

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 03:33:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004129.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_SRR6004129 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004129.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 03:33:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004129.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,159,020
Mapped reads	1,338,086 / 61.98%
Unmapped reads	820,934 / 38.02%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,929 / 0.41%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	145,669 / 6.75%
Duplication rate	8.85%
Clipped reads	841,891 / 38.99%

2.2. ACGT Content

Number/percentage of A's	21,545,225 / 25.71%
Number/percentage of C's	15,024,077 / 17.93%
Number/percentage of T's	27,730,761 / 33.09%
Number/percentage of G's	19,502,828 / 23.27%
Number/percentage of N's	9,965 / 0.01%
GC Percentage	41.2%

2.3. Coverage

Mean	0.0271

Standard Deviation	0.2876
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2.4. Mapping Quality

Mean Mapping Quality	45.01
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2.5. Mismatches and indels

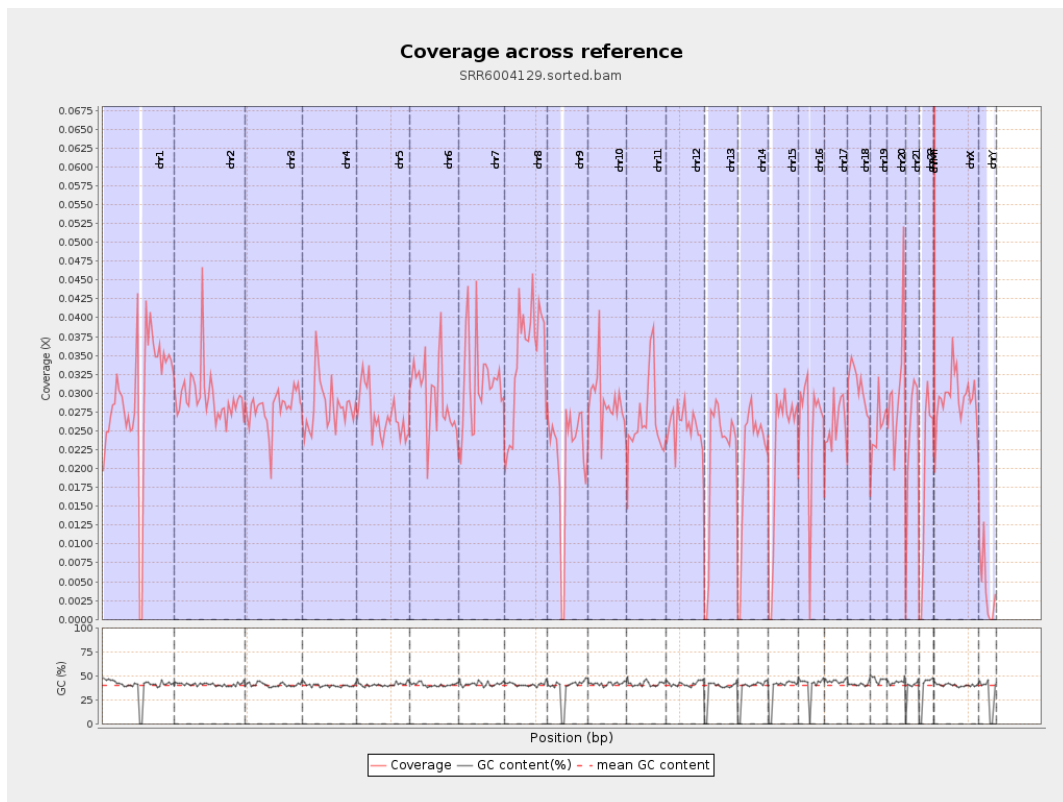
General error rate	1.12%
Mismatches	924,489
Insertions	7,265
Mapped reads with at least one insertion	0.54%
Deletions	26,623
Mapped reads with at least one deletion	1.97%
Homopolymer indels	46.77%

