

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 22:05:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8751222.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_SRR8751222 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8751222.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 22:05:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8751222.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,118,220
Mapped reads	3,942,707 / 95.74%
Unmapped reads	175,513 / 4.26%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	71,240 / 1.73%
Read min/max/mean length	30 / 101 / 101.72
Duplicated reads (estimated)	50,246 / 1.22%
Duplication rate	1.14%
Clipped reads	481,828 / 11.7%

2.2. ACGT Content

Number/percentage of A's	114,641,322 / 29.38%
Number/percentage of C's	80,621,560 / 20.66%
Number/percentage of T's	115,372,475 / 29.57%
Number/percentage of G's	79,545,420 / 20.39%
Number/percentage of N's	2,229 / 0%
GC Percentage	41.05%

2.3. Coverage

Mean	0.1261

Standard Deviation	0.4488
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2.4. Mapping Quality

Mean Mapping Quality	51.79
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2.5. Mismatches and indels

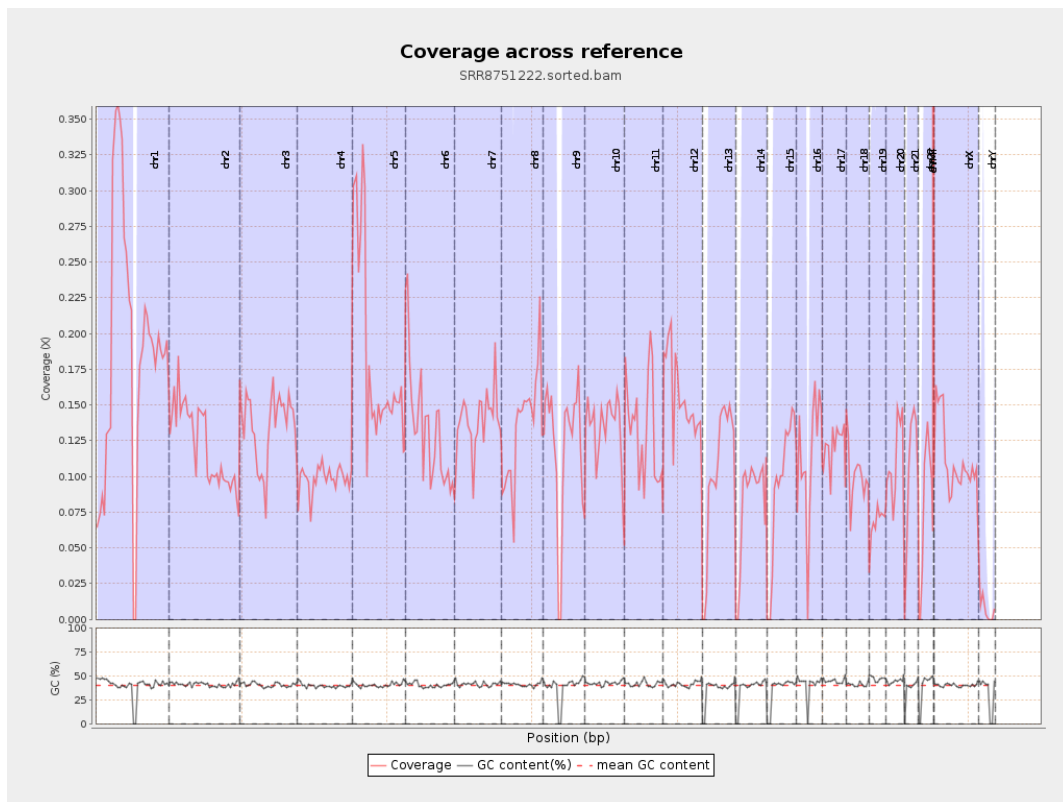
General error rate	0.28%
Mismatches	1,027,382
Insertions	39,876
Mapped reads with at least one insertion	1%
Deletions	44,616
Mapped reads with at least one deletion	1.11%
Homopolymer indels	46.1%

