

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 04:23:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240056.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_SRR6240056 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240056.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 04:23:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240056.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,822,803
Mapped reads	1,496,274 / 82.09%
Unmapped reads	326,529 / 17.91%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,791 / 0.37%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	101,609 / 5.57%
Duplication rate	5.66%
Clipped reads	917,980 / 50.36%

2.2. ACGT Content

Number/percentage of A's	25,594,961 / 27.34%
Number/percentage of C's	16,256,560 / 17.37%
Number/percentage of T's	30,431,981 / 32.51%
Number/percentage of G's	21,265,533 / 22.72%
Number/percentage of N's	62,883 / 0.07%
GC Percentage	40.08%

2.3. Coverage

Mean	0.0303

Standard Deviation	0.2981
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2.4. Mapping Quality

Mean Mapping Quality	45.89
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2.5. Mismatches and indels

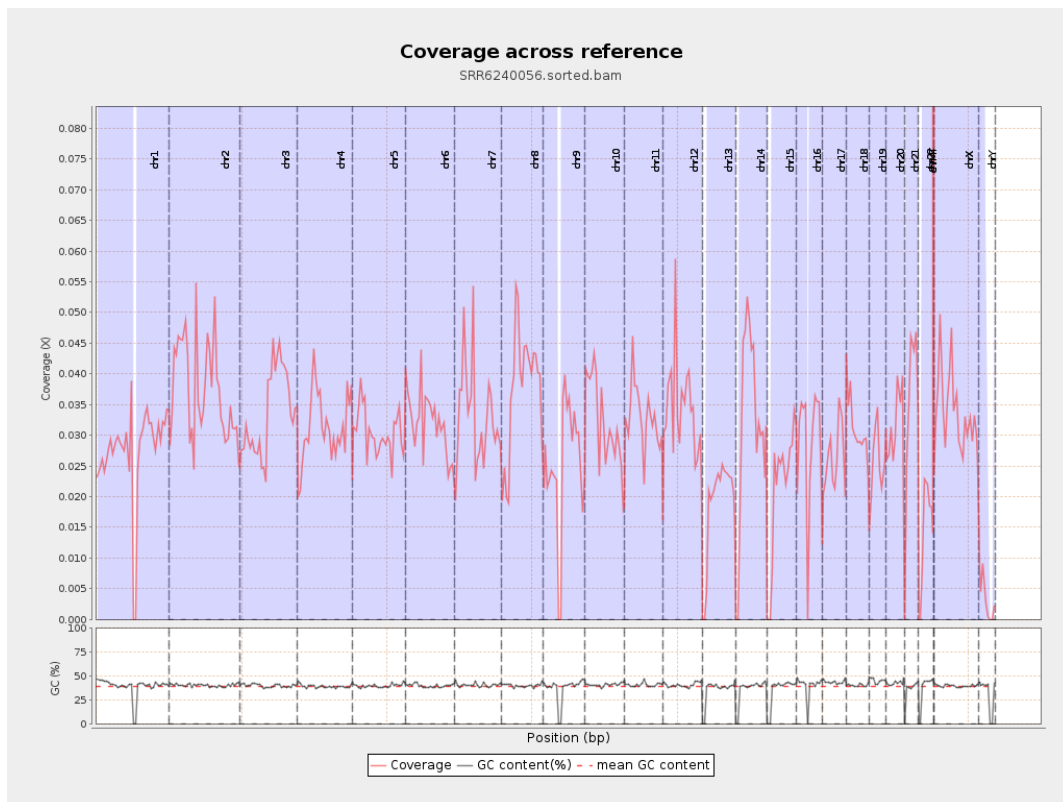
General error rate	0.98%
Mismatches	905,575
Insertions	6,421
Mapped reads with at least one insertion	0.43%
Deletions	28,573
Mapped reads with at least one deletion	1.89%
Homopolymer indels	49.34%