2.6. Chromosome stats

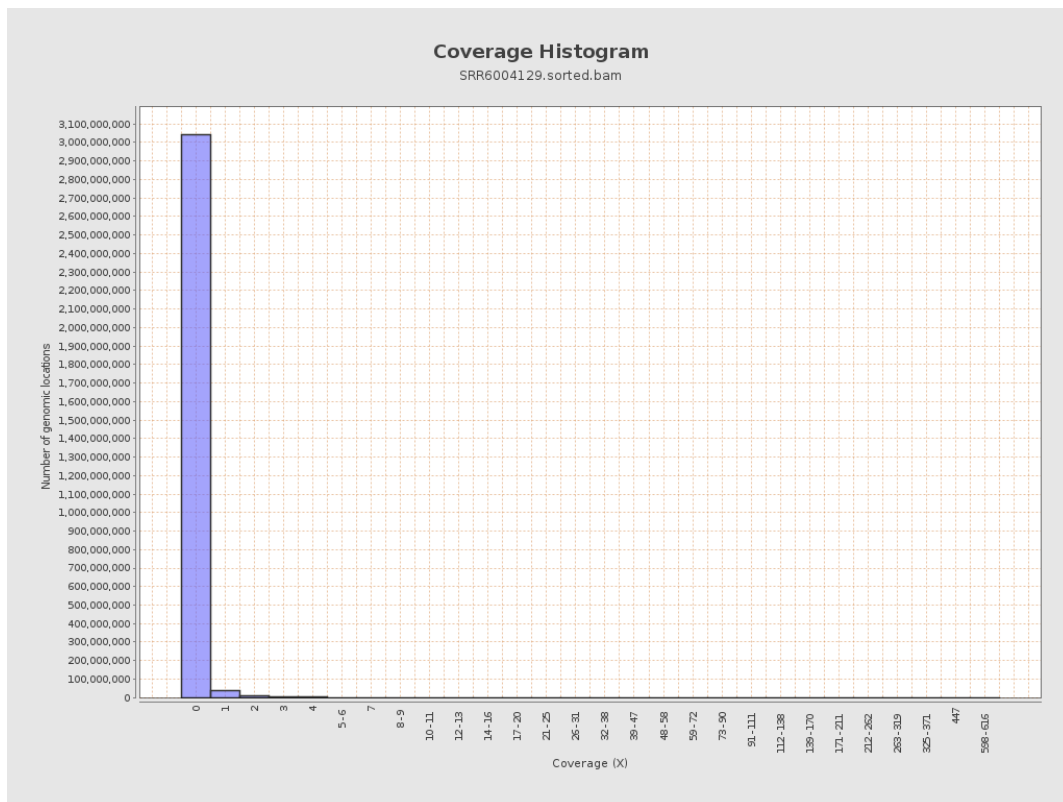
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	7331827	0.0294	0.3845
chr2	243199373	7172565	0.0295	0.3788
chr3	198022430	5537686	0.028	0.2397
chr4	191154276	5408802	0.0283	0.2452
chr5	180915260	4908376	0.0271	0.2351
chr6	171115067	5044304	0.0295	0.2708
chr7	159138663	4981243	0.0313	0.3687

chr8	146364022	5063853	0.0346	0.3367
chr9	141213431	3057207	0.0216	0.2472
chr10	135534747	3917397	0.0289	0.2796
chr11	135006516	3565181	0.0264	0.2722
chr12	133851895	3417641	0.0255	0.2355
chr13	115169878	2467177	0.0214	0.2137
chr14	107349540	2296946	0.0214	0.2164
chr15	102531392	2316258	0.0226	0.216
chr16	90354753	2314141	0.0256	0.2354
chr17	81195210	2105416	0.0259	0.235
chr18	78077248	2418489	0.031	0.4077
chr19	59128983	1500826	0.0254	0.3212
chr20	63025520	1954467	0.031	0.2611
chr21	48129895	1174956	0.0244	0.2302
chr22	51304566	986018	0.0192	0.1963
chrMT	16571	89973	5.4295	4.3099
chrX	155270560	4577858	0.0295	0.2555
chrY	59373566	246138	0.0041	0.1011