2.6. Chromosome stats

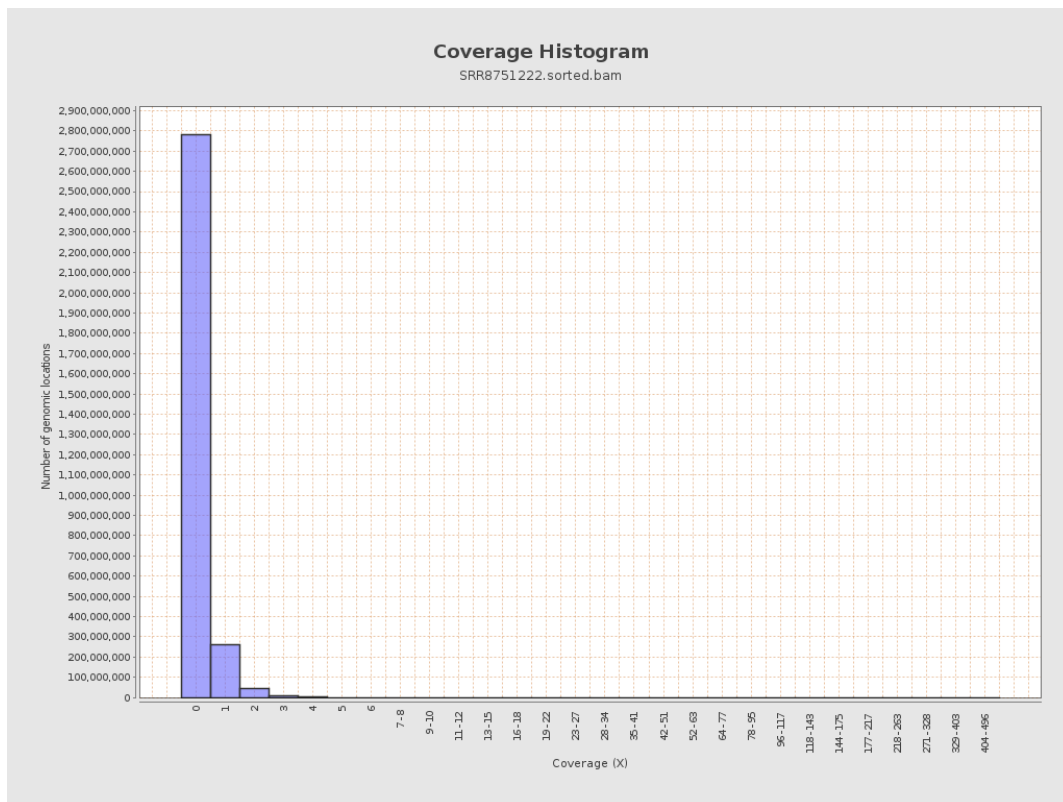
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	46962522	0.1884	0.6829
chr2	243199373	29575041	0.1216	0.4031
chr3	198022430	26837527	0.1355	0.4203
chr4	191154276	18859874	0.0987	0.3598
chr5	180915260	33136196	0.1832	0.4976
chr6	171115067	22682505	0.1326	0.4634
chr7	159138663	22230327	0.1397	0.433

chr8	146364022	19740107	0.1349	0.4252
chr9	141213431	17079244	0.1209	0.4057
chr10	135534747	18484285	0.1364	0.5243
chr11	135006516	17811711	0.1319	0.4363
chr12	133851895	20800200	0.1554	0.4541
chr13	115169878	11866059	0.103	0.3683
chr14	107349540	8597757	0.0801	0.324
chr15	102531392	9647829	0.0941	0.3554
chr16	90354753	10297117	0.114	0.394
chr17	81195210	9777447	0.1204	0.4356
chr18	78077248	7824696	0.1002	0.4081
chr19	59128983	4061548	0.0687	0.431
chr20	63025520	6961950	0.1105	0.3875
chr21	48129895	4912923	0.1021	0.3719
chr22	51304566	3988526	0.0777	0.3271
chrMT	16571	417991	25.2242	14.0743
chrX	155270560	17284623	0.1113	0.3833
chrY	59373566	442985	0.0075	0.1592

