

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/01 20:07:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524609.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_SRR10524609 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524609.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 01 20:07:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524609.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,212,496
Mapped reads	2,057,388 / 92.99%
Unmapped reads	155,108 / 7.01%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,371 / 0.2%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	116,912 / 5.28%
Duplication rate	4.4%
Clipped reads	2,060,269 / 93.12%

2.2. ACGT Content

Number/percentage of A's	30,894,949 / 25.75%
Number/percentage of C's	21,042,953 / 17.54%
Number/percentage of T's	37,893,632 / 31.58%
Number/percentage of G's	30,167,318 / 25.14%
Number/percentage of N's	705 / 0%
GC Percentage	42.68%

2.3. Coverage

Mean	0.0388

Standard Deviation	0.3366
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2.4. Mapping Quality

Mean Mapping Quality	45.6
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2.5. Mismatches and indels

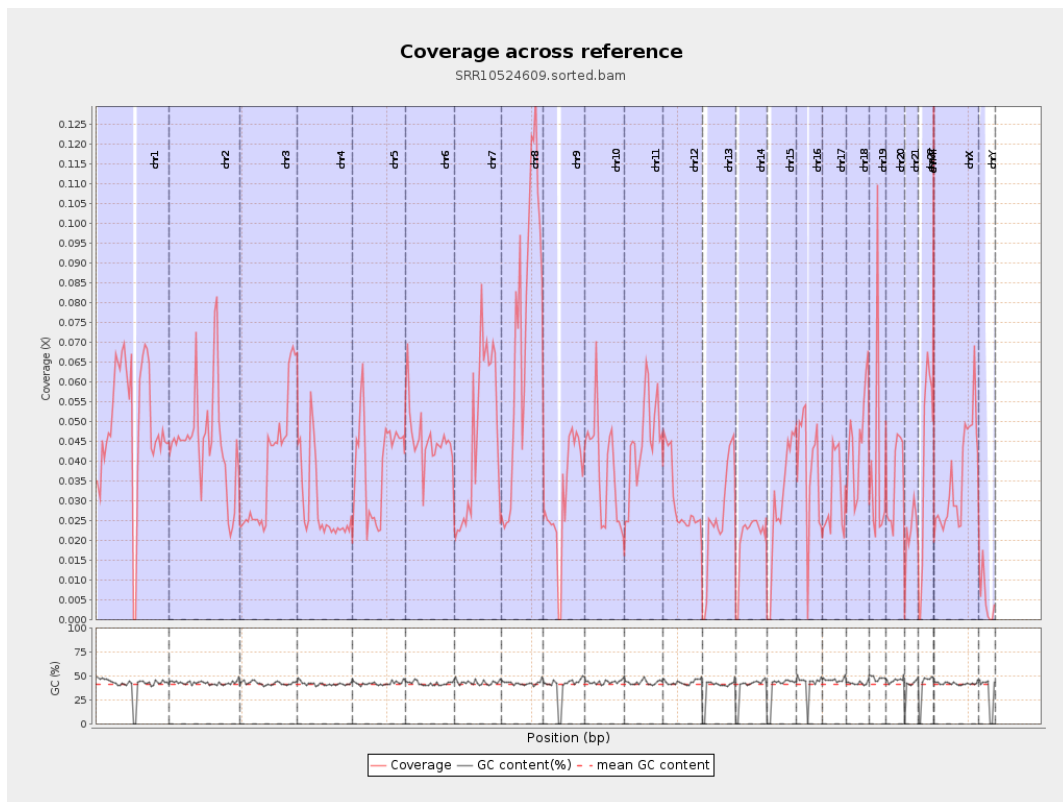
General error rate	0.47%
Mismatches	549,978
Insertions	6,474
Mapped reads with at least one insertion	0.31%
Deletions	22,417
Mapped reads with at least one deletion	1.08%
Homopolymer indels	45.2%