2.6. Chromosome stats

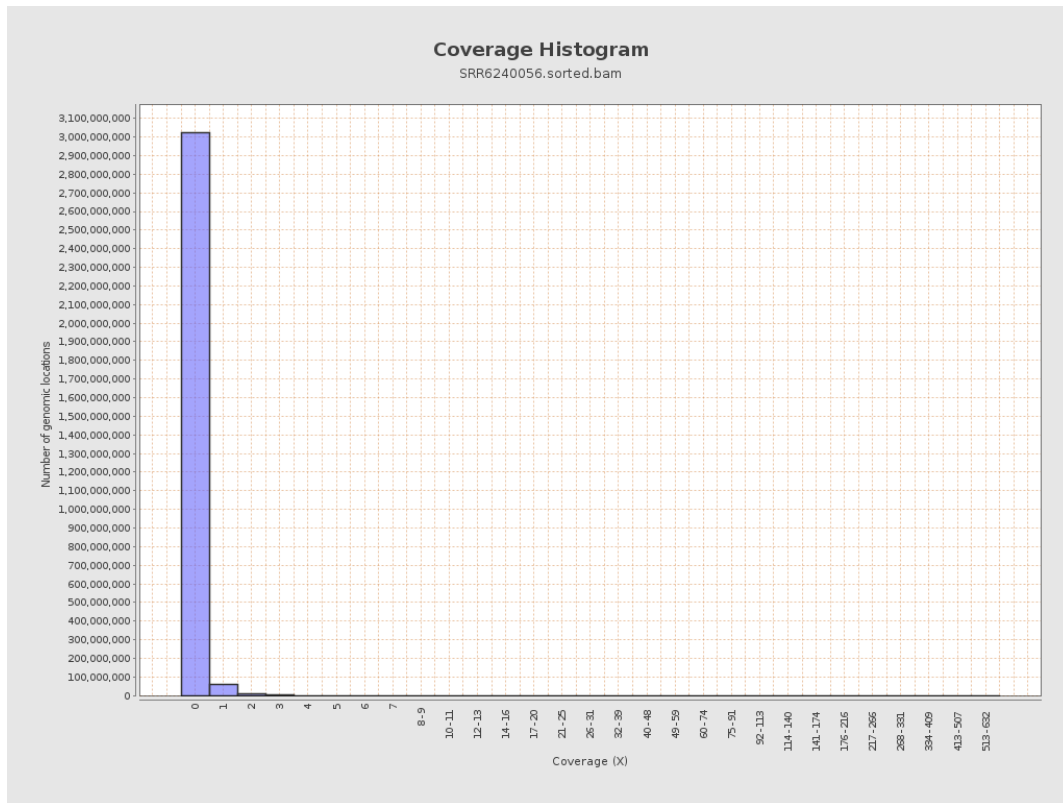
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	6847753	0.0275	0.4498
chr2	243199373	9112888	0.0375	0.3535
chr3	198022430	6649108	0.0336	0.2215
chr4	191154276	5980586	0.0313	0.2204
chr5	180915260	5491314	0.0304	0.2135
chr6	171115067	5464893	0.0319	0.2612
chr7	159138663	5316290	0.0334	0.4622

chr8	146364022	5479105	0.0374	0.4426
chr9	141213431	3566793	0.0253	0.2678
chr10	135534747	4402374	0.0325	0.2527
chr11	135006516	4416080	0.0327	0.2841
chr12	133851895	4613392	0.0345	0.2278
chr13	115169878	2160355	0.0188	0.1641
chr14	107349540	3456818	0.0322	0.2254
chr15	102531392	2202037	0.0215	0.1887
chr16	90354753	2594139	0.0287	0.2098
chr17	81195210	2113918	0.026	0.2183
chr18	78077248	2433186	0.0312	0.4197
chr19	59128983	1540455	0.0261	0.3148
chr20	63025520	1971262	0.0313	0.2187
chr21	48129895	1690510	0.0351	0.2356
chr22	51304566	729815	0.0142	0.1389
chrMT	16571	29754	1.7955	2.2453
chrX	155270560	5206936	0.0335	0.2425
chrY	59373566	191912	0.0032	0.0747