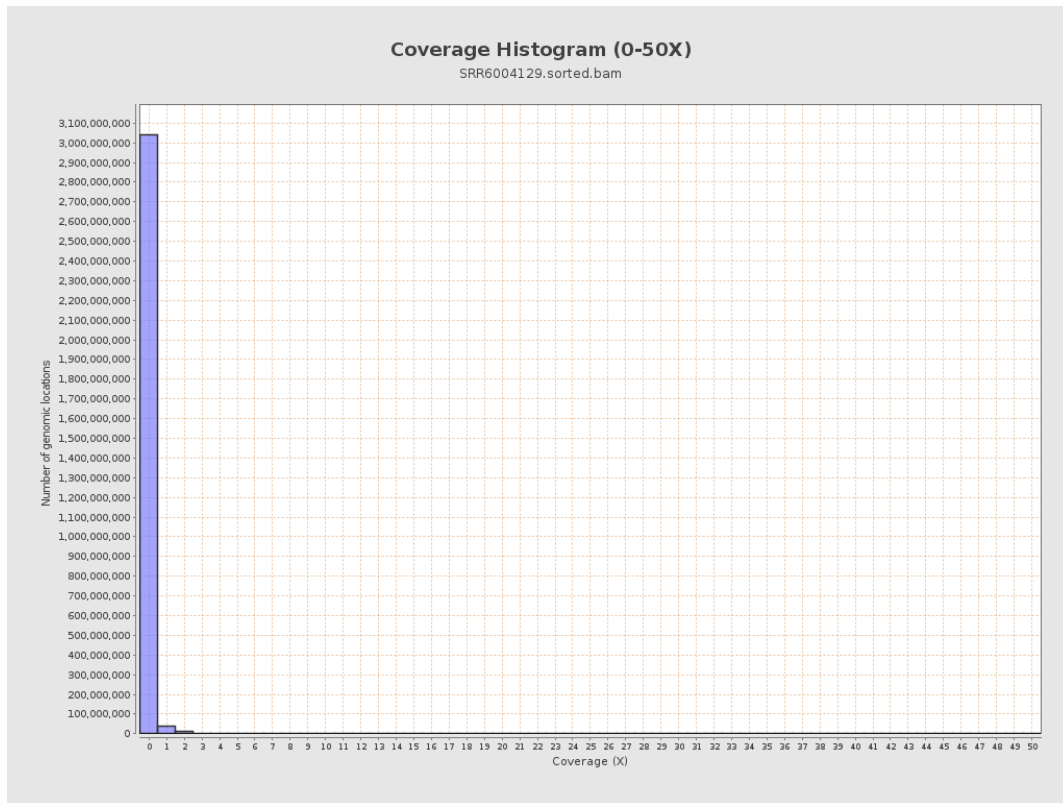
3. Results : Coverage across reference



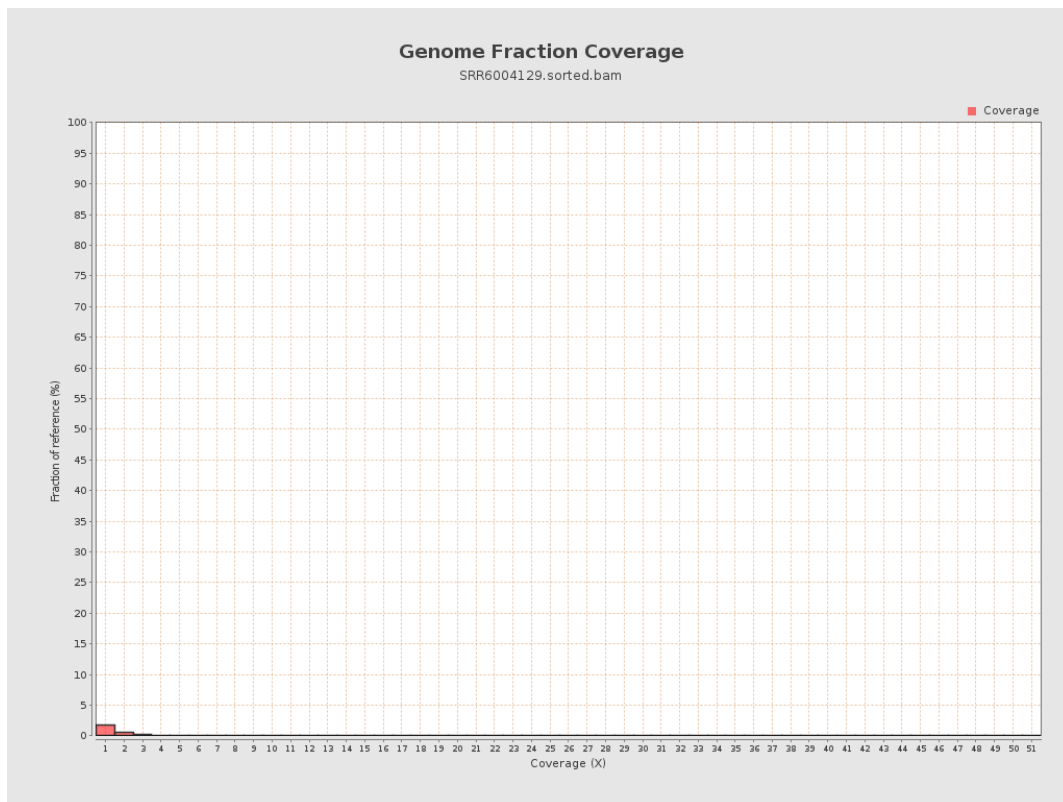