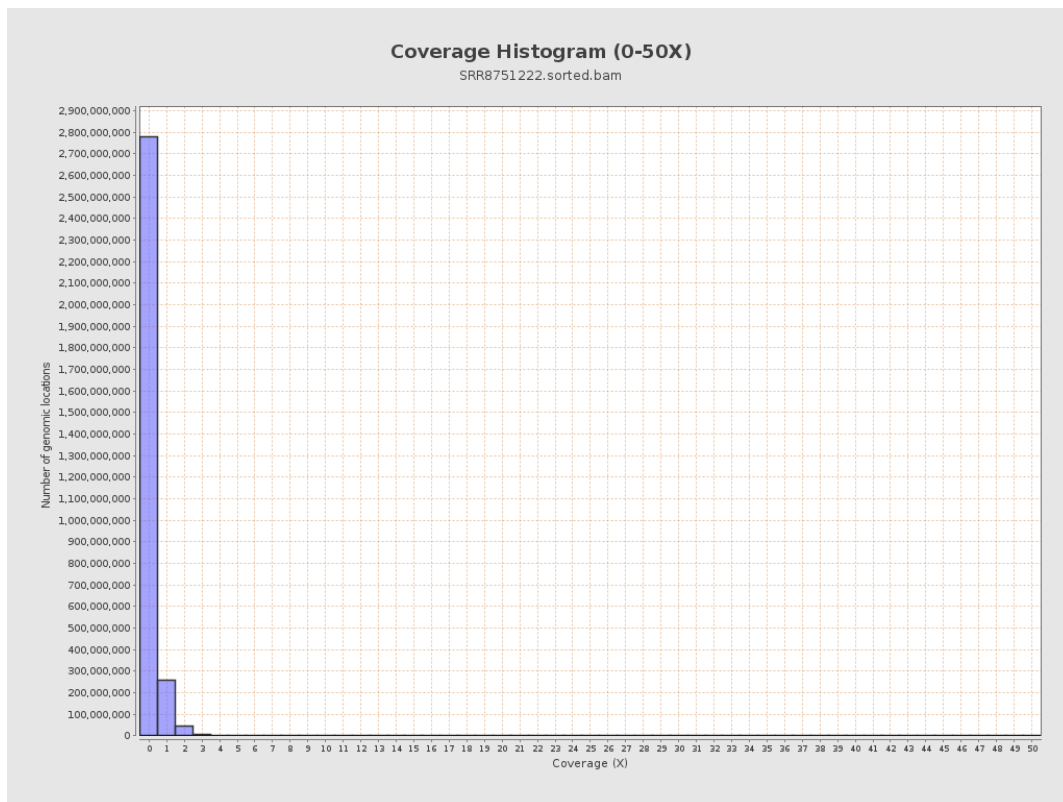
3. Results : Coverage across reference



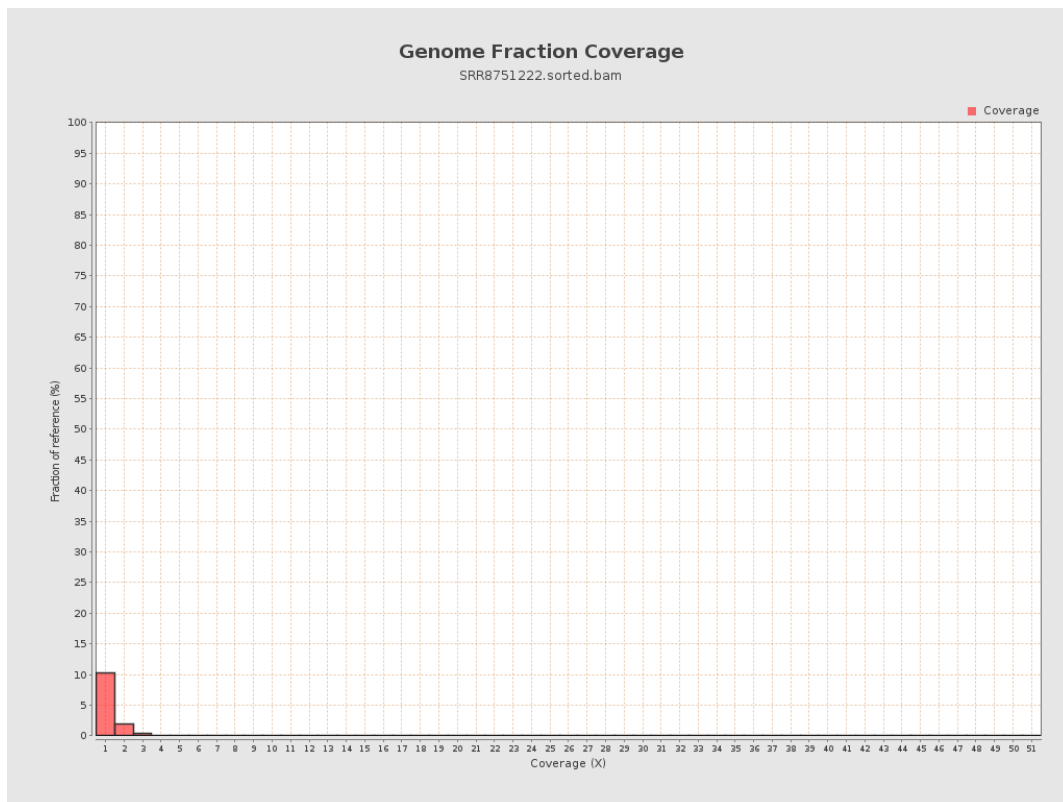