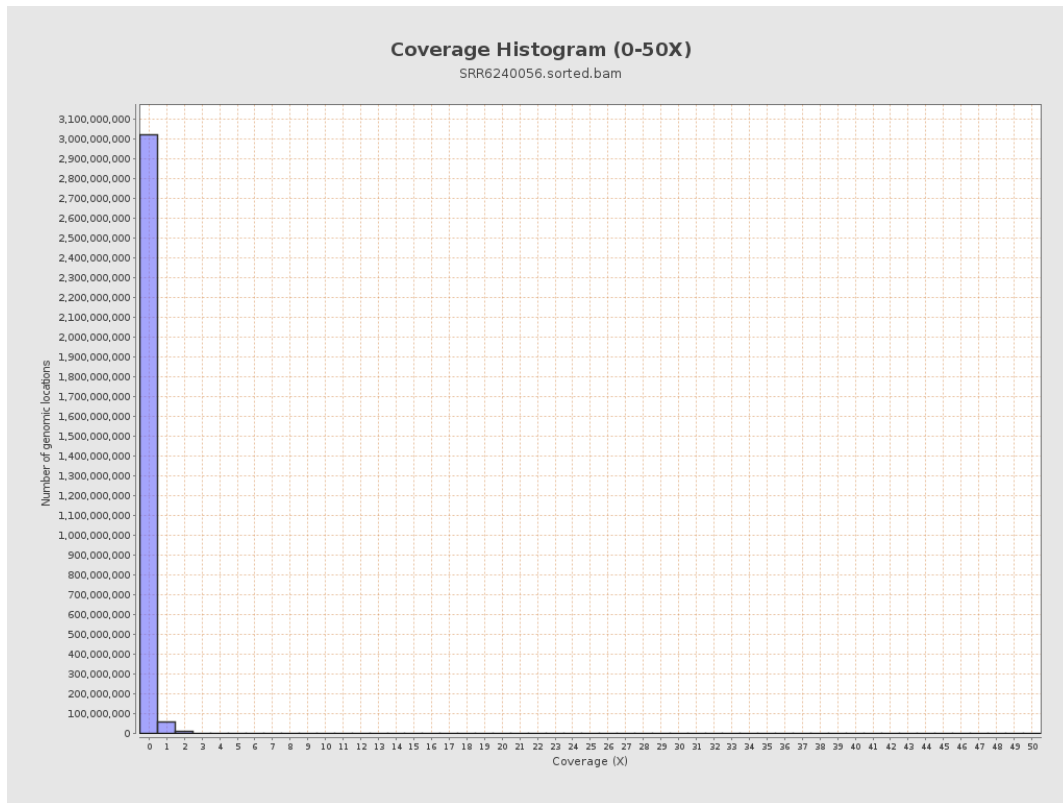
3. Results : Coverage across reference



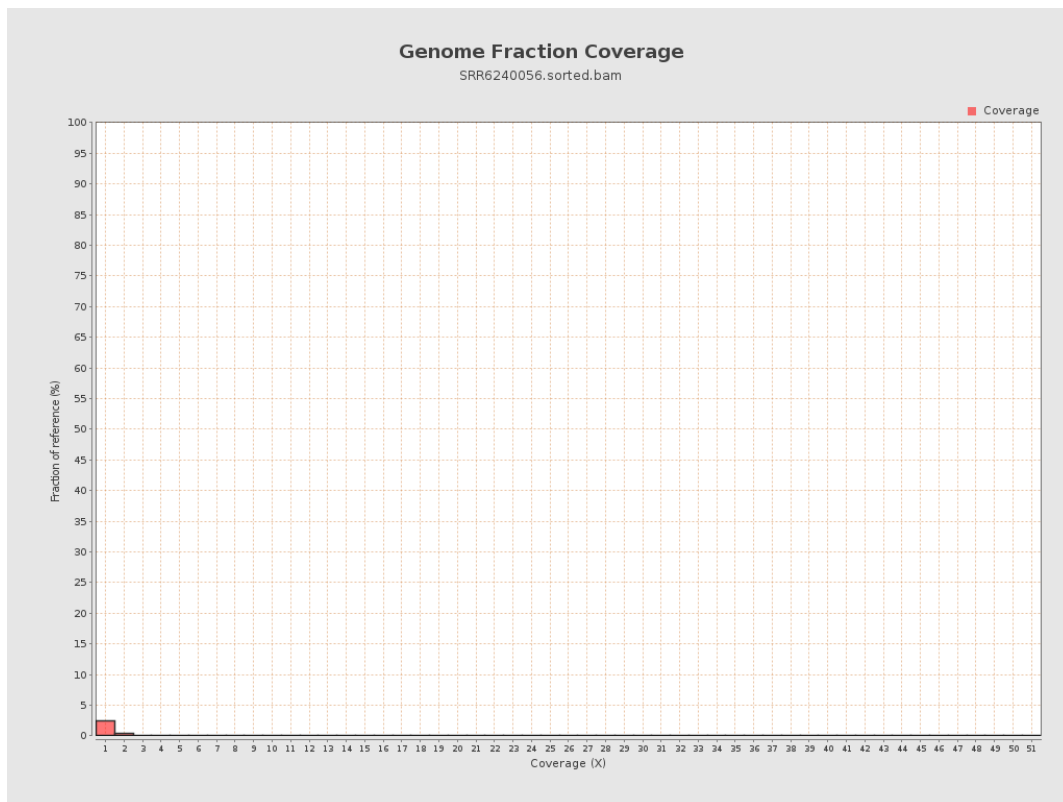