2.6. Chromosome stats

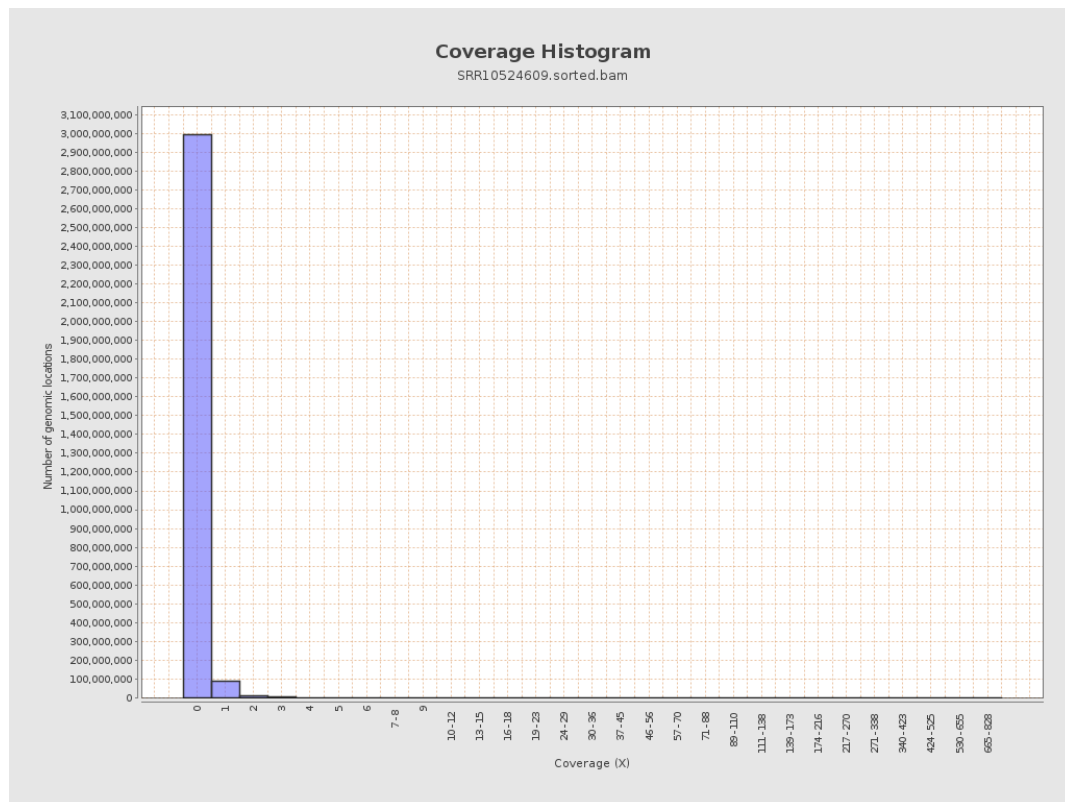
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	12339596	0.0495	0.6298
chr2	243199373	10959947	0.0451	0.3876
chr3	198022430	7712147	0.0389	0.2272
chr4	191154276	5418076	0.0283	0.2258
chr5	180915260	7133395	0.0394	0.2263
chr6	171115067	7767784	0.0454	0.2682
chr7	159138663	7373894	0.0463	0.4441

chr8	146364022	10657787	0.0728	0.4447
chr9	141213431	4371289	0.031	0.2957
chr10	135534747	5079158	0.0375	0.3266
chr11	135006516	6047890	0.0448	0.3249
chr12	133851895	3995782	0.0299	0.2066
chr13	115169878	2977886	0.0259	0.1879
chr14	107349540	2162727	0.0201	0.1704
chr15	102531392	3051336	0.0298	0.2092
chr16	90354753	3461665	0.0383	0.2396
chr17	81195210	2574846	0.0317	0.2107
chr18	78077248	3569811	0.0457	0.4725
chr19	59128983	2278561	0.0385	0.4213
chr20	63025520	2199208	0.0349	0.2191
chr21	48129895	1033733	0.0215	0.1897
chr22	51304566	2080826	0.0406	0.2296
chrMT	16571	2319	0.1399	0.4338
chrX	155270560	5492546	0.0354	0.2453
chrY	59373566	295489	0.005	0.1398

