

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 08:50:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008729.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_SRR6008729 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008729.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 08:50:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008729.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,886,373
Mapped reads	1,641,437 / 87.02%
Unmapped reads	244,936 / 12.98%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,763 / 0.73%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	99,268 / 5.26%
Duplication rate	4.85%
Clipped reads	883,608 / 46.84%

2.2. ACGT Content

Number/percentage of A's	28,522,120 / 26.99%
Number/percentage of C's	19,688,043 / 18.63%
Number/percentage of T's	33,283,761 / 31.49%
Number/percentage of G's	24,118,357 / 22.82%
Number/percentage of N's	77,245 / 0.07%
GC Percentage	41.45%

2.3. Coverage

Mean	0.0342

Standard Deviation	0.3294
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2.4. Mapping Quality

Mean Mapping Quality	45.22
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2.5. Mismatches and indels

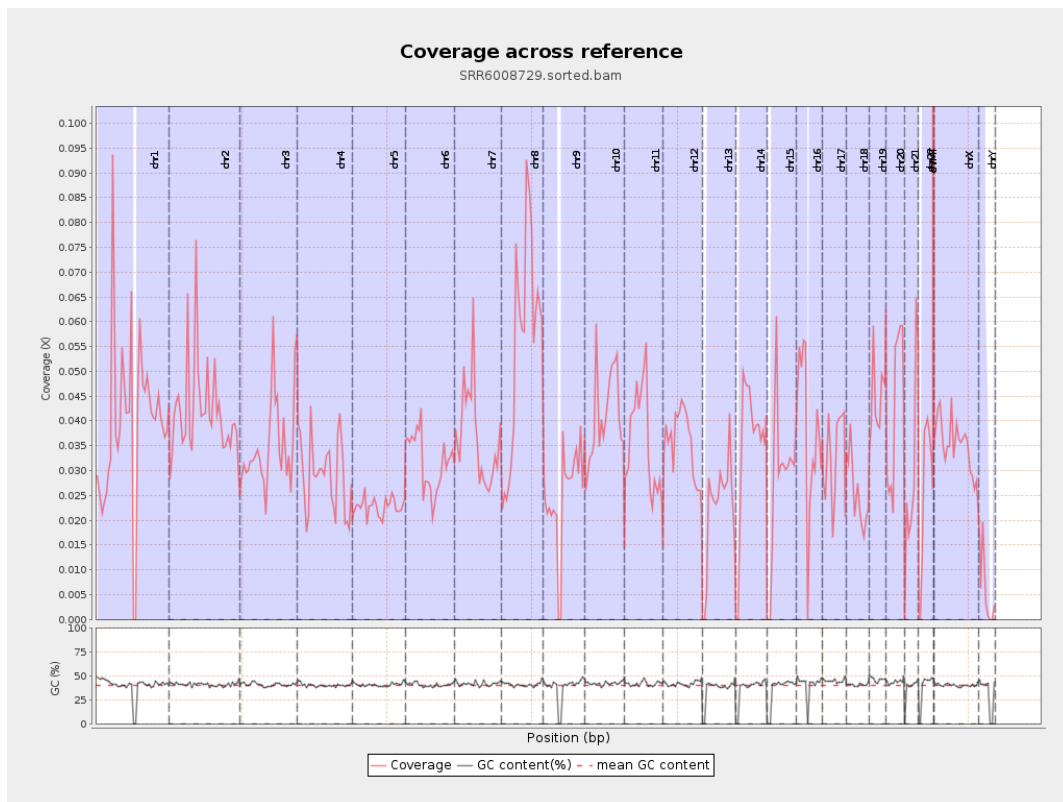
General error rate	0.96%
Mismatches	998,314
Insertions	8,457
Mapped reads with at least one insertion	0.51%
Deletions	49,171
Mapped reads with at least one deletion	2.95%
Homopolymer indels	43.72%