4. Results : Coverage Histogram



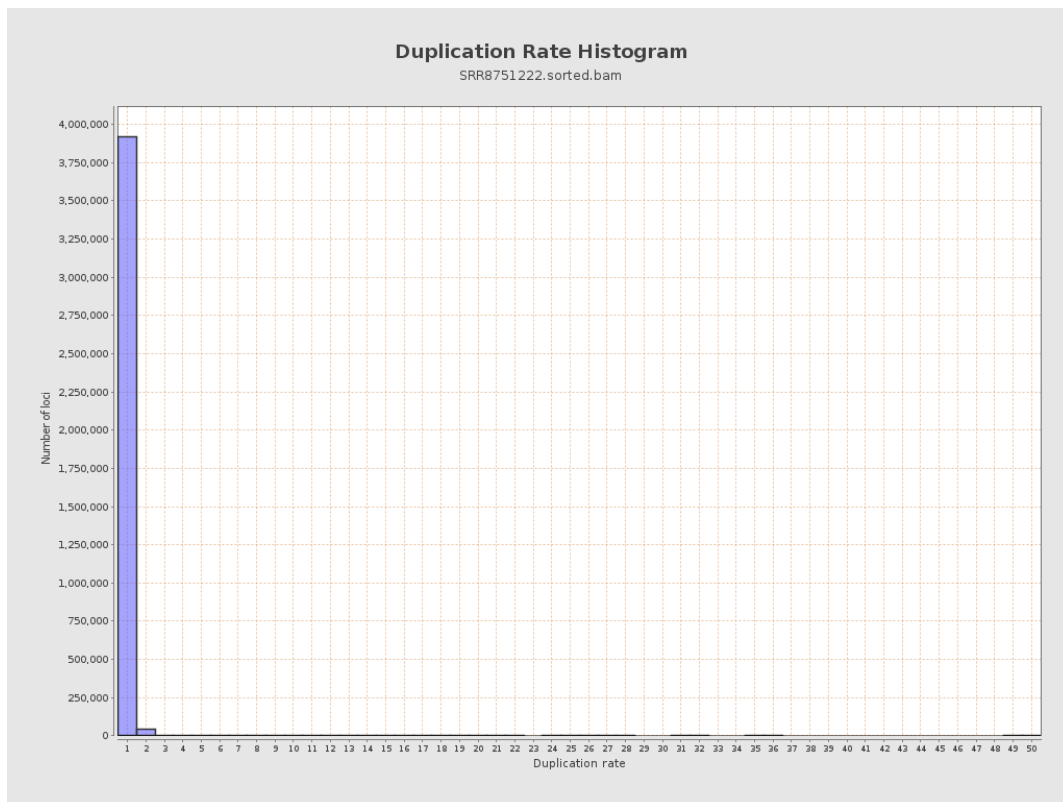
5. Results : Coverage Histogram (0-50X)



