

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/13 22:08:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004040.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_SRR6004040 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004040.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 13 22:08:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004040.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,949,126
Mapped reads	2,681,910 / 90.94%
Unmapped reads	267,216 / 9.06%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	24,260 / 0.82%
Read min/max/mean length	30 / 76 / 76.29
Duplicated reads (estimated)	150,410 / 5.1%
Duplication rate	4.3%
Clipped reads	1,221,301 / 41.41%

2.2. ACGT Content

Number/percentage of A's	49,874,787 / 27.91%
Number/percentage of C's	33,552,669 / 18.78%
Number/percentage of T's	55,577,560 / 31.1%
Number/percentage of G's	39,653,630 / 22.19%
Number/percentage of N's	33,945 / 0.02%
GC Percentage	40.97%

2.3. Coverage

Mean	0.0578

Standard Deviation	0.5246
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2.4. Mapping Quality

Mean Mapping Quality	45.31
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2.5. Mismatches and indels

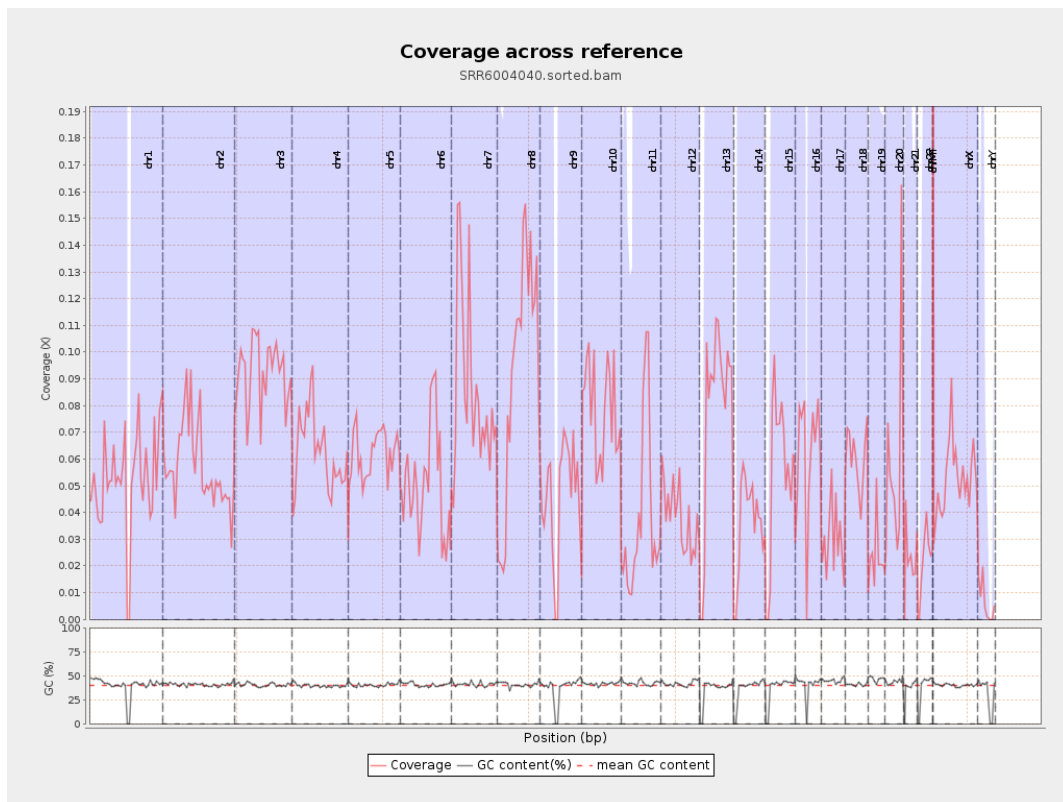
General error rate	0.8%
Mismatches	1,403,991
Insertions	12,484
Mapped reads with at least one insertion	0.46%
Deletions	49,721
Mapped reads with at least one deletion	1.83%
Homopolymer indels	46.16%