2.6. Chromosome stats

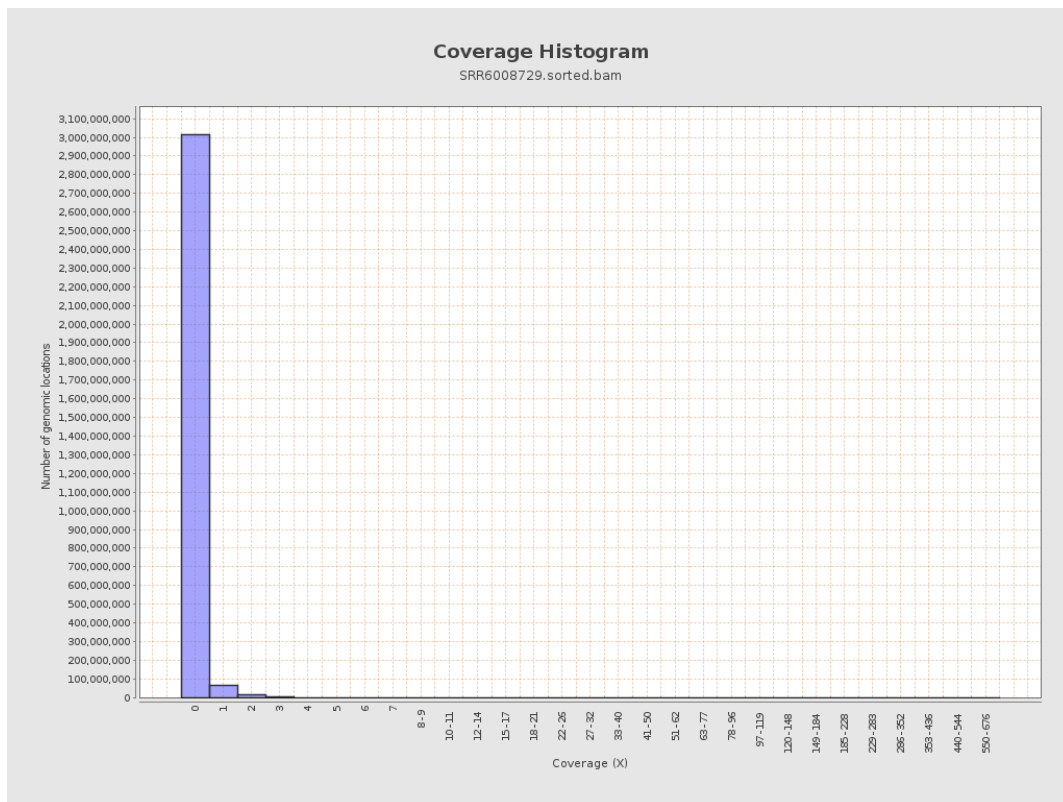
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	9797532	0.0393	0.5608
chr2	243199373	10219498	0.042	0.4411
chr3	198022430	6895659	0.0348	0.2259
chr4	191154276	5508494	0.0288	0.2251
chr5	180915260	4118447	0.0228	0.1847
chr6	171115067	5412460	0.0316	0.2444
chr7	159138663	5830208	0.0366	0.42

chr8	146364022	8095380	0.0553	0.4415
chr9	141213431	3514950	0.0249	0.2721
chr10	135534747	5527405	0.0408	0.3008
chr11	135006516	4812484	0.0356	0.3624
chr12	133851895	4771726	0.0356	0.2325
chr13	115169878	2582458	0.0224	0.1814
chr14	107349540	3748844	0.0349	0.2294
chr15	102531392	2945552	0.0287	0.2112
chr16	90354753	3435987	0.038	0.2542
chr17	81195210	2635316	0.0325	0.2727
chr18	78077248	1985422	0.0254	0.4358
chr19	59128983	2662161	0.045	0.3848
chr20	63025520	2656305	0.0421	0.2562
chr21	48129895	1439833	0.0299	0.2244
chr22	51304566	1298313	0.0253	0.1881
chrMT	16571	62584	3.7767	3.2373
chrX	155270560	5475666	0.0353	0.2441
chrY	59373566	340131	0.0057	0.1817

