

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 05:00:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240069.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_SRR6240069 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240069.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 05:00:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240069.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,878,397
Mapped reads	965,905 / 51.42%
Unmapped reads	912,492 / 48.58%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,016 / 0.43%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	142,771 / 7.6%
Duplication rate	11.57%
Clipped reads	594,033 / 31.62%

2.2. ACGT Content

Number/percentage of A's	16,056,562 / 26.63%
Number/percentage of C's	10,802,725 / 17.92%
Number/percentage of T's	19,327,654 / 32.06%
Number/percentage of G's	14,060,355 / 23.32%
Number/percentage of N's	40,917 / 0.07%
GC Percentage	41.24%

2.3. Coverage

Mean	0.0195

Standard Deviation	0.2722
--------------------	--------

2.4. Mapping Quality

Mean Mapping Quality	44.82
----------------------	-------

2.5. Mismatches and indels

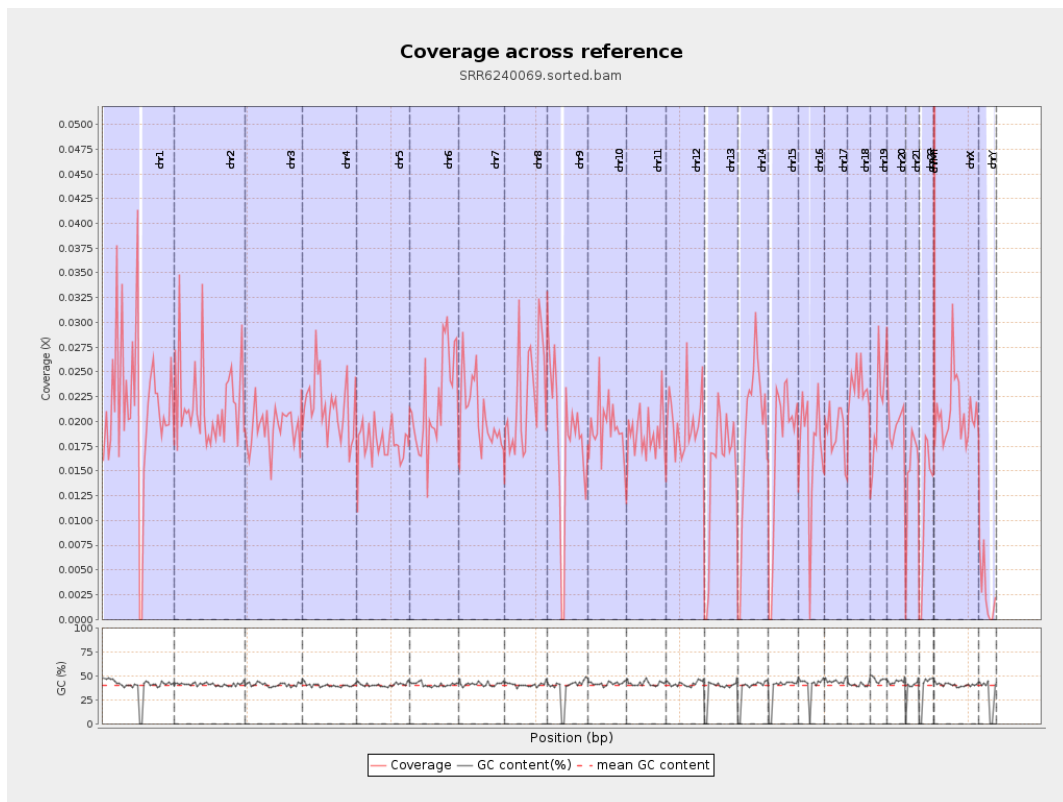
General error rate	0.89%
Mismatches	526,317
Insertions	4,183
Mapped reads with at least one insertion	0.43%
Deletions	12,915
Mapped reads with at least one deletion	1.32%
Homopolymer indels	47.35%