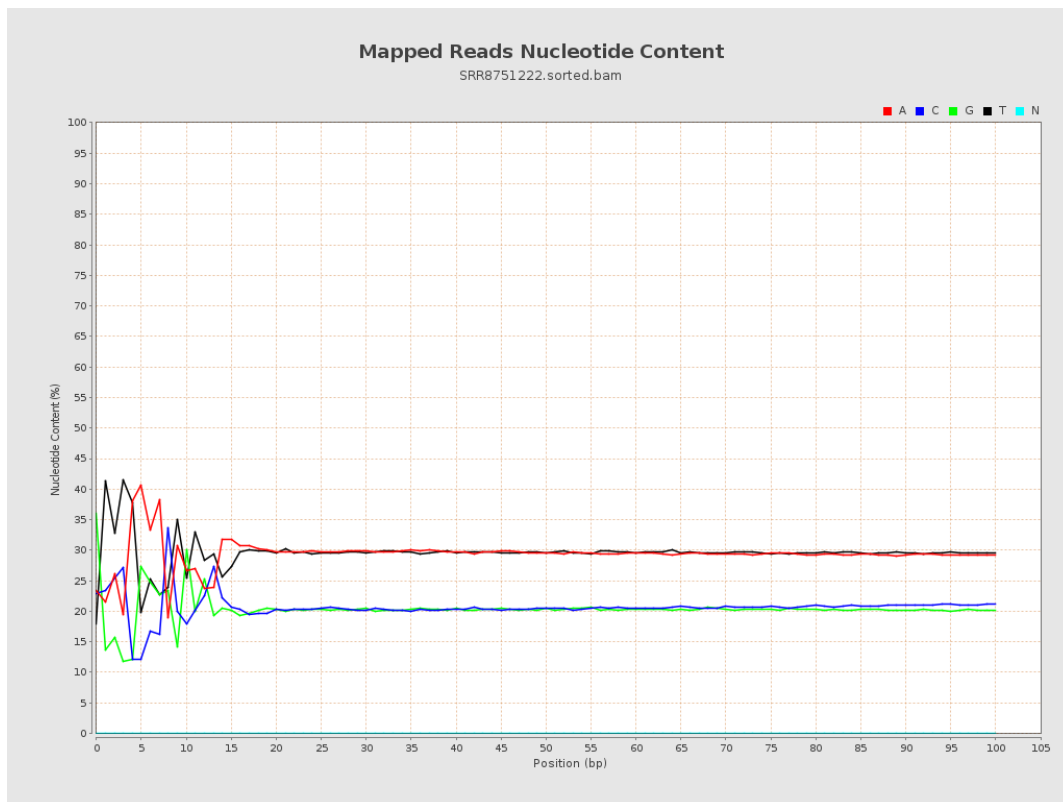
6. Results : Genome Fraction Coverage



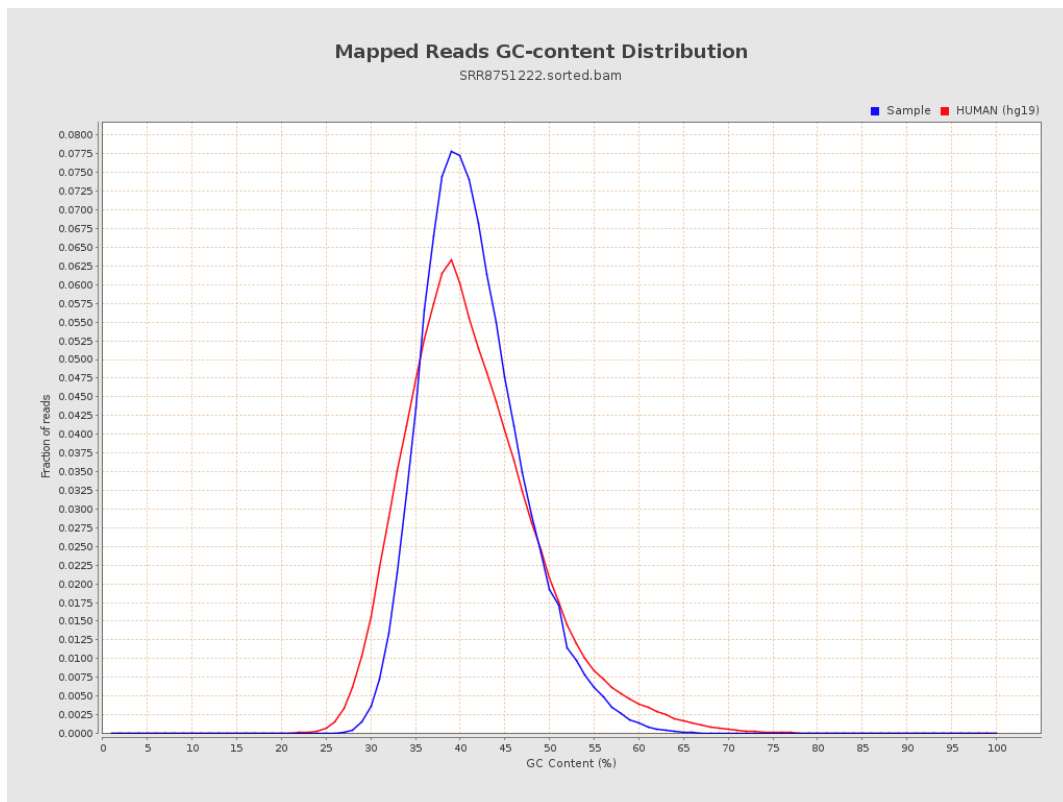