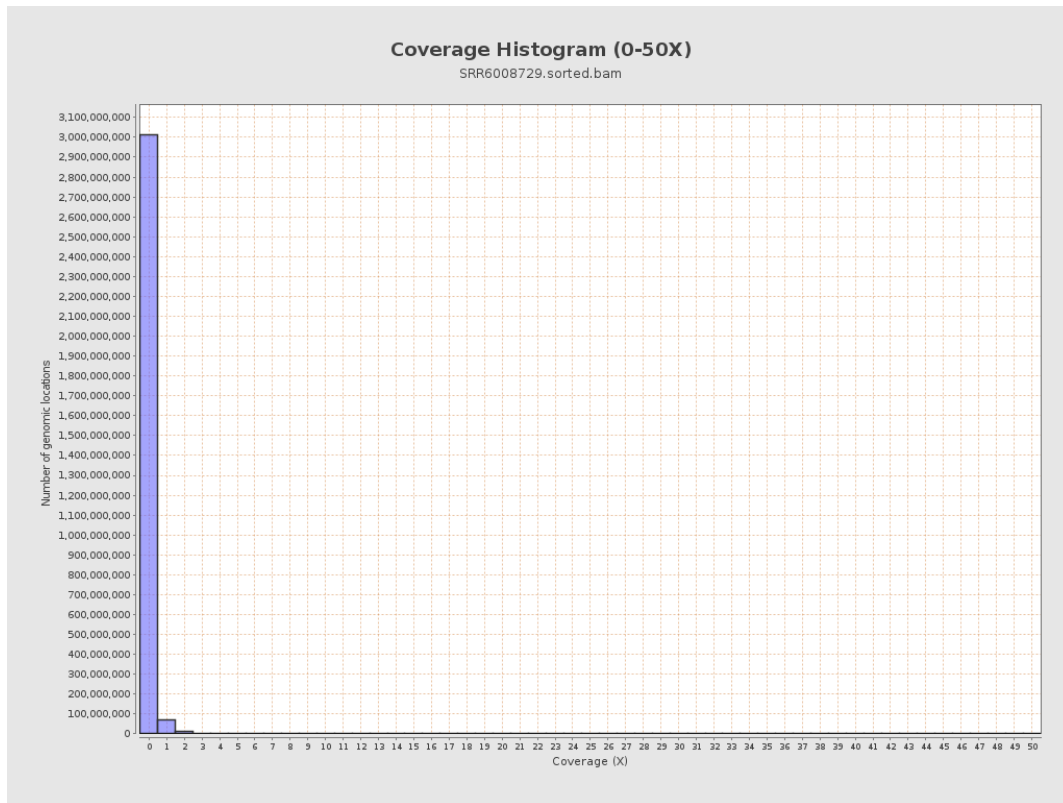
3. Results : Coverage across reference



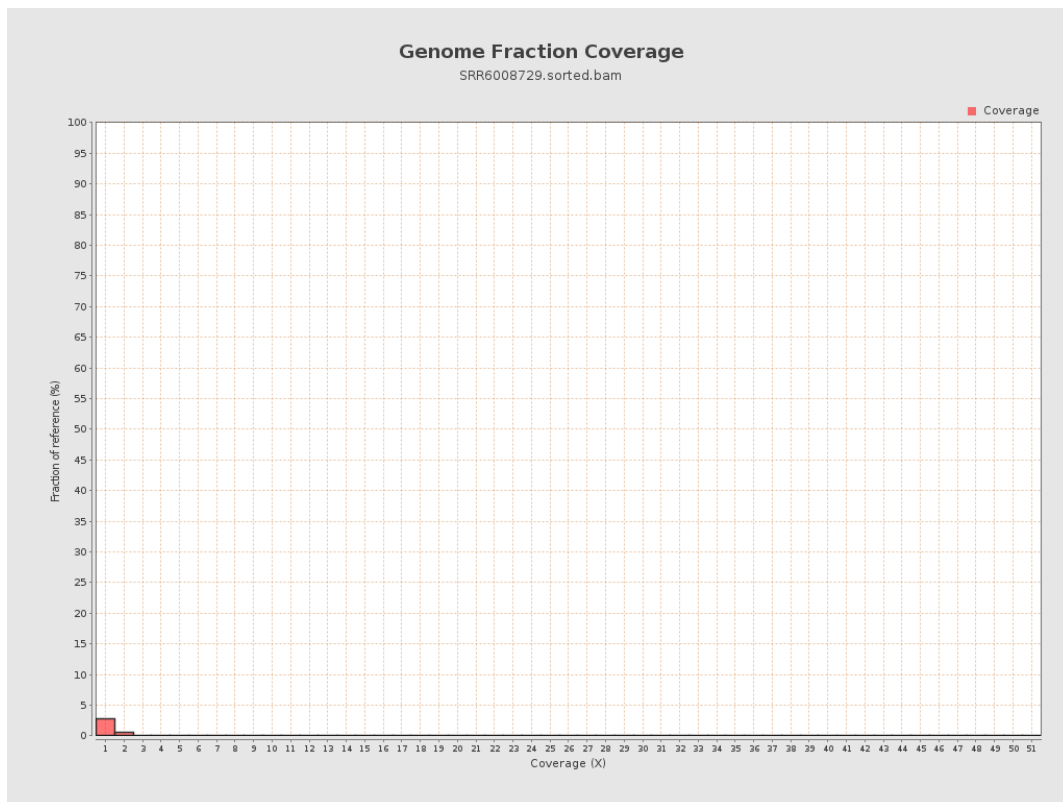