4. Results : Coverage Histogram



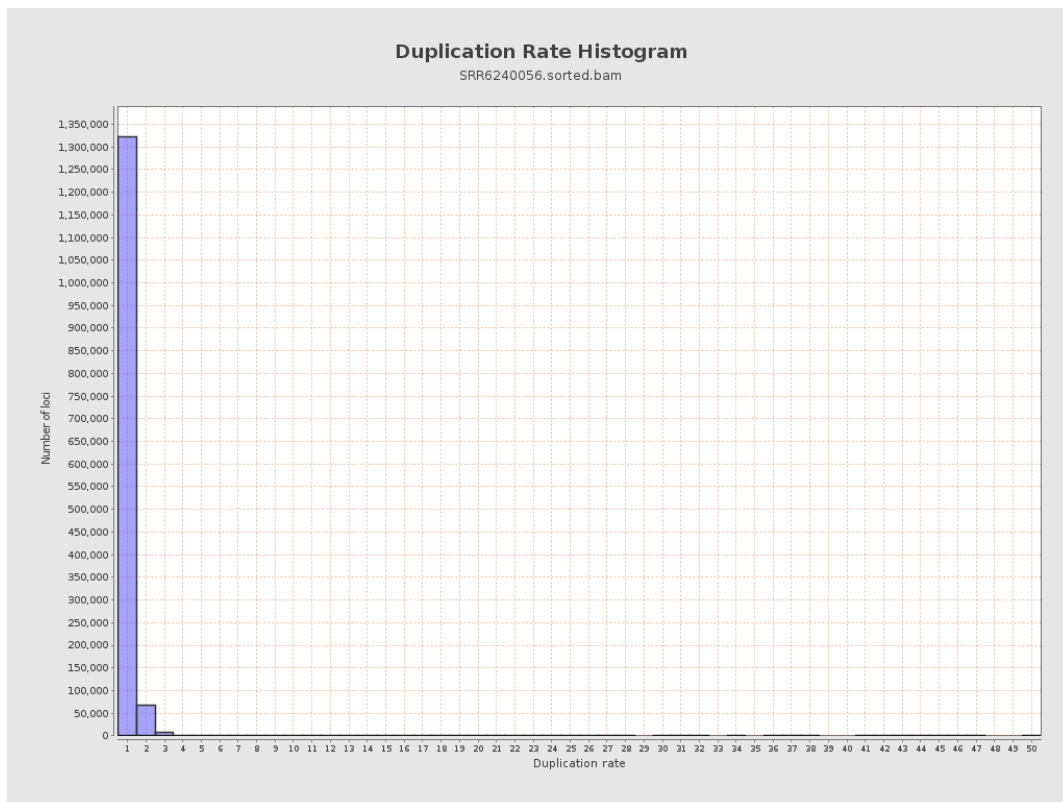
5. Results : Coverage Histogram (0-50X)