7. Results : Duplication Rate Histogram



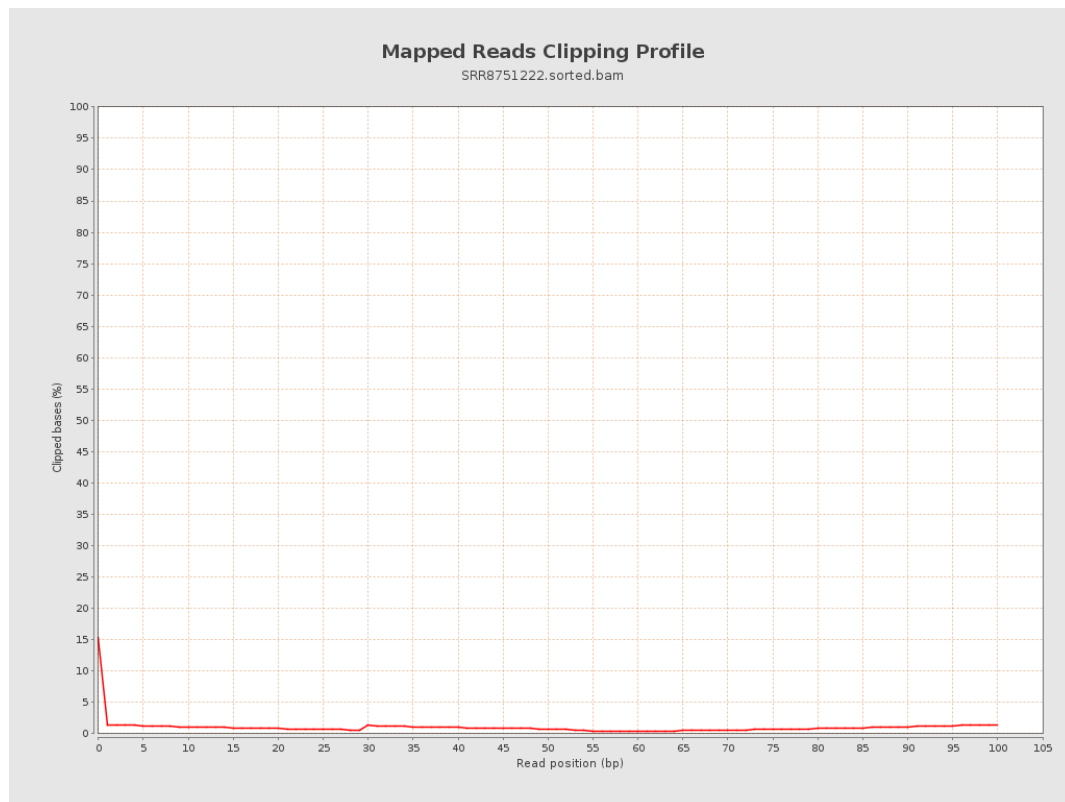
8. Results : Mapped Reads Nucleotide Content