4. Results : Coverage Histogram



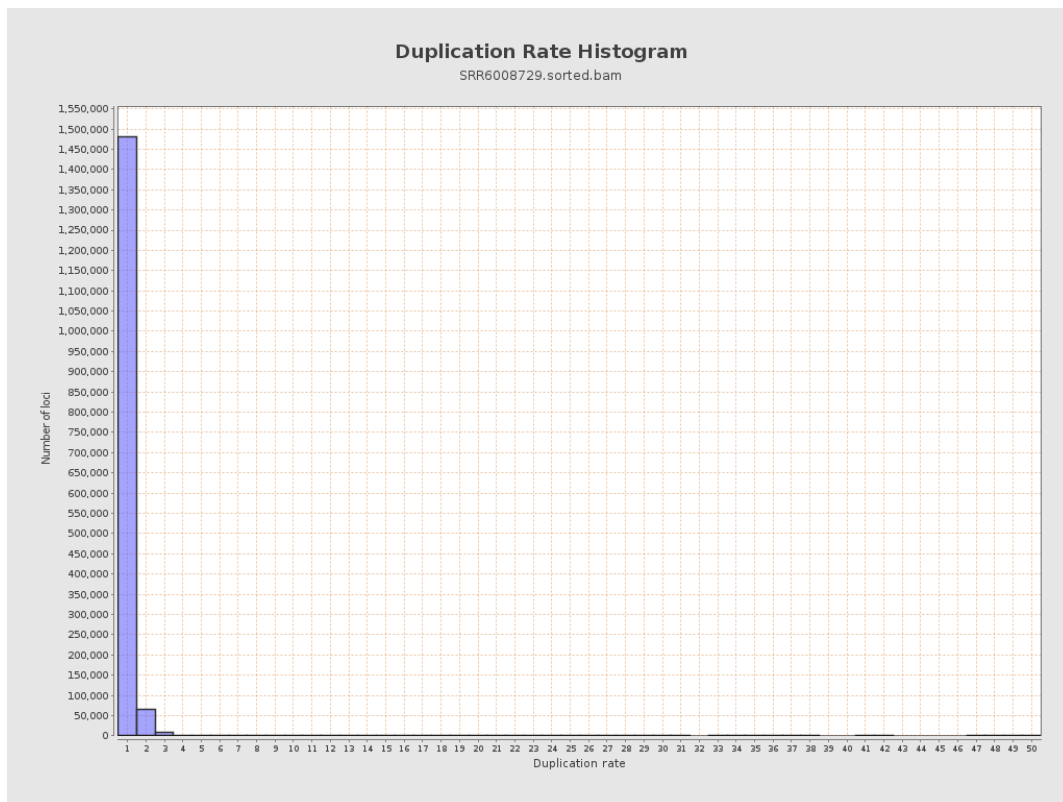
5. Results : Coverage Histogram (0-50X)