2.6. Chromosome stats

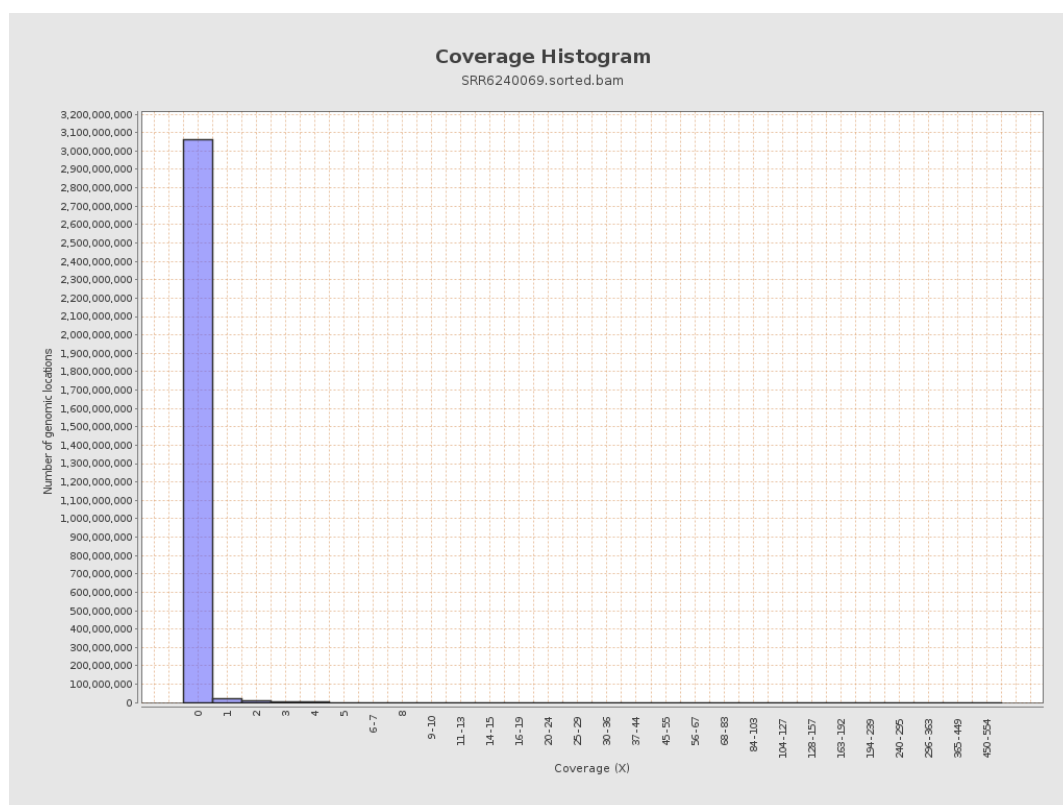
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	5279593	0.0212	0.4746
chr2	243199373	5316051	0.0219	0.3278
chr3	198022430	3820878	0.0193	0.2117
chr4	191154276	4107646	0.0215	0.2301
chr5	180915260	3256826	0.018	0.2027
chr6	171115067	3748065	0.0219	0.2376
chr7	159138663	3284811	0.0206	0.2533

chr8	146364022	3297556	0.0225	0.341
chr9	141213431	2570615	0.0182	0.2531
chr10	135534747	2597178	0.0192	0.234
chr11	135006516	2545723	0.0189	0.2292
chr12	133851895	2673788	0.02	0.2165
chr13	115169878	1728449	0.015	0.1878
chr14	107349540	2030226	0.0189	0.2172
chr15	102531392	1783251	0.0174	0.2084
chr16	90354753	1543101	0.0171	0.2003
chr17	81195210	1529832	0.0188	0.213
chr18	78077248	1839143	0.0236	0.38
chr19	59128983	1271472	0.0215	0.3194
chr20	63025520	1233848	0.0196	0.216
chr21	48129895	735353	0.0153	0.1906
chr22	51304566	603608	0.0118	0.1609
chrMT	16571	88048	5.3134	4.5433
chrX	155270560	3266079	0.021	0.2353
chrY	59373566	158795	0.0027	0.0752