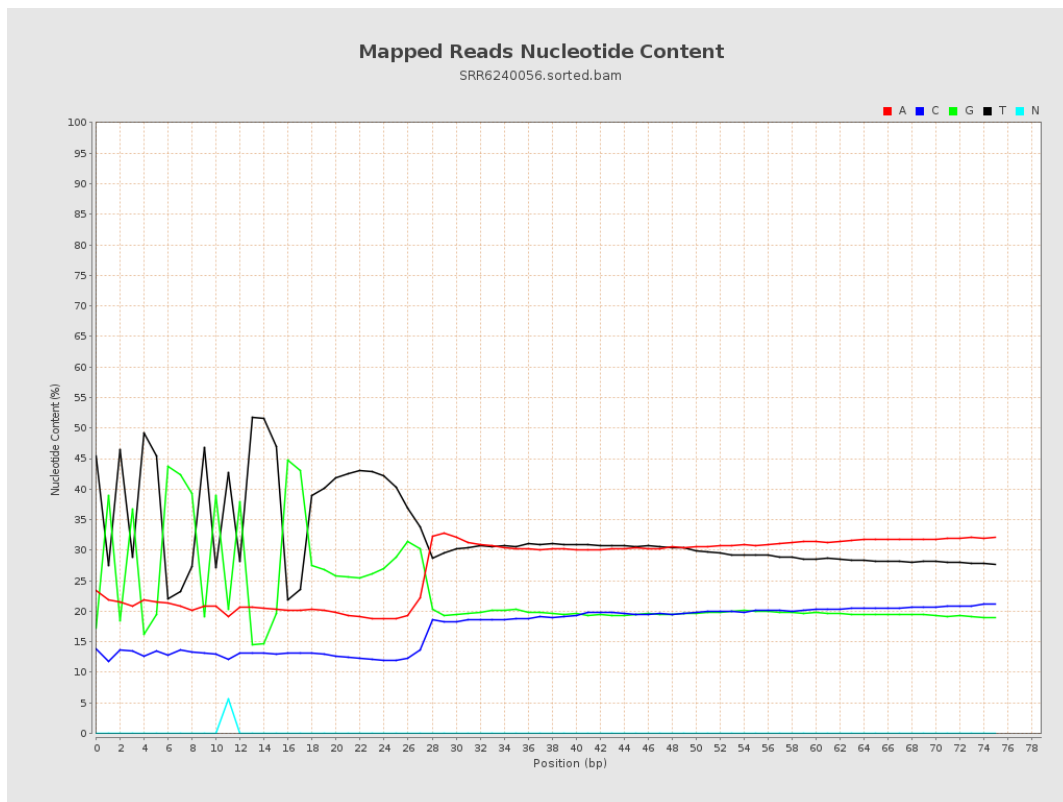
6. Results : Genome Fraction Coverage



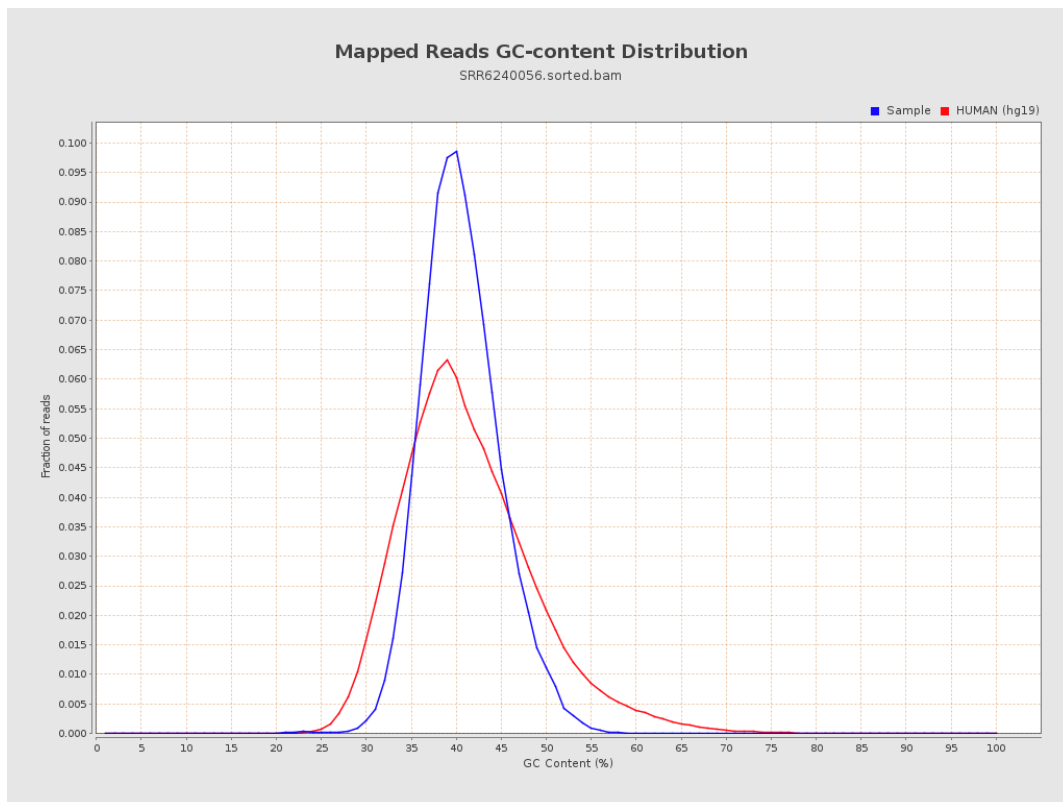