2.6. Chromosome stats

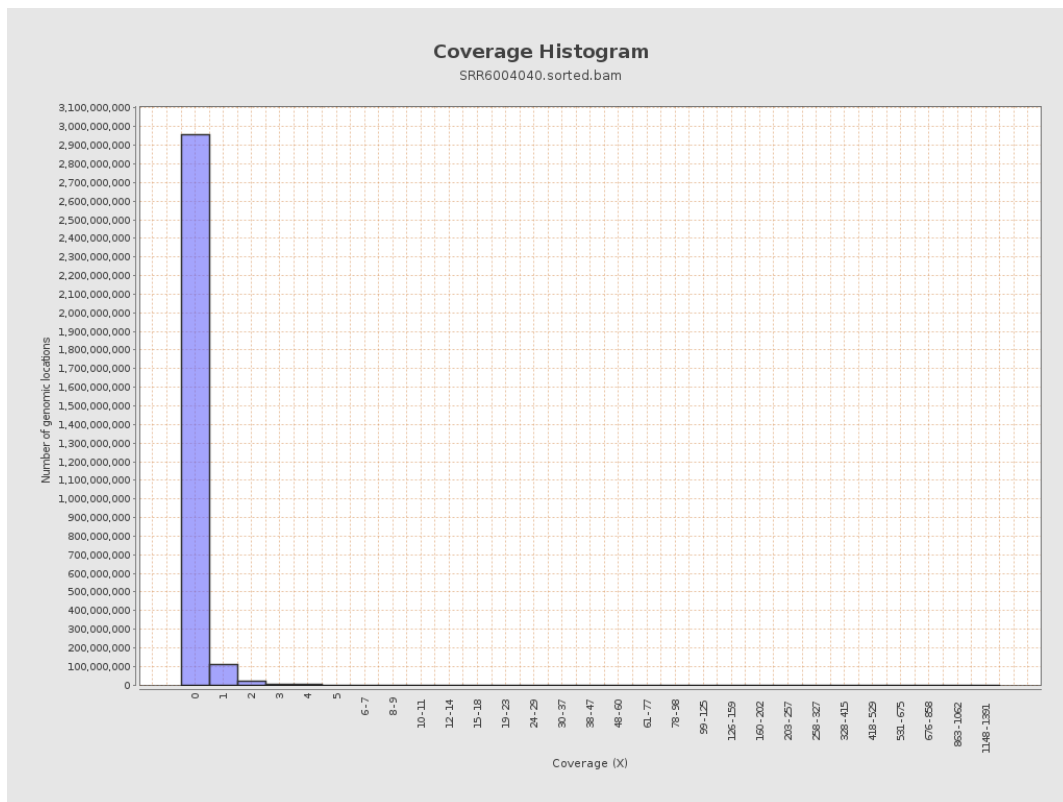
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	13108931	0.0526	0.7452
chr2	243199373	13841682	0.0569	0.5753
chr3	198022430	18277350	0.0923	0.3755
chr4	191154276	12074642	0.0632	0.3297
chr5	180915260	11141233	0.0616	0.3077
chr6	171115067	8660279	0.0506	0.3094
chr7	159138663	13476141	0.0847	1.1062

chr8	146364022	13704255	0.0936	0.9078
chr9	141213431	6496188	0.046	0.46
chr10	135534747	10569743	0.078	0.4972
chr11	135006516	5071217	0.0376	0.3051
chr12	133851895	5158627	0.0385	0.2584
chr13	115169878	9147207	0.0794	0.351
chr14	107349540	3921060	0.0365	0.2786
chr15	102531392	5614501	0.0548	0.3018
chr16	90354753	5424117	0.06	0.3365
chr17	81195210	2400126	0.0296	0.223
chr18	78077248	4677587	0.0599	0.7947
chr19	59128983	1414706	0.0239	0.6458
chr20	63025520	3870027	0.0614	0.3302
chr21	48129895	1117982	0.0232	0.2198
chr22	51304566	1114856	0.0217	0.1776
chrMT	16571	8967	0.5411	0.8611
chrX	155270560	8105062	0.0522	0.3339
chrY	59373566	382229	0.0064	0.1266