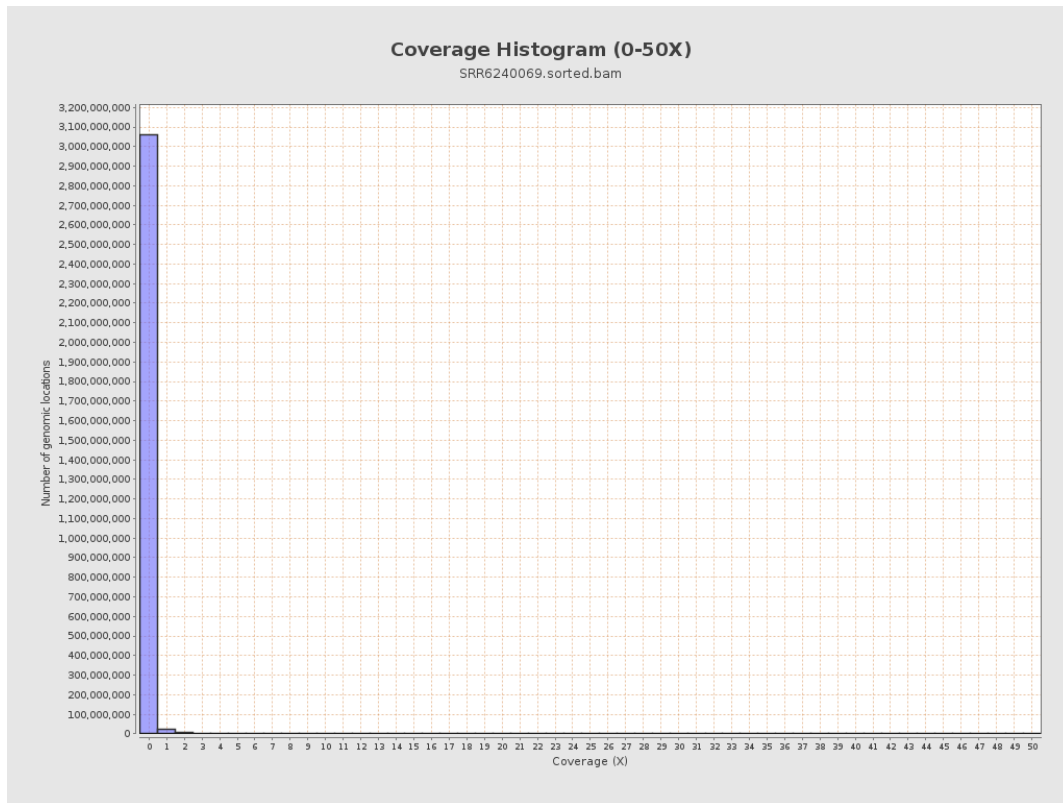
3. Results : Coverage across reference



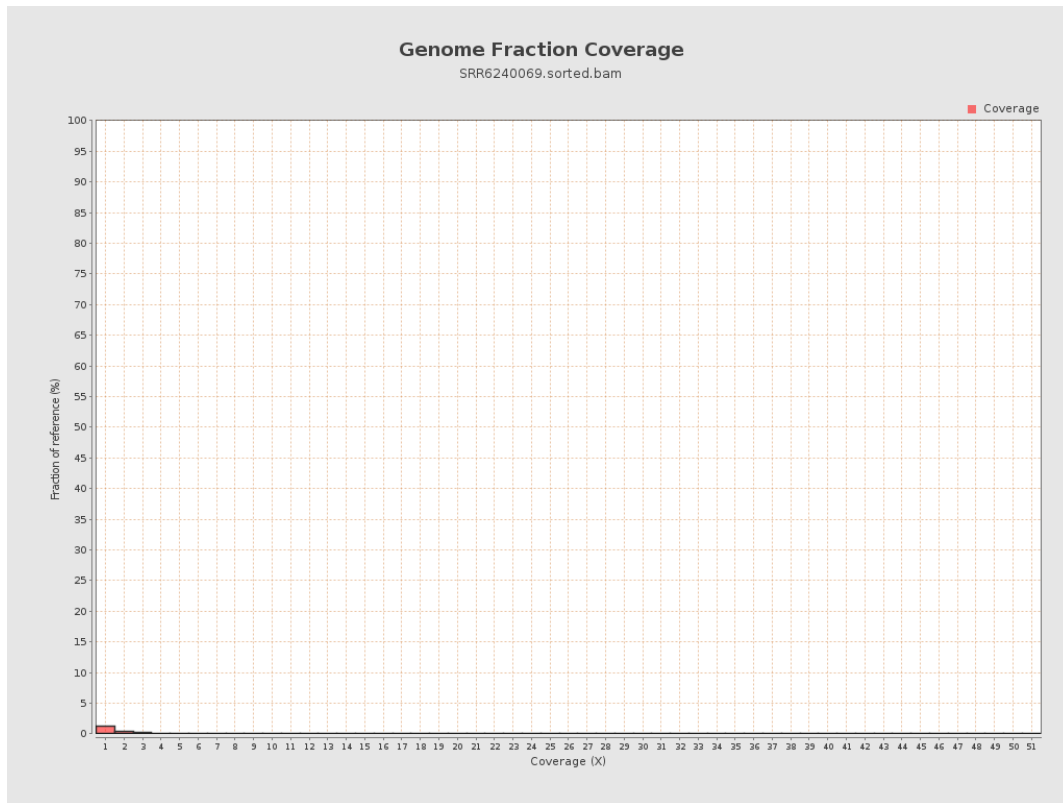