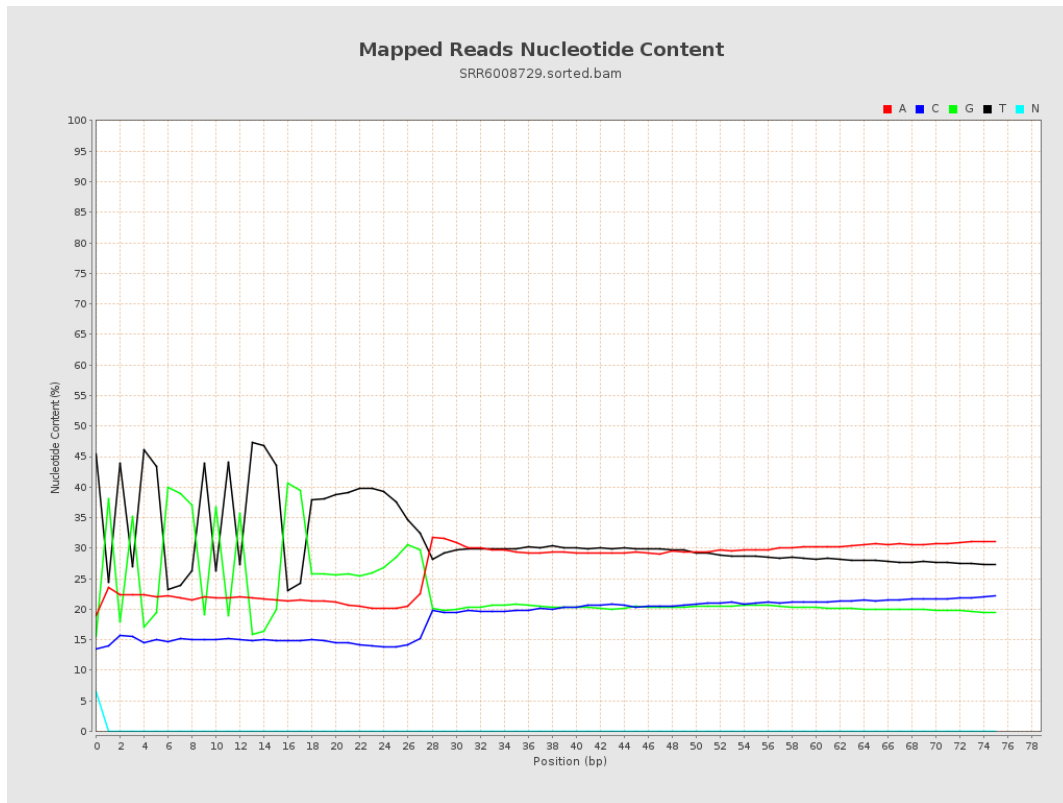
6. Results : Genome Fraction Coverage



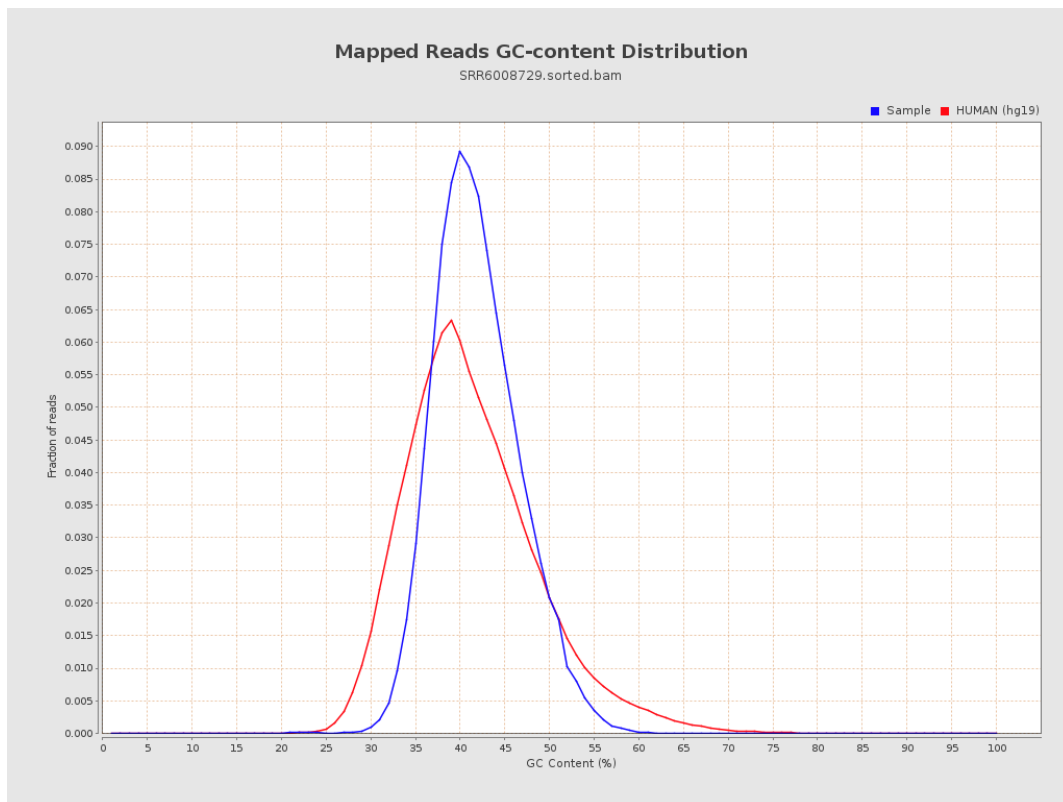