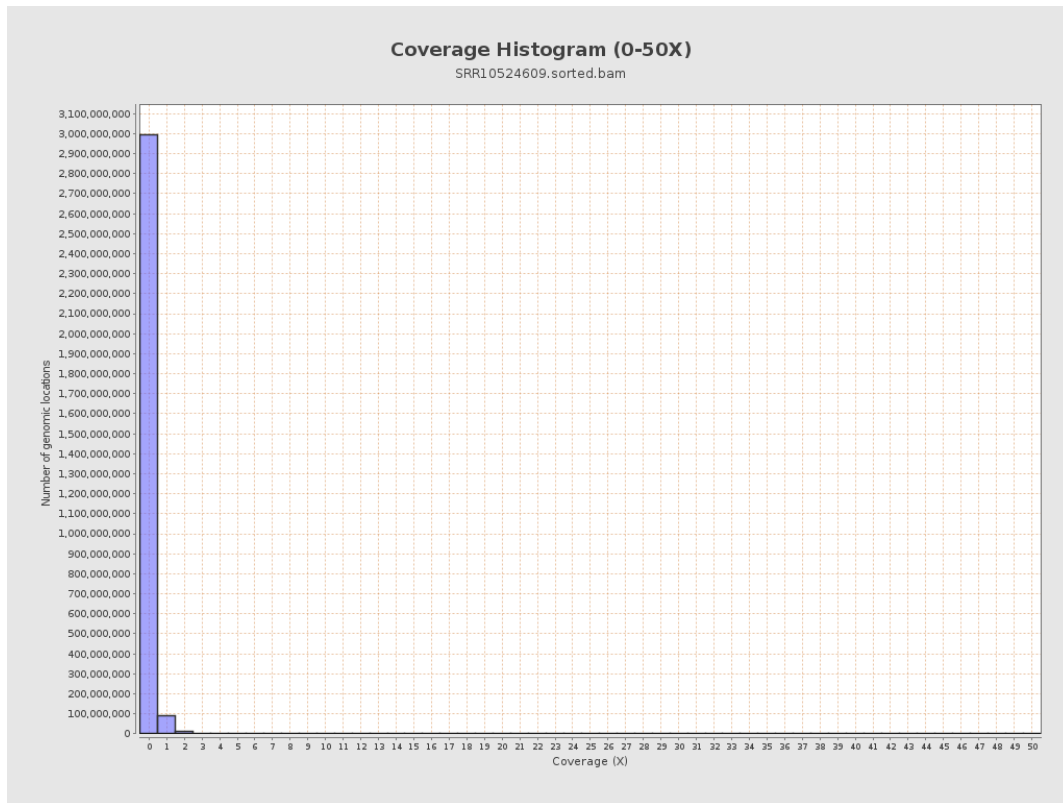
3. Results : Coverage across reference



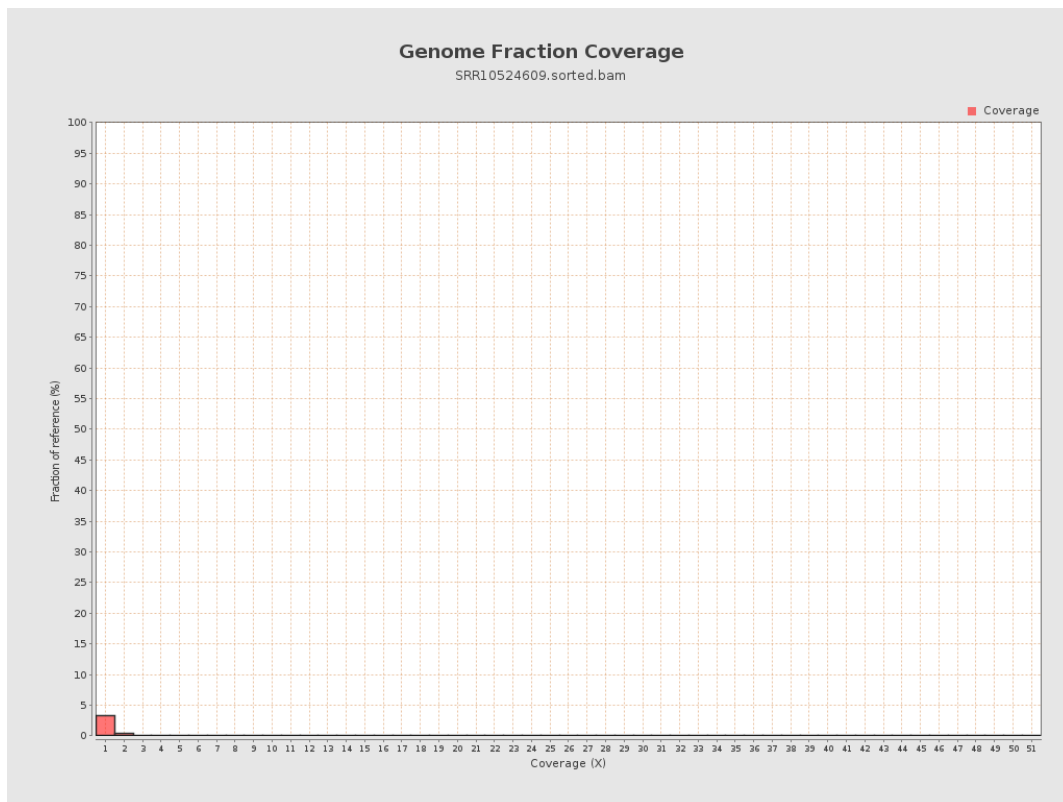