4. Results : Coverage Histogram



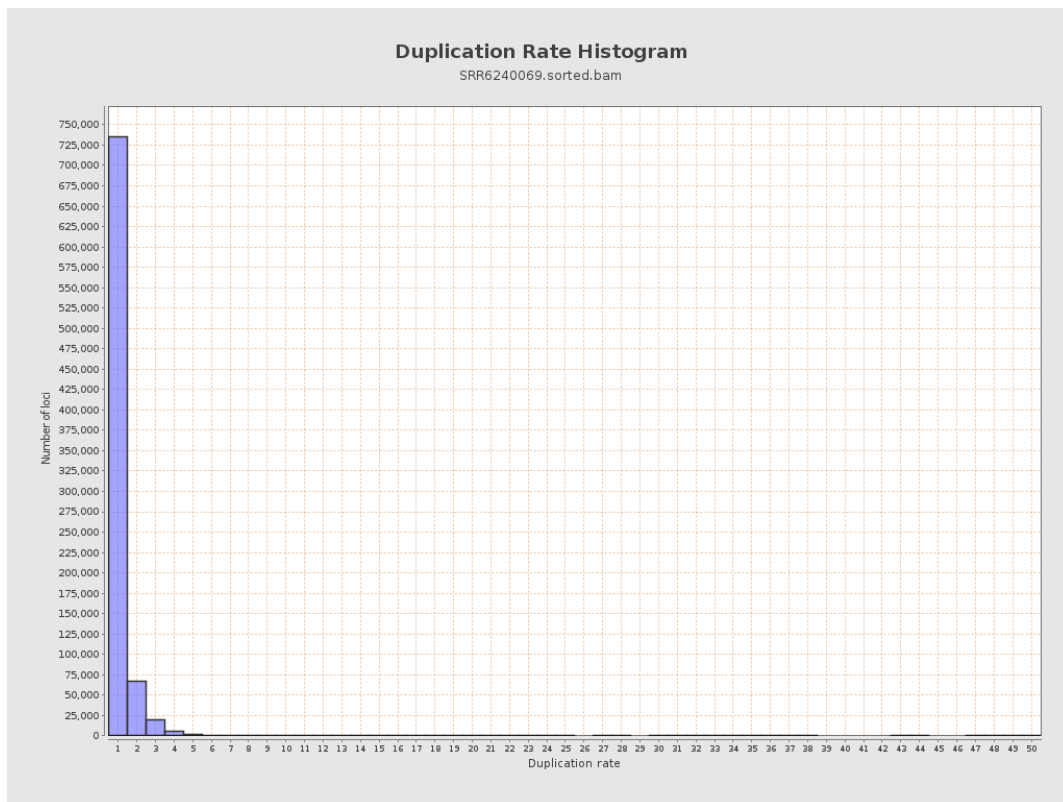
5. Results : Coverage Histogram (0-50X)