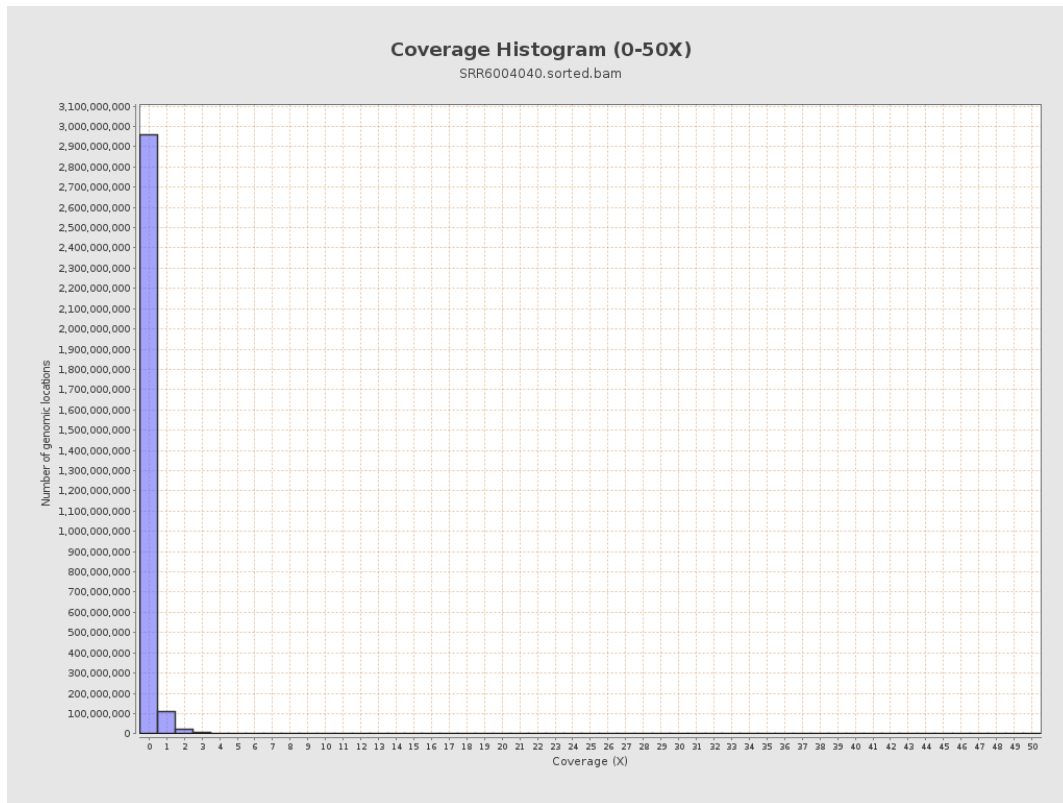
3. Results : Coverage across reference



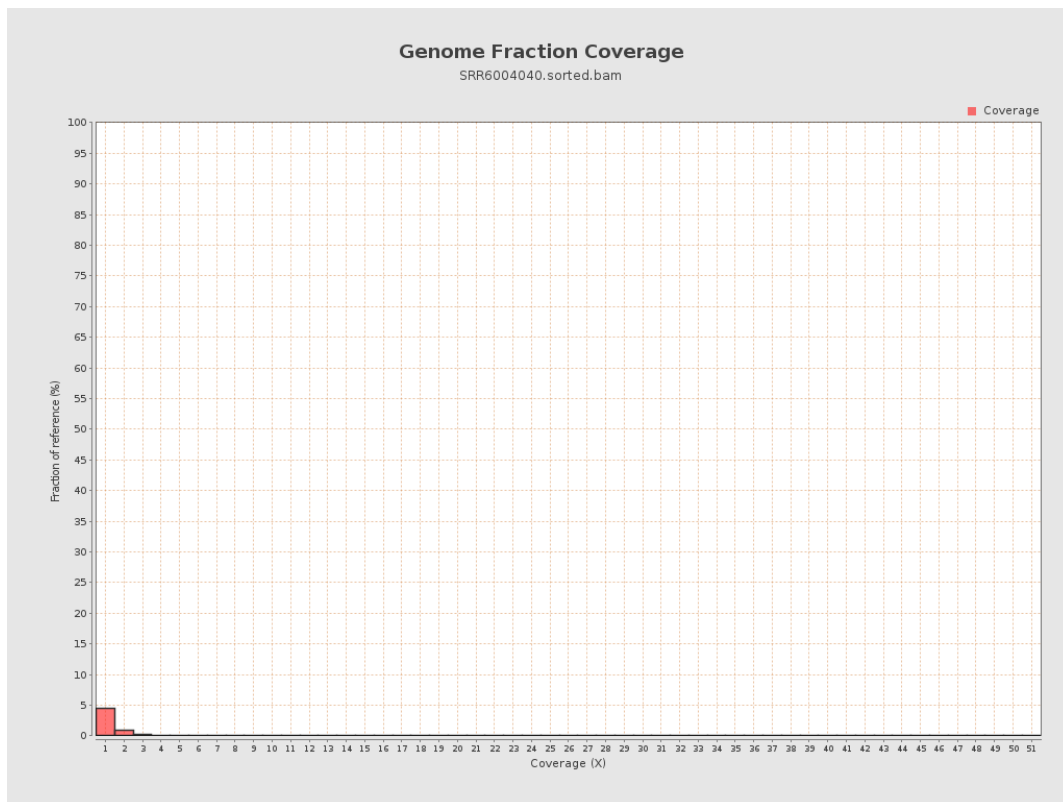