7. Results : Duplication Rate Histogram



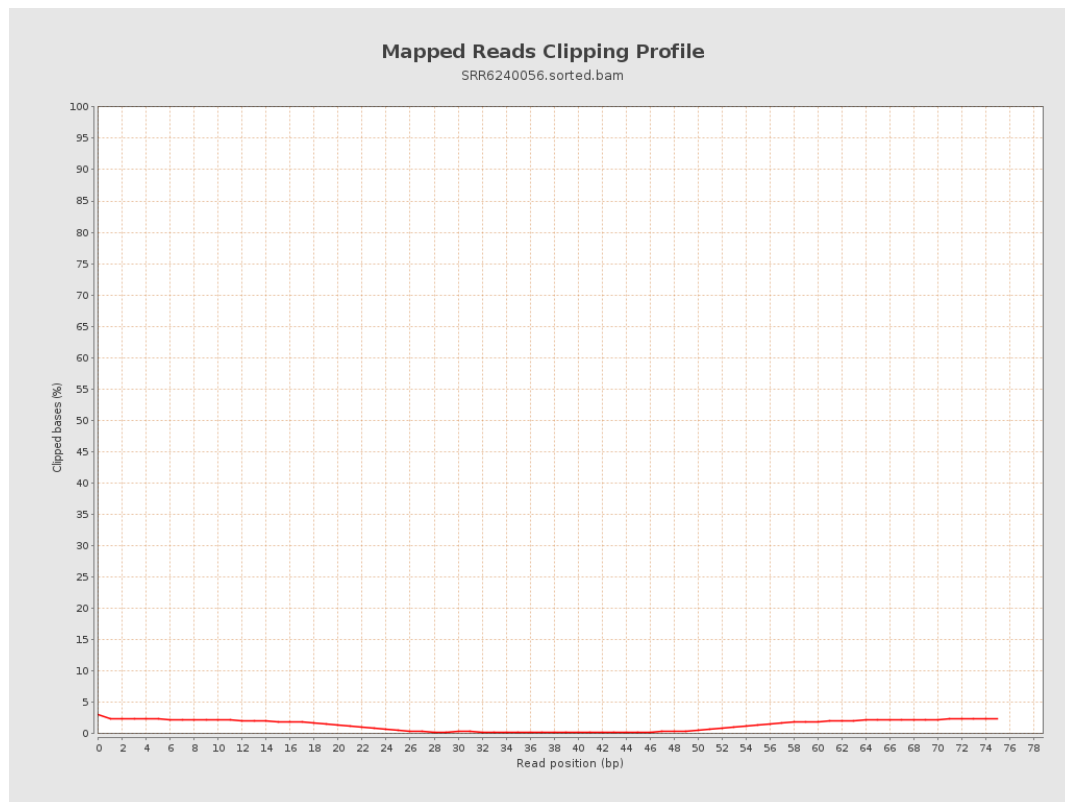
8. Results : Mapped Reads Nucleotide Content