4. Results : Coverage Histogram



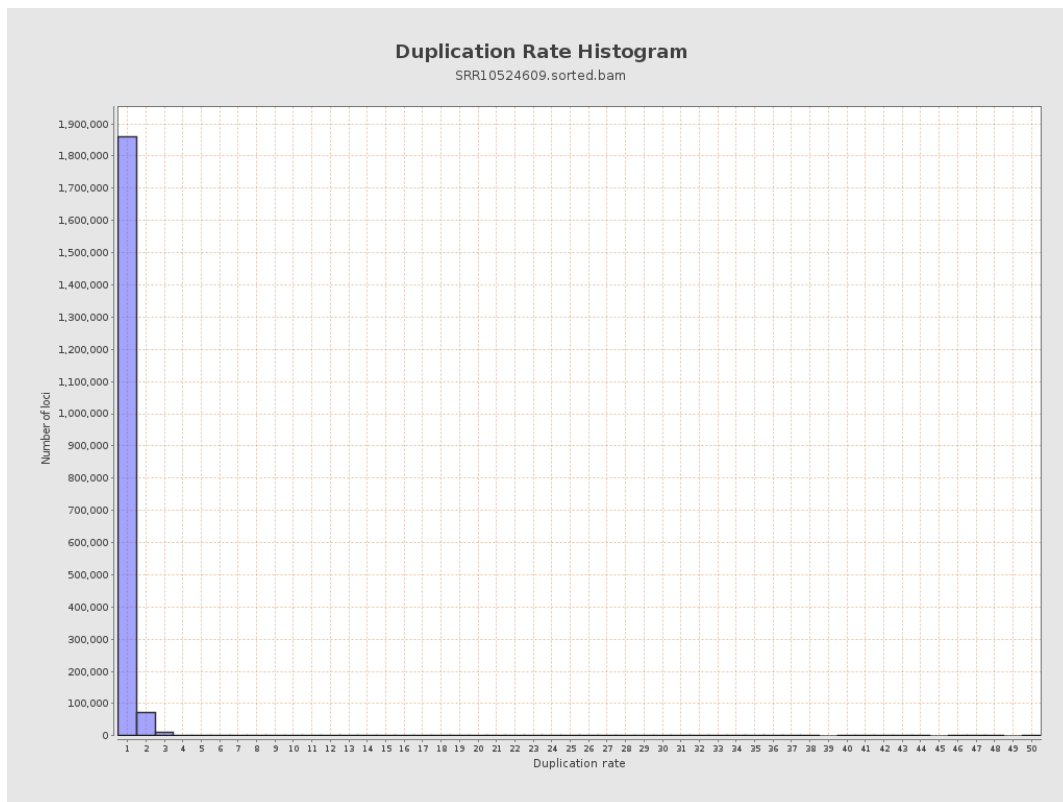
5. Results : Coverage Histogram (0-50X)