4. Results : Coverage Histogram



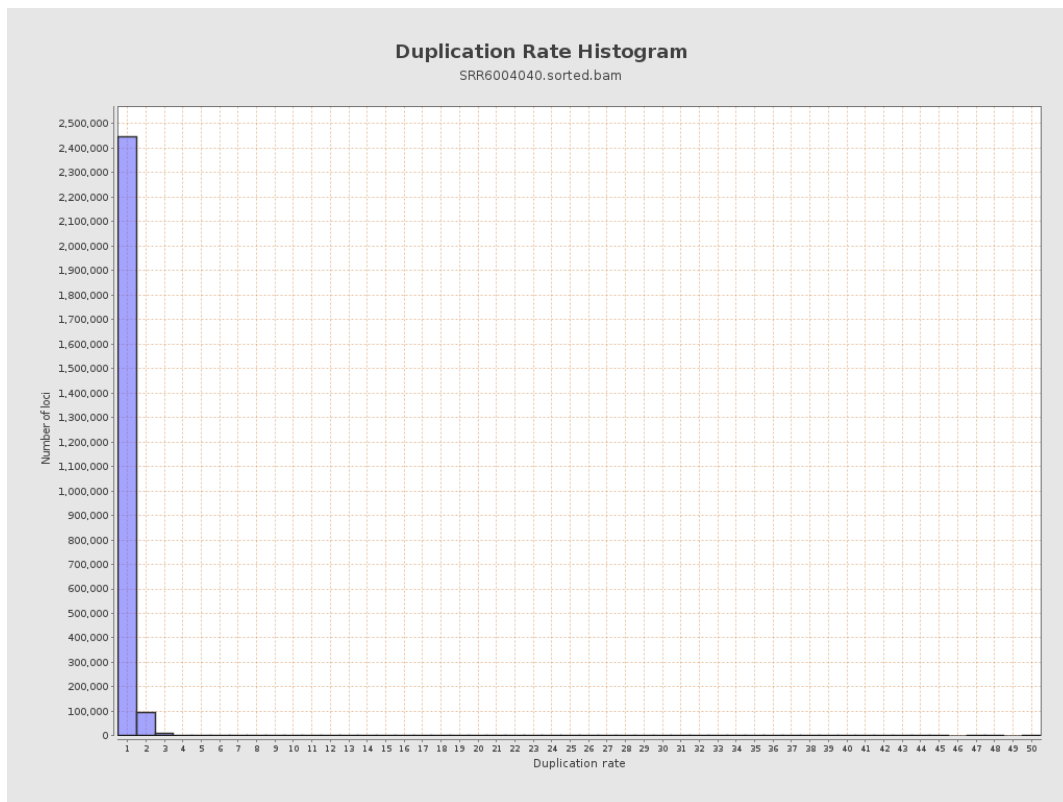
5. Results : Coverage Histogram (0-50X)