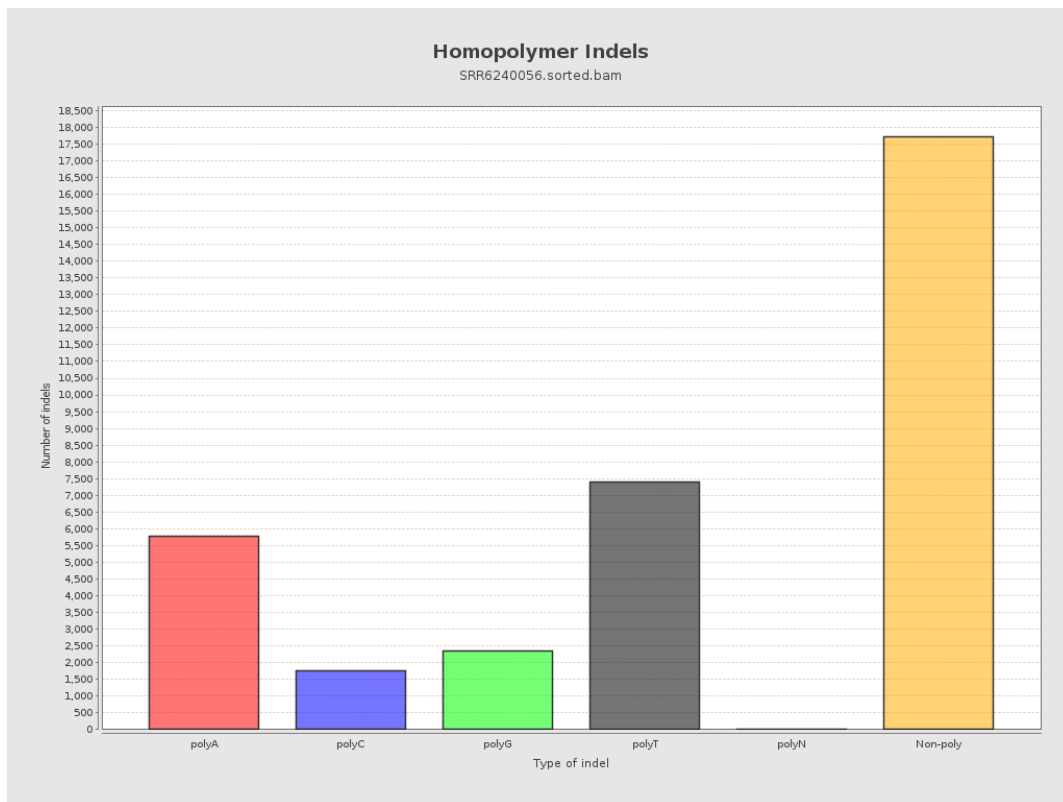
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