4. Results : Coverage Histogram



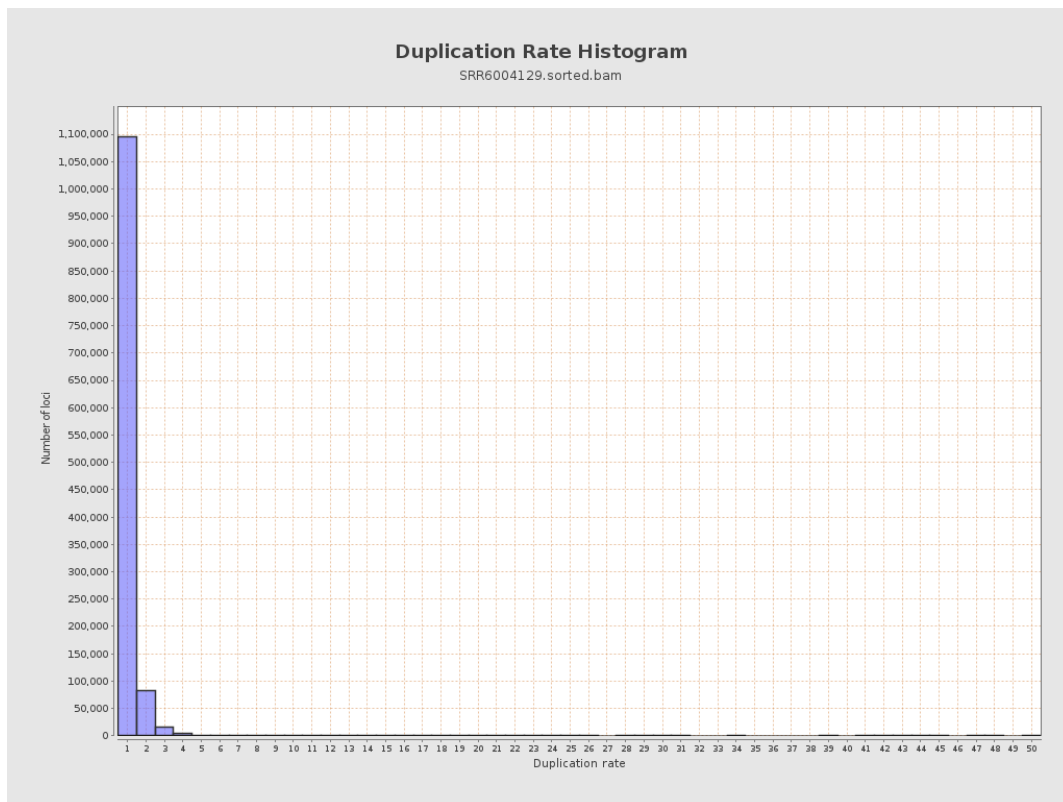
5. Results : Coverage Histogram (0-50X)