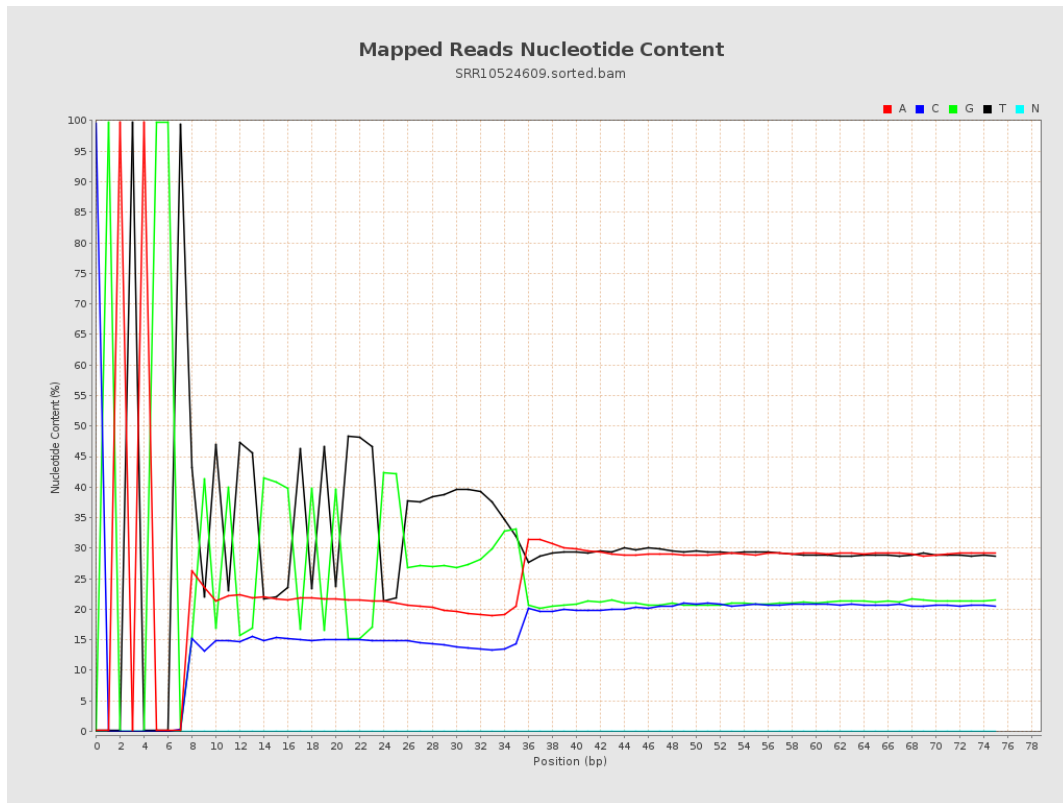
6. Results : Genome Fraction Coverage



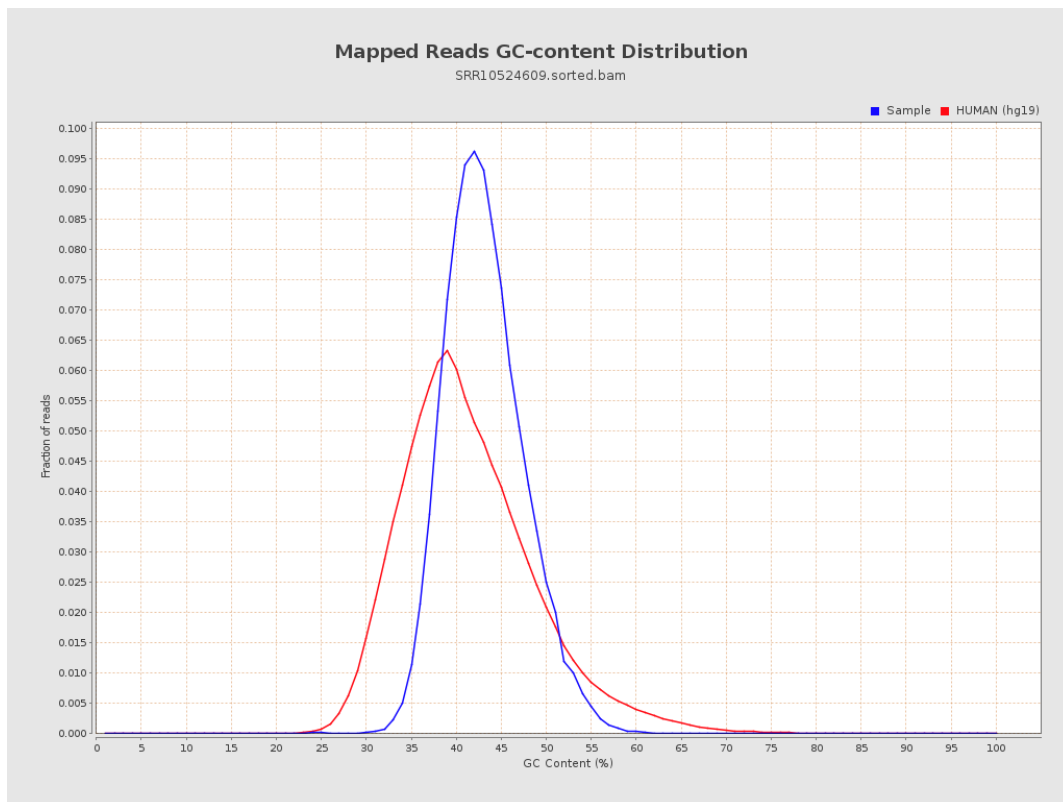