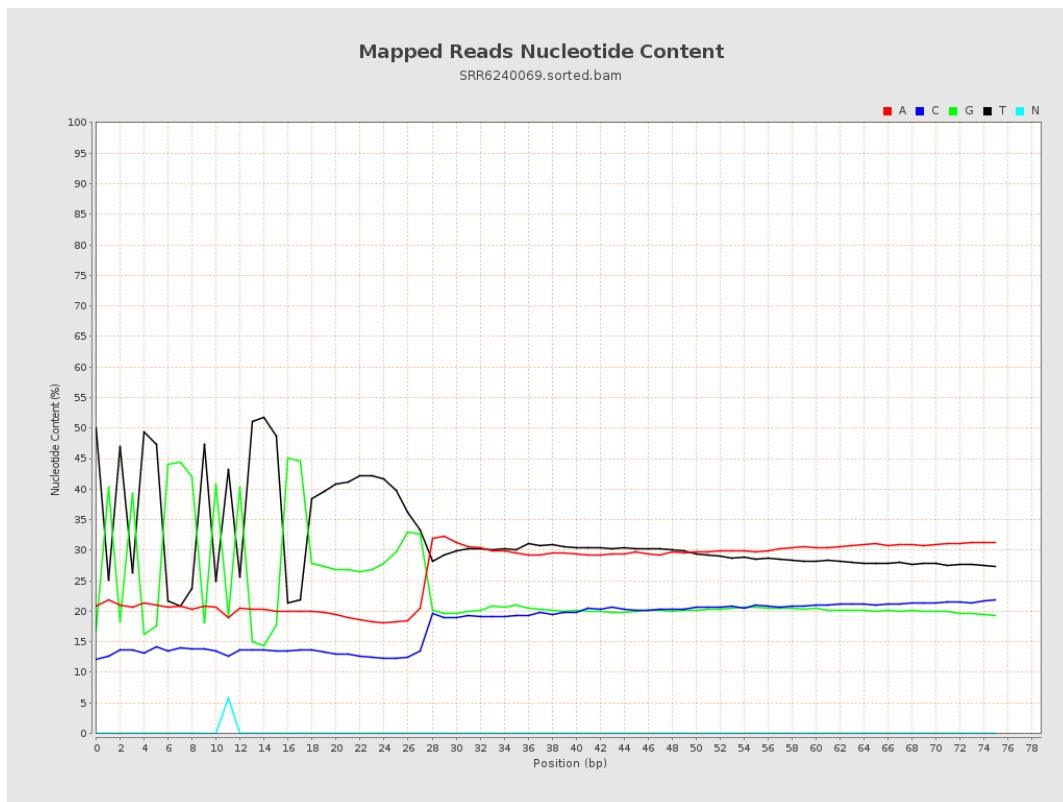
6. Results : Genome Fraction Coverage



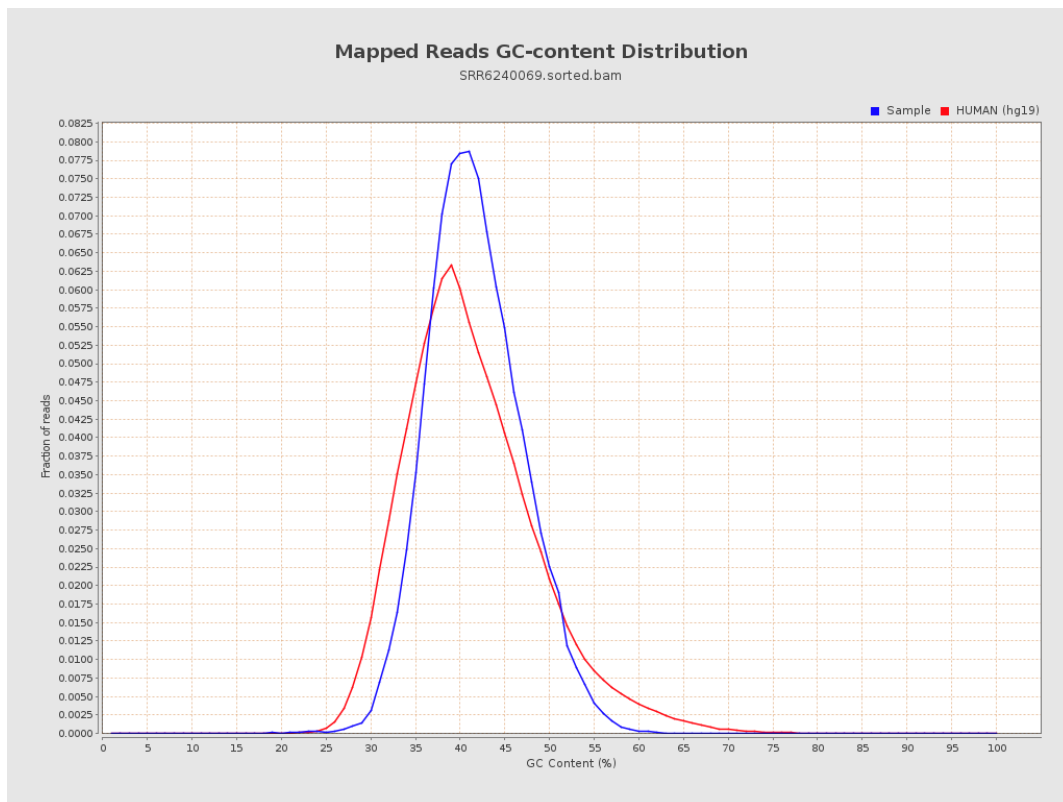
