

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 15:32:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013199.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_SRR6013199 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013199.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 15:32:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013199.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,612,502
Mapped reads	1,314,664 / 81.53%
Unmapped reads	297,838 / 18.47%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,736 / 0.6%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	72,844 / 4.52%
Duplication rate	4.66%
Clipped reads	705,057 / 43.72%

2.2. ACGT Content

Number/percentage of A's	22,927,850 / 27.11%
Number/percentage of C's	15,101,613 / 17.86%
Number/percentage of T's	27,490,714 / 32.51%
Number/percentage of G's	19,039,866 / 22.52%
Number/percentage of N's	1,168 / 0%
GC Percentage	40.37%

2.3. Coverage

Mean	0.0273

Standard Deviation	0.2568
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2.4. Mapping Quality

Mean Mapping Quality	45.83
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2.5. Mismatches and indels

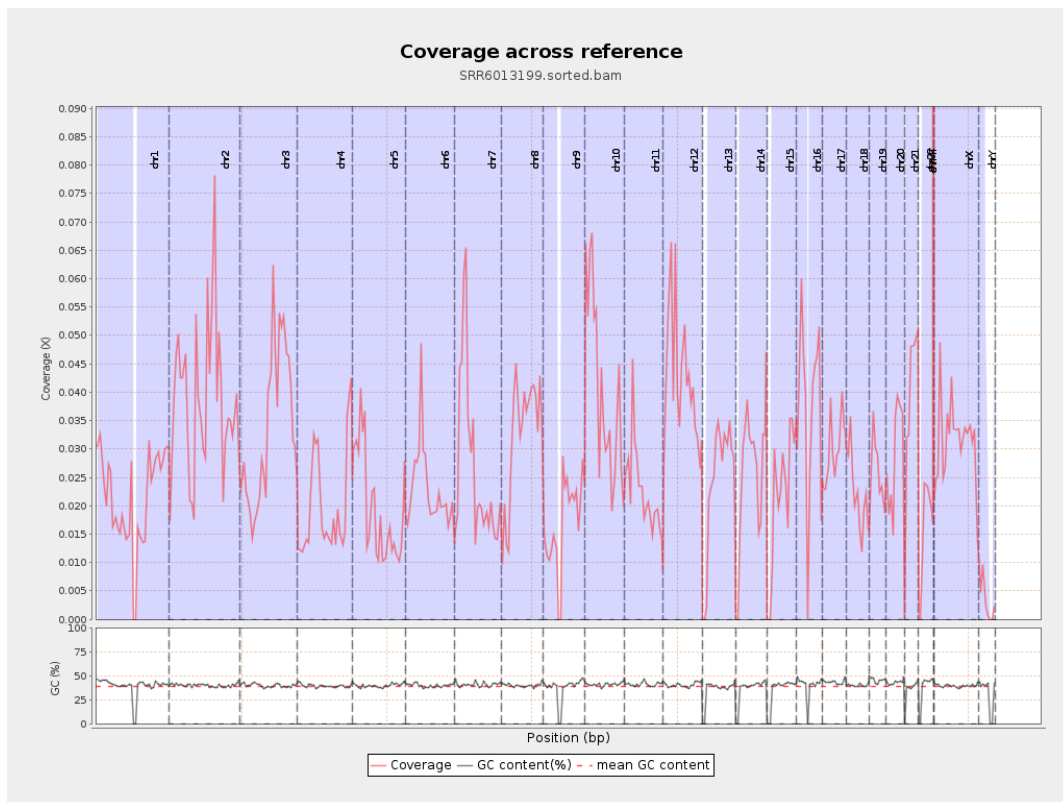
General error rate	0.83%
Mismatches	694,963
Insertions	5,816
Mapped reads with at least one insertion	0.44%
Deletions	27,282
Mapped reads with at least one deletion	2.05%
Homopolymer indels	46.56%

