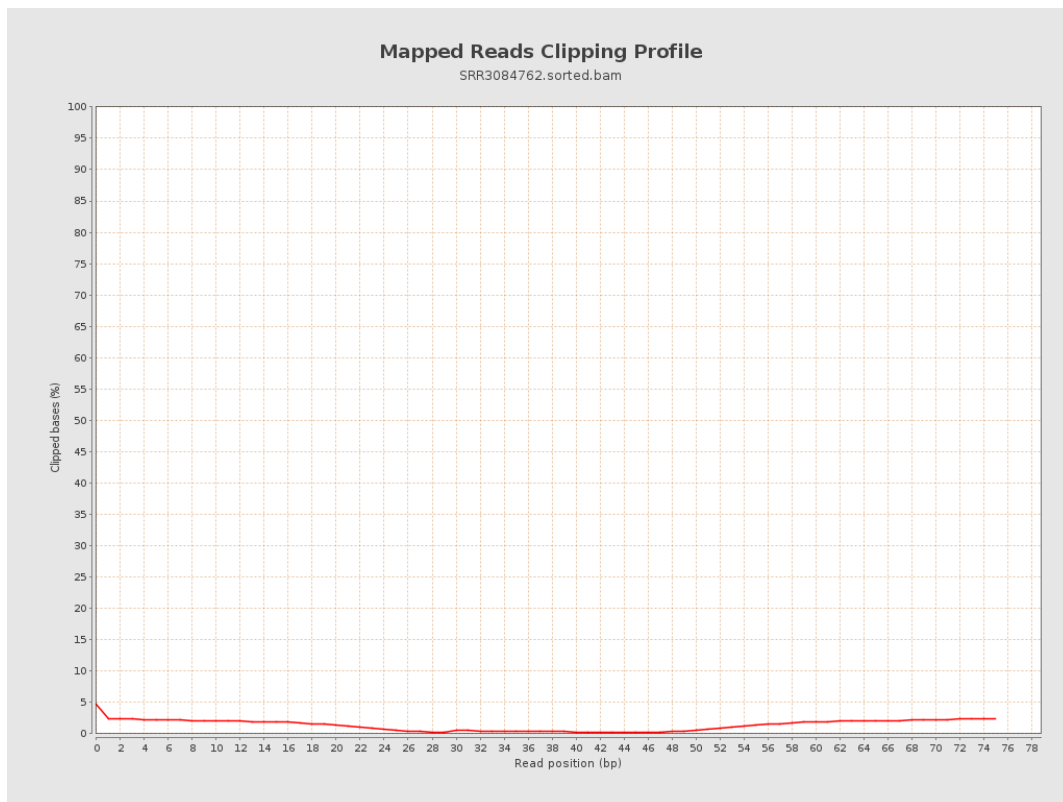
8. Results : Mapped Reads Nucleotide Content



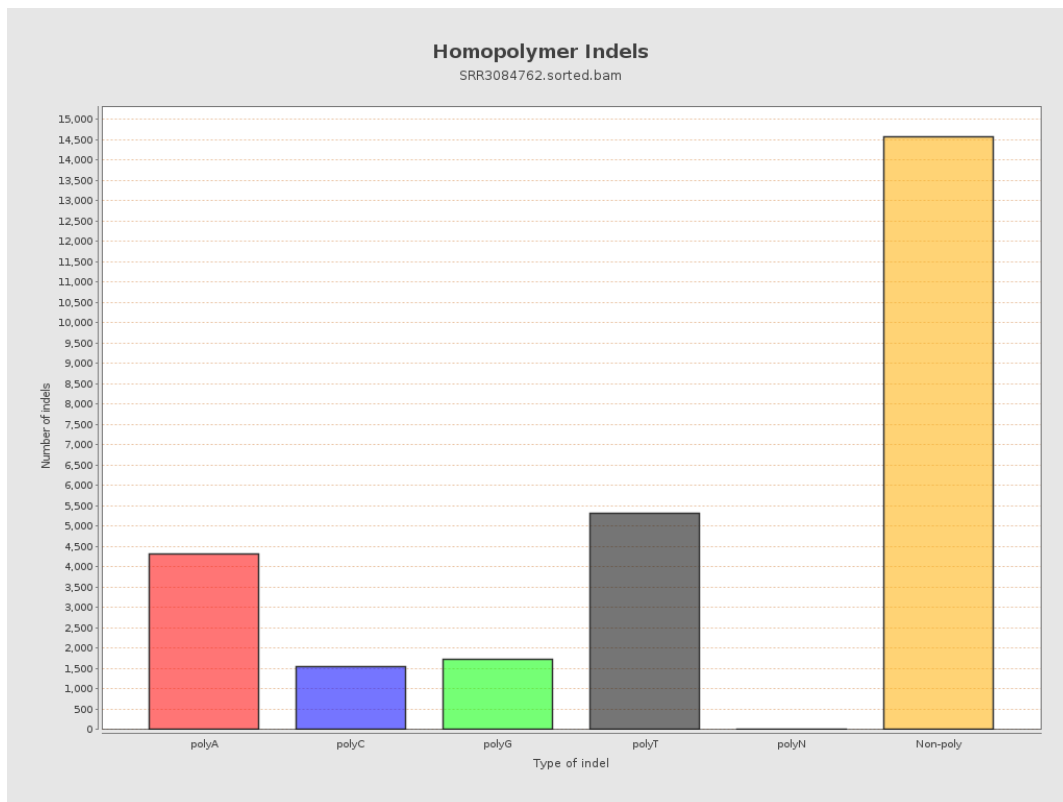
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