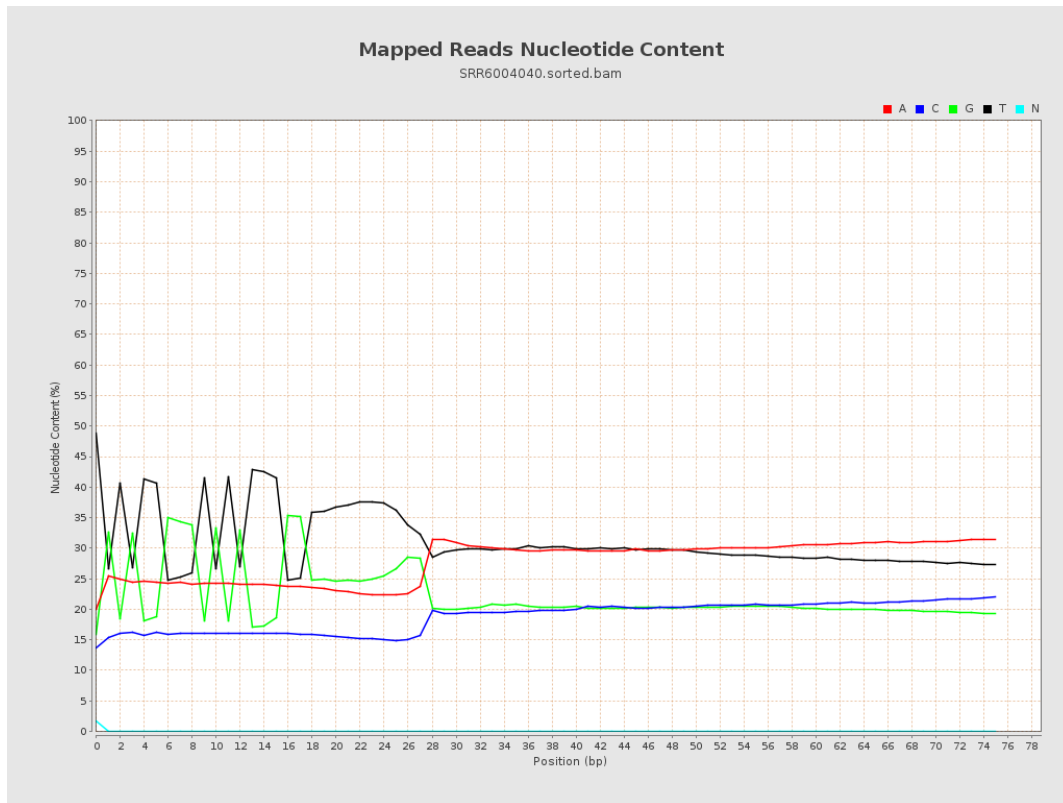
6. Results : Genome Fraction Coverage



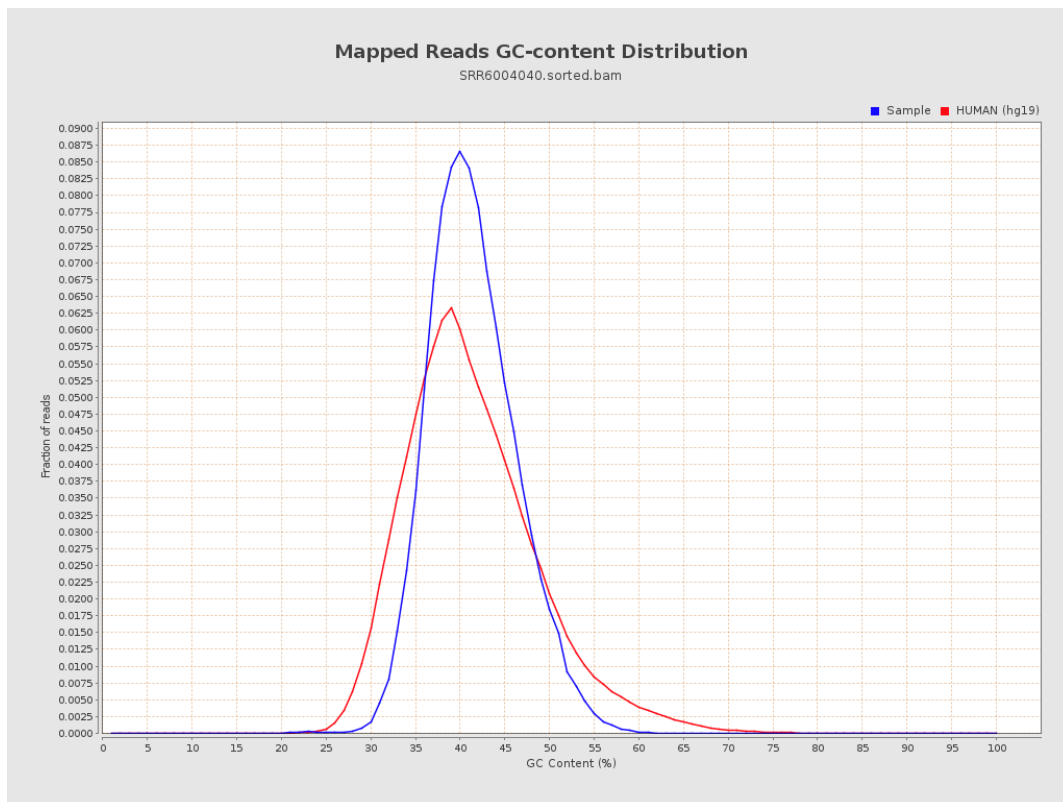