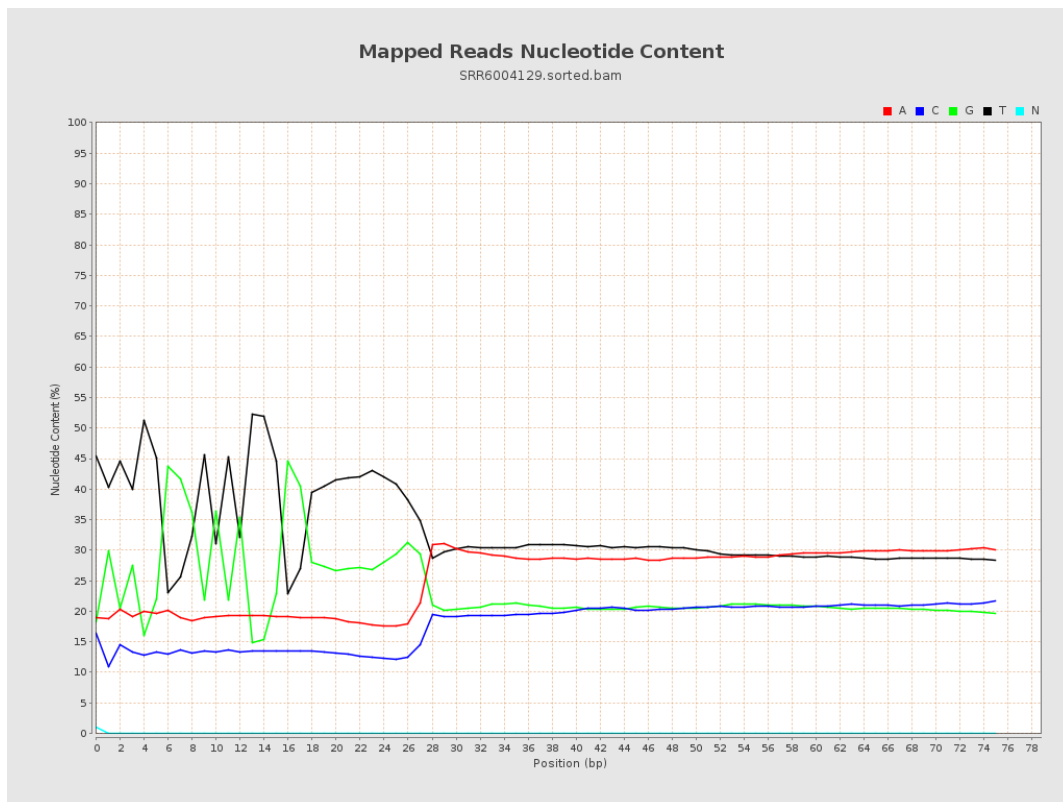
6. Results : Genome Fraction Coverage



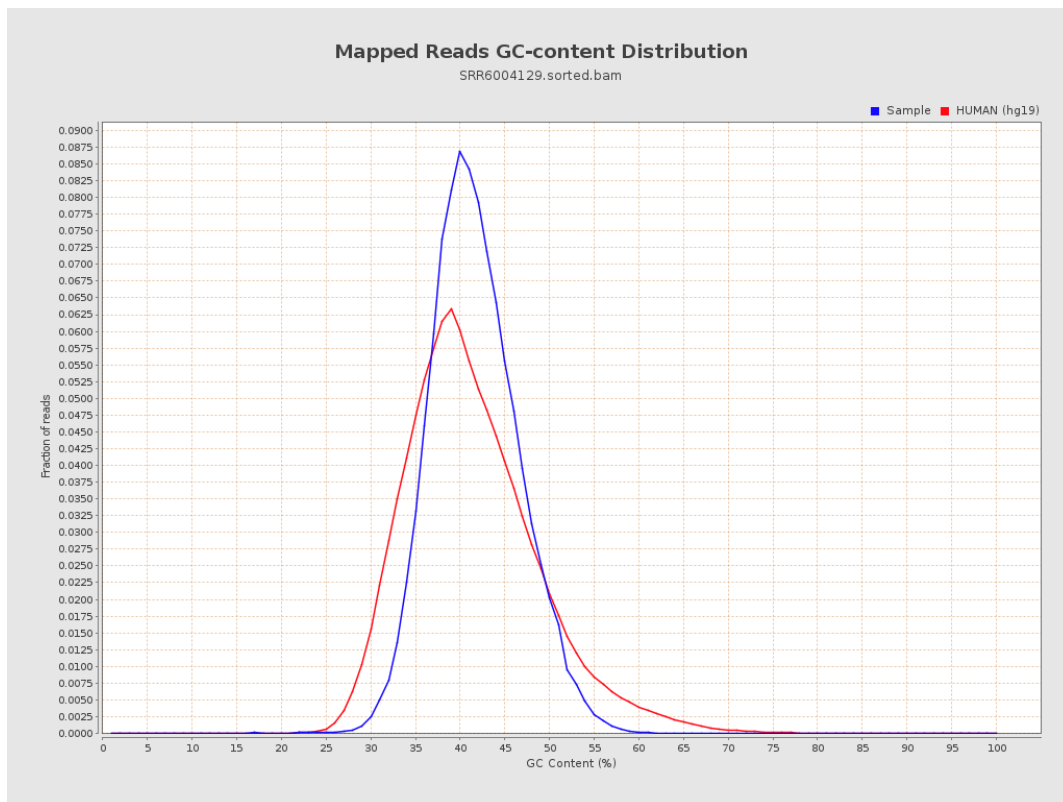