7. Results : Duplication Rate Histogram



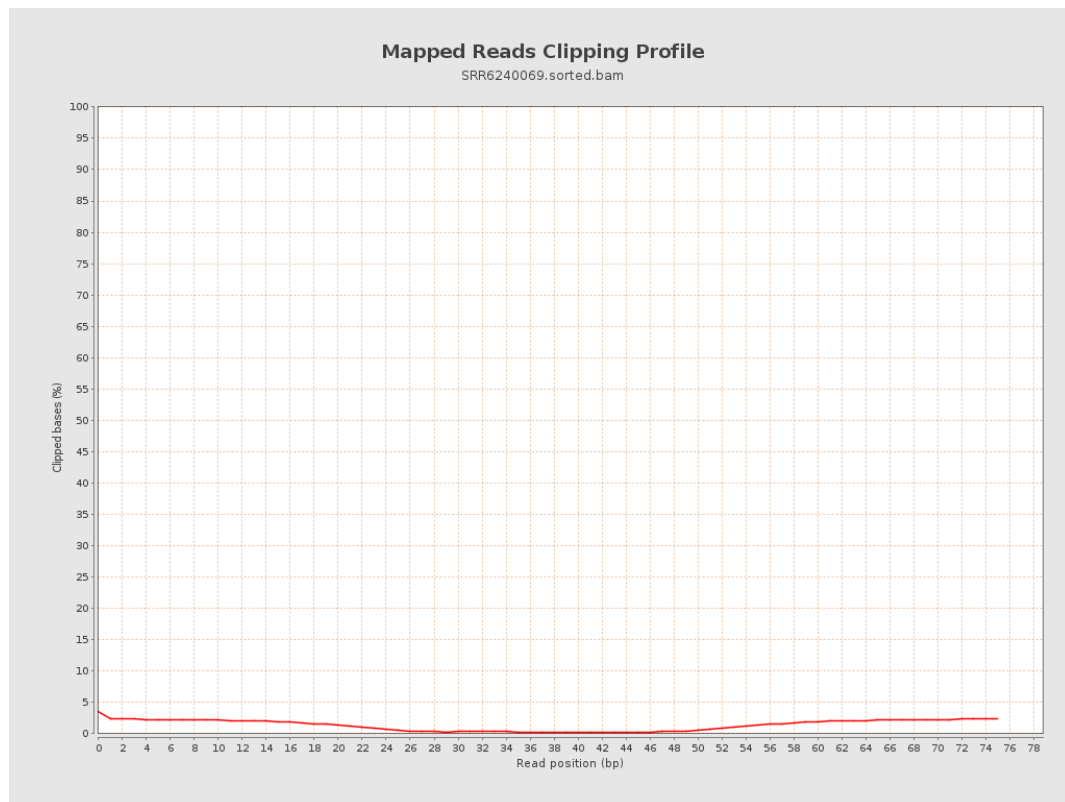
8. Results : Mapped Reads Nucleotide Content