7. Results : Duplication Rate Histogram



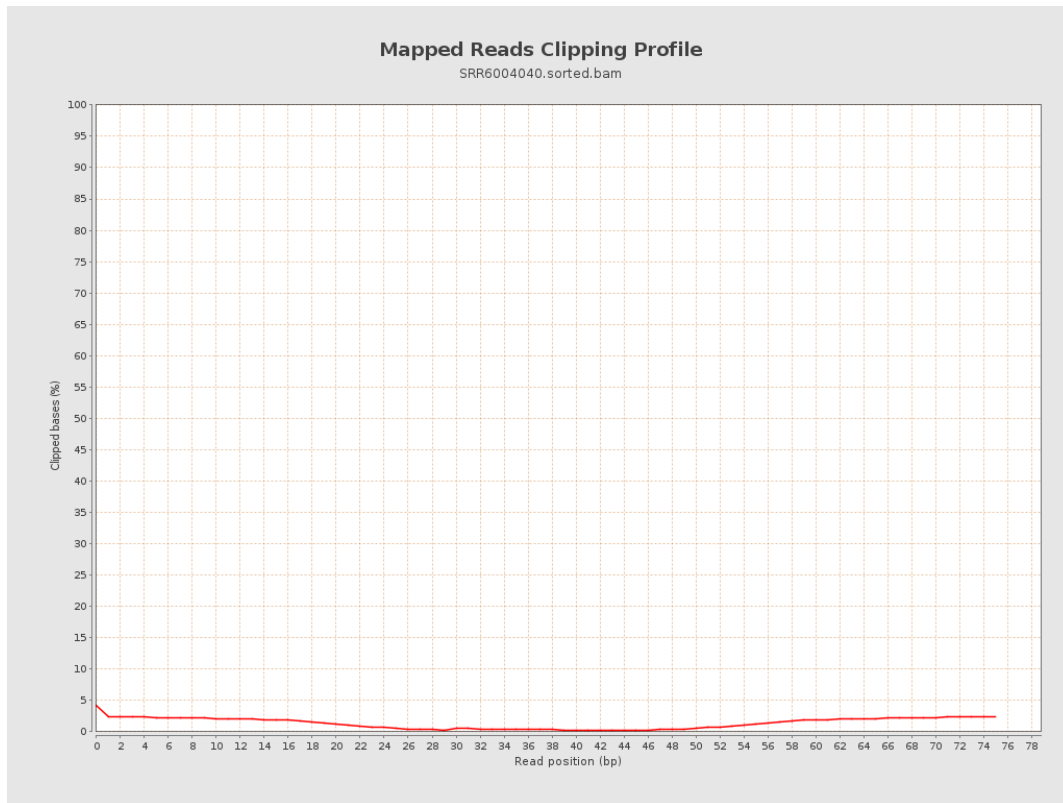
8. Results : Mapped Reads Nucleotide Content