7. Results : Duplication Rate Histogram



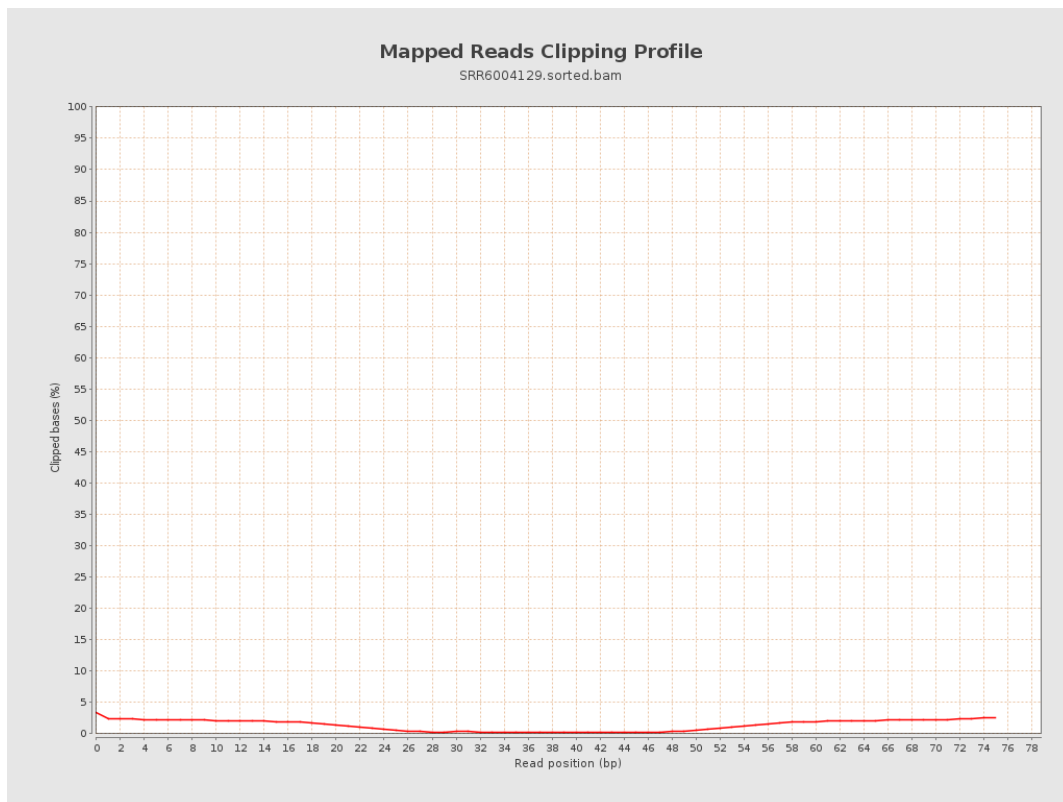
8. Results : Mapped Reads Nucleotide Content