7. Results : Duplication Rate Histogram



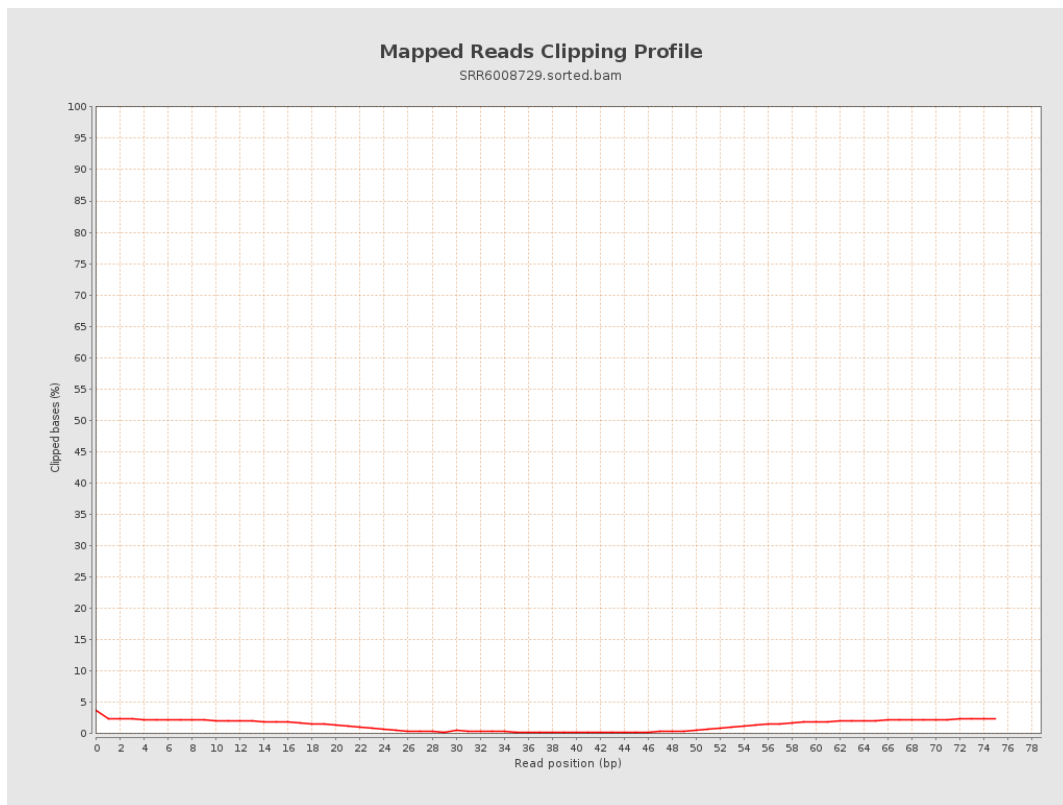
8. Results : Mapped Reads Nucleotide Content