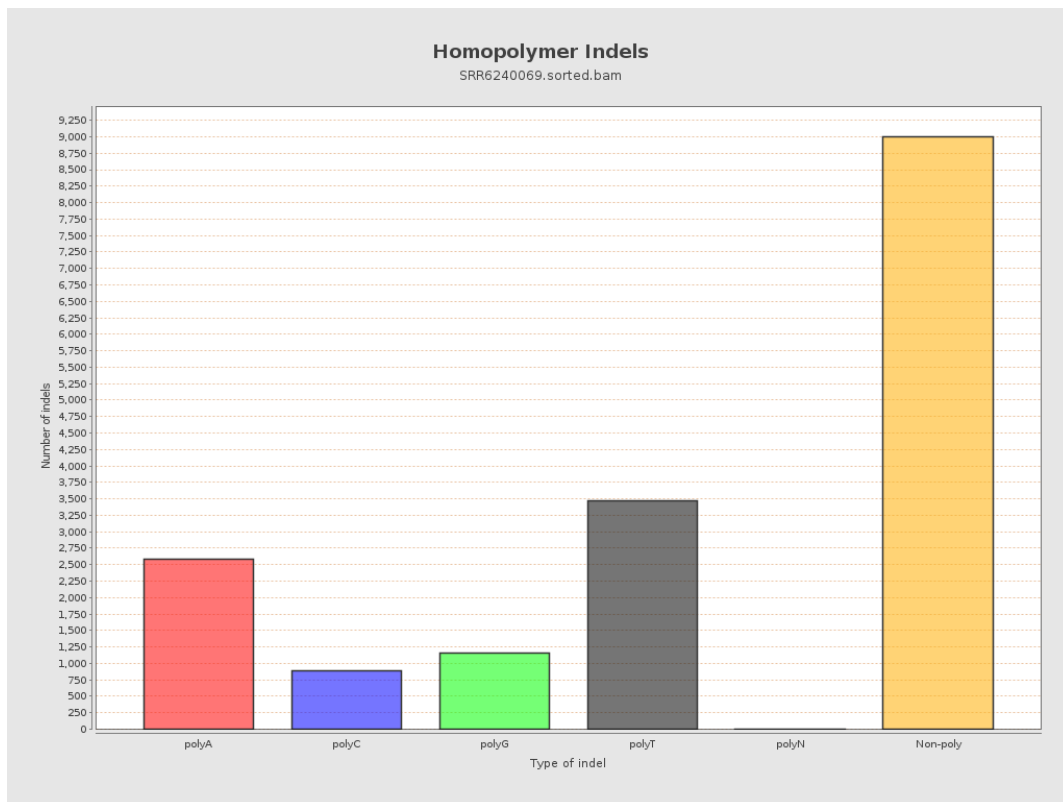
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