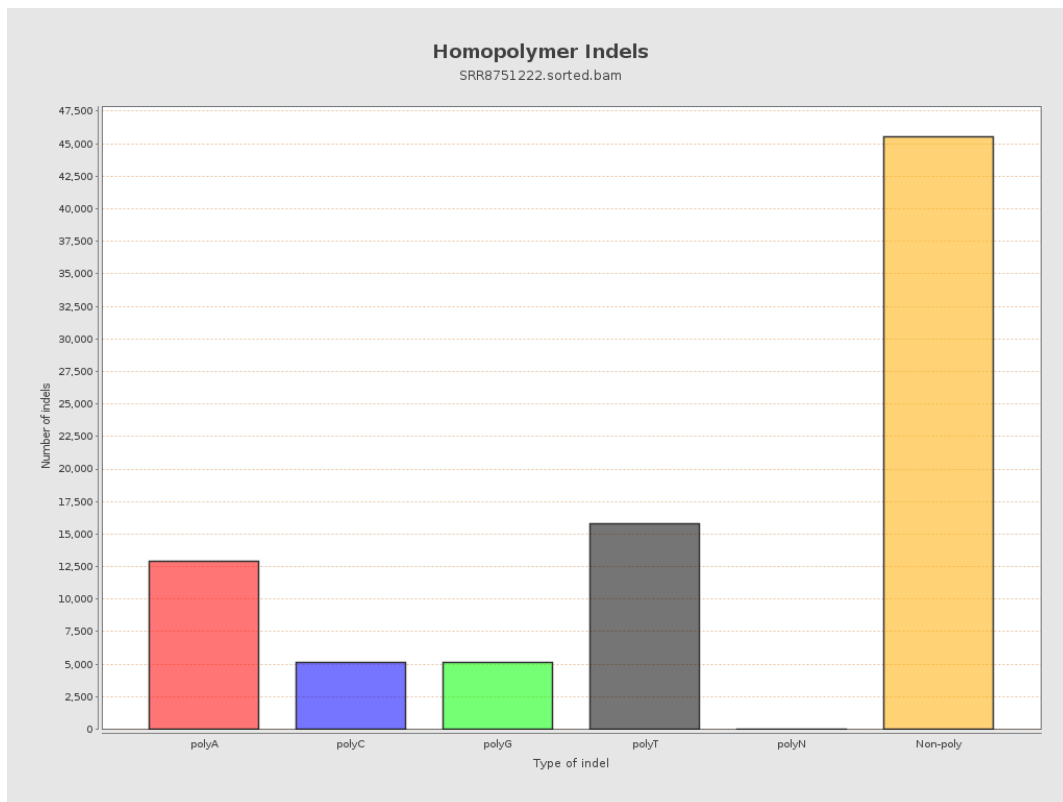
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