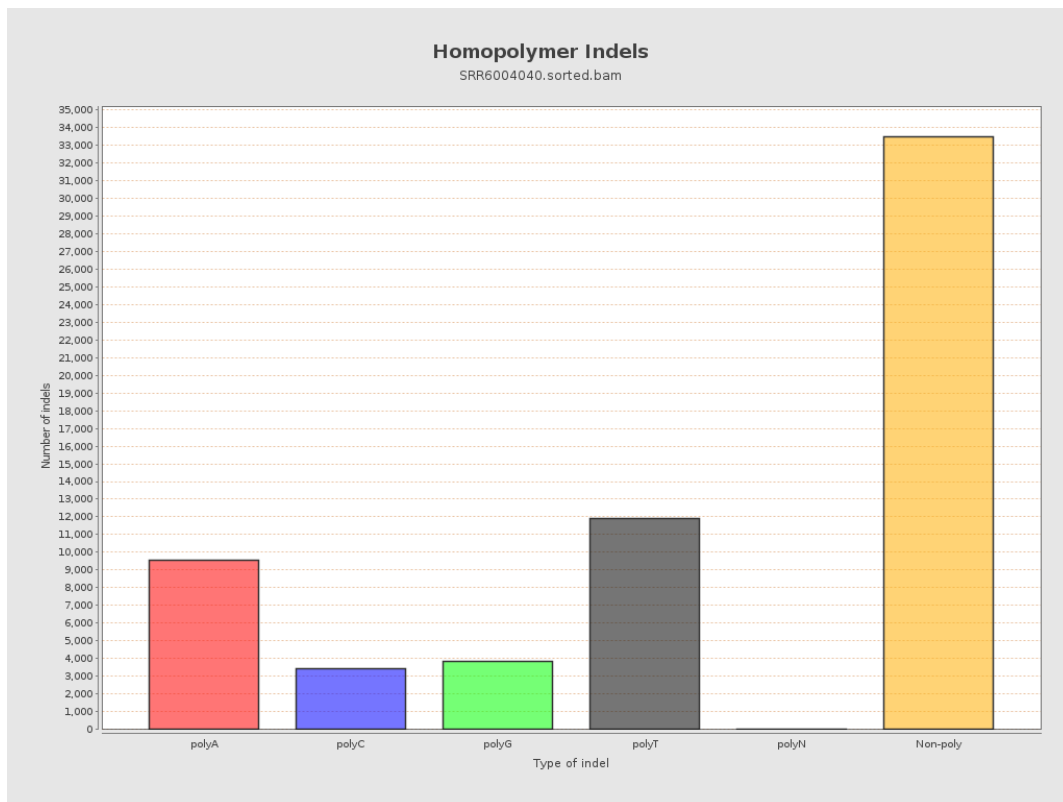
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