7. Results : Duplication Rate Histogram



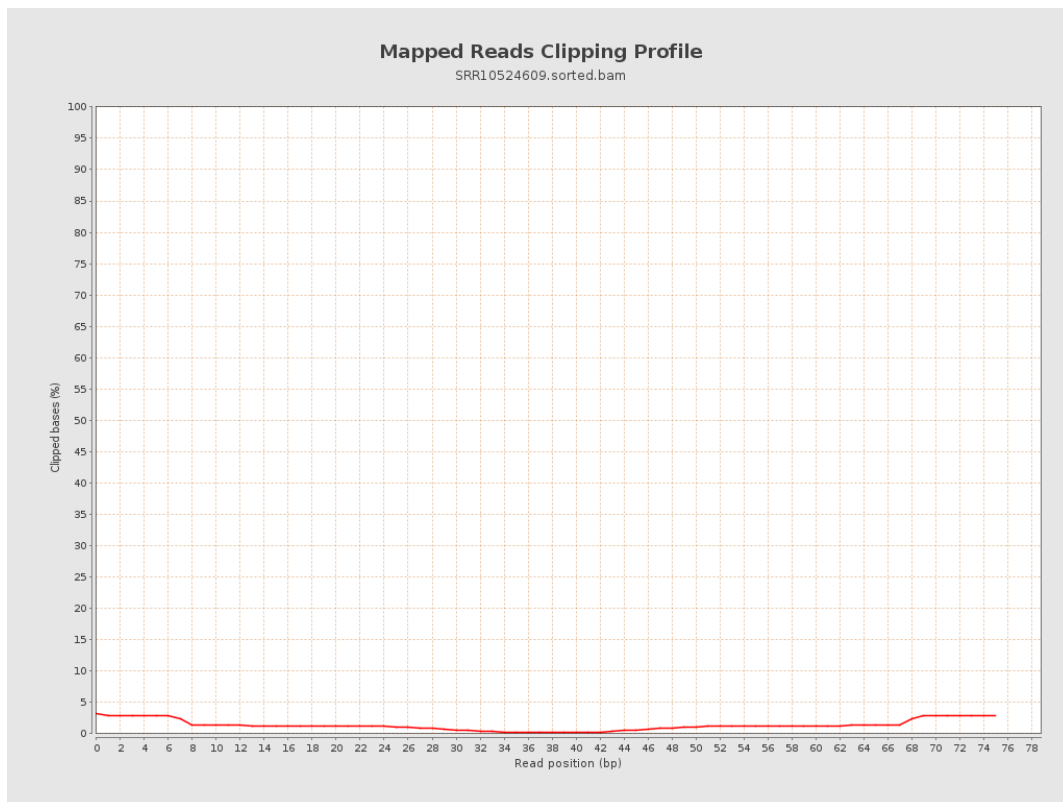
8. Results : Mapped Reads Nucleotide Content