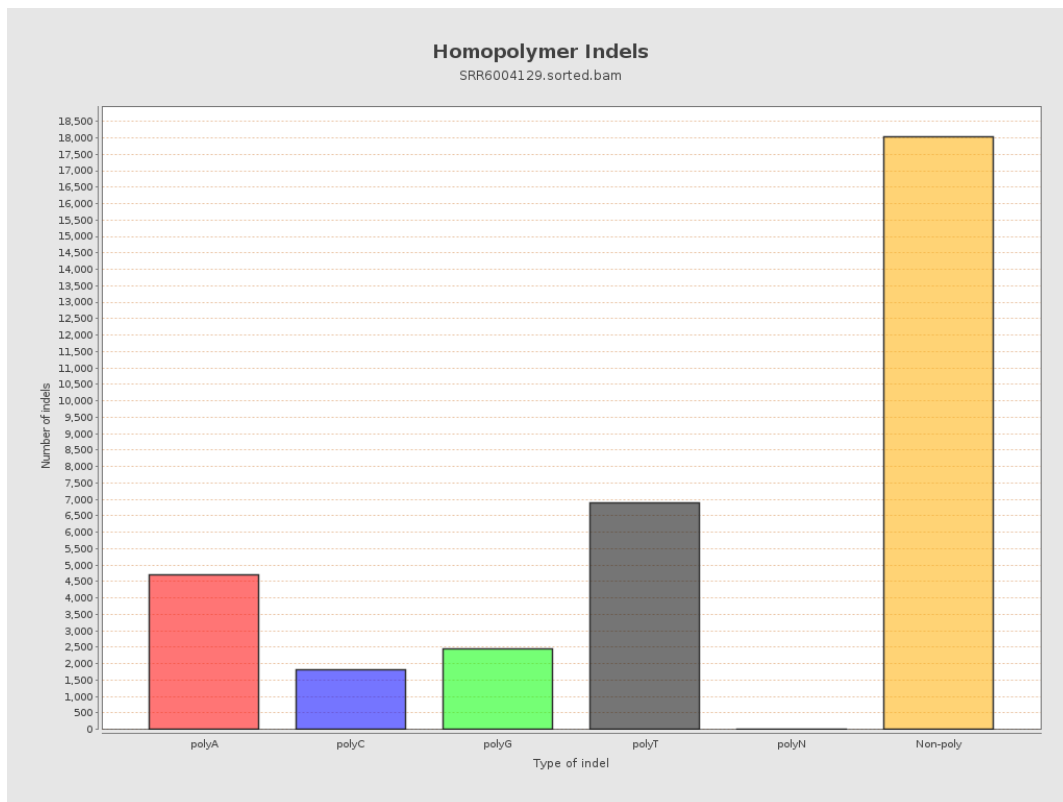
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