2.6. Chromosome stats

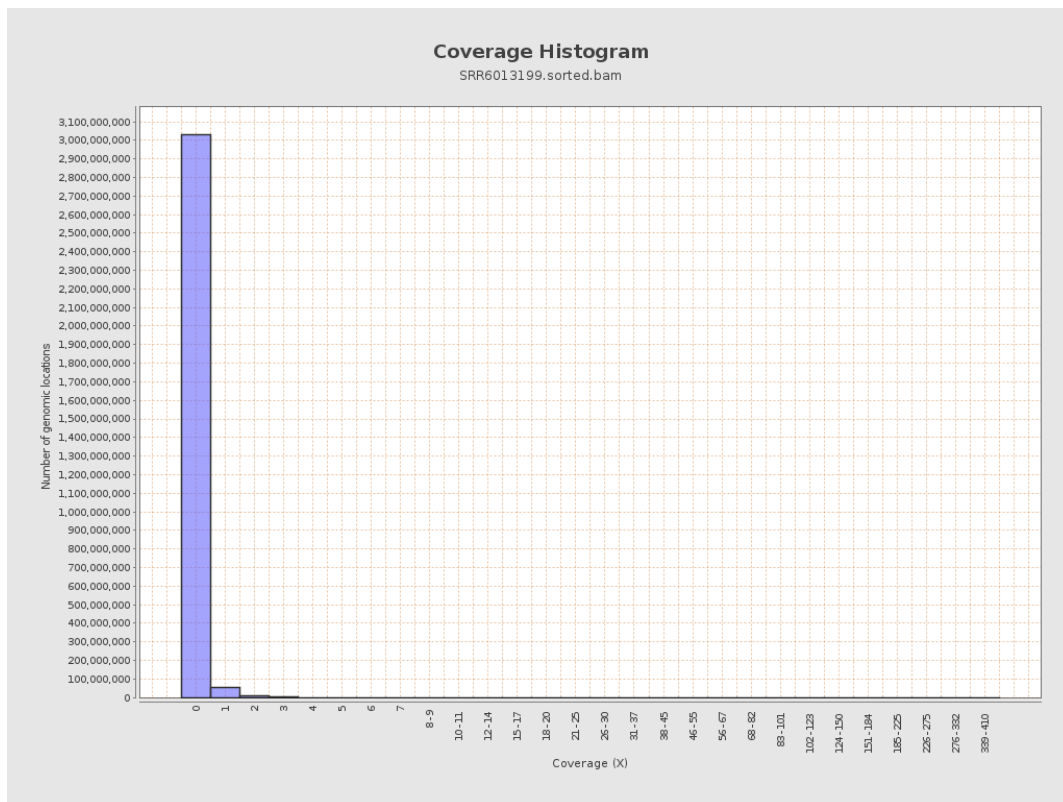
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	5315894	0.0213	0.353
chr2	243199373	9322627	0.0383	0.3451
chr3	198022430	6662470	0.0336	0.2216
chr4	191154276	3849114	0.0201	0.1763
chr5	180915260	3522454	0.0195	0.1704
chr6	171115067	3893116	0.0228	0.2515
chr7	159138663	4288724	0.0269	0.2992

chr8	146364022	4750012	0.0325	0.2908
chr9	141213431	2380522	0.0169	0.226
chr10	135534747	5534357	0.0408	0.3099
chr11	135006516	3059846	0.0227	0.2079
chr12	133851895	5650979	0.0422	0.2497
chr13	115169878	2786255	0.0242	0.1867
chr14	107349540	2666457	0.0248	0.1946
chr15	102531392	2242173	0.0219	0.1784
chr16	90354753	3388408	0.0375	0.2401
chr17	81195210	2444565	0.0301	0.2205
chr18	78077248	1748566	0.0224	0.366
chr19	59128983	1541314	0.0261	0.2969
chr20	63025520	1792919	0.0284	0.2023
chr21	48129895	1878769	0.039	0.2475
chr22	51304566	796456	0.0155	0.1476
chrMT	16571	26409	1.5937	1.7378
chrX	155270560	4871867	0.0314	0.2257
chrY	59373566	193836	0.0033	0.081