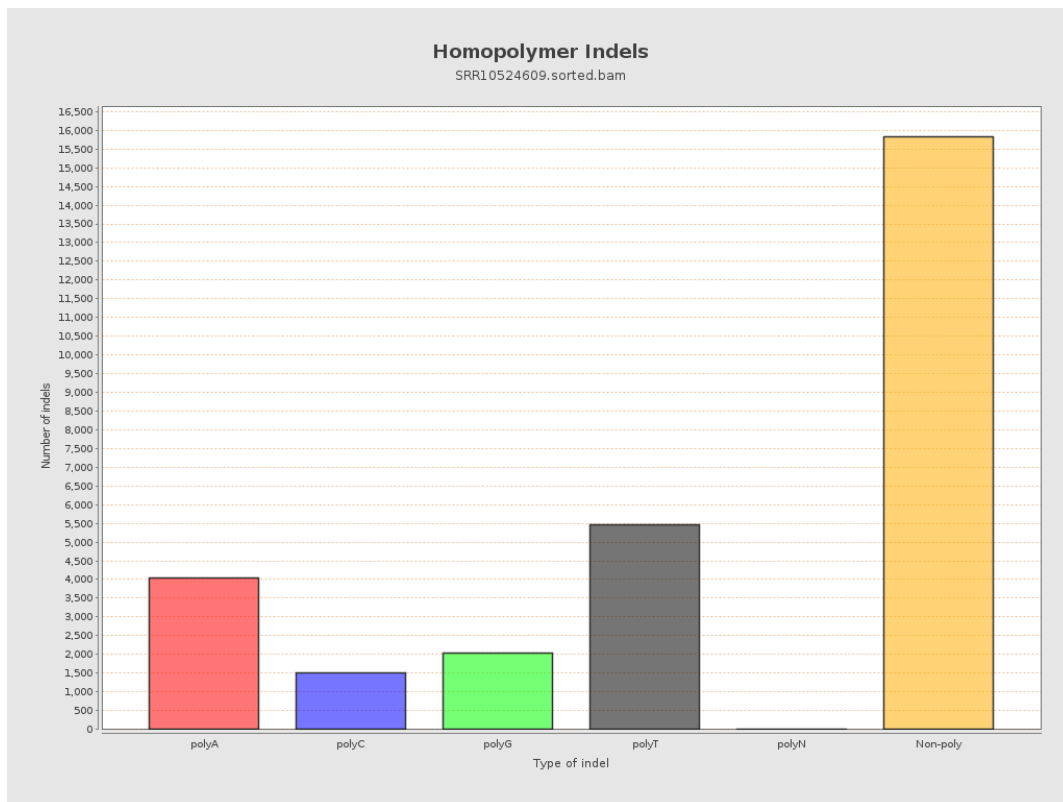
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