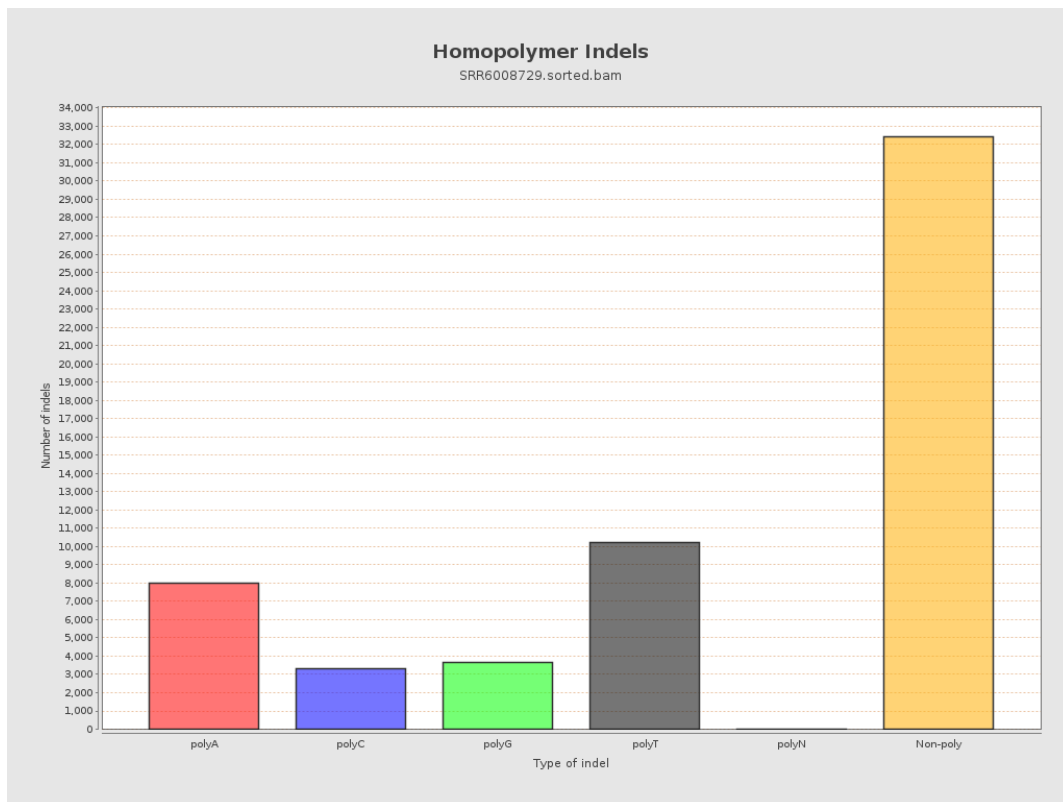
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