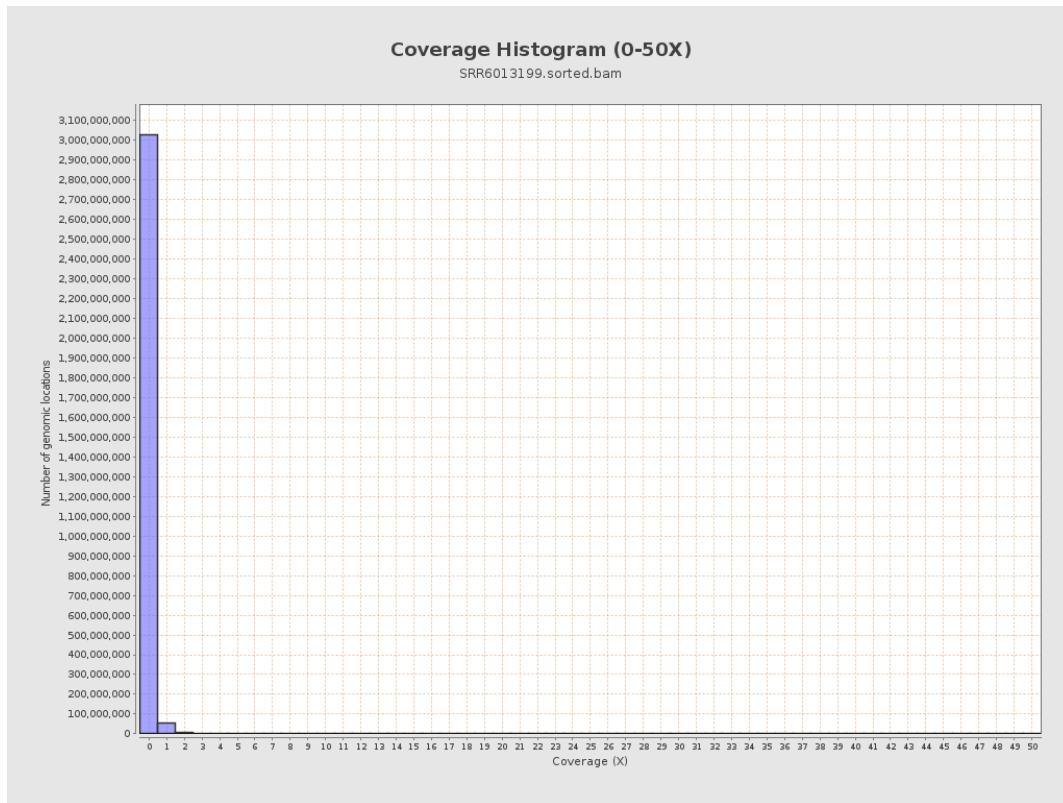
3. Results : Coverage across reference



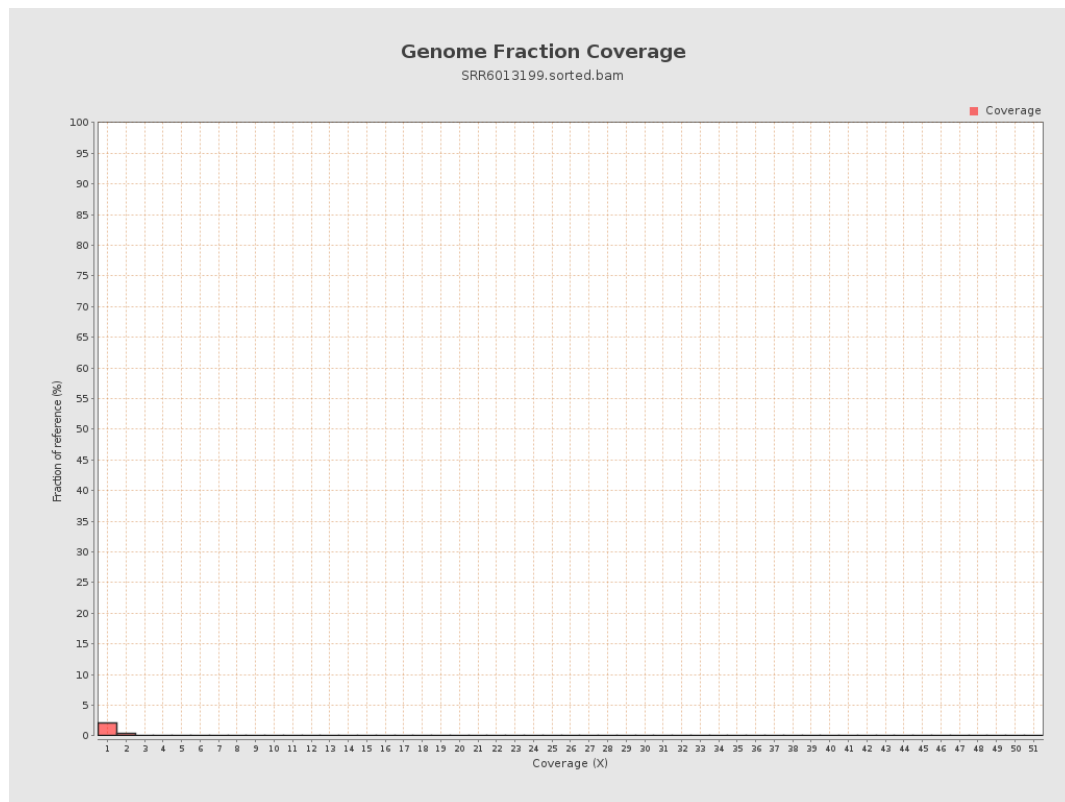
4. Results : Coverage Histogram



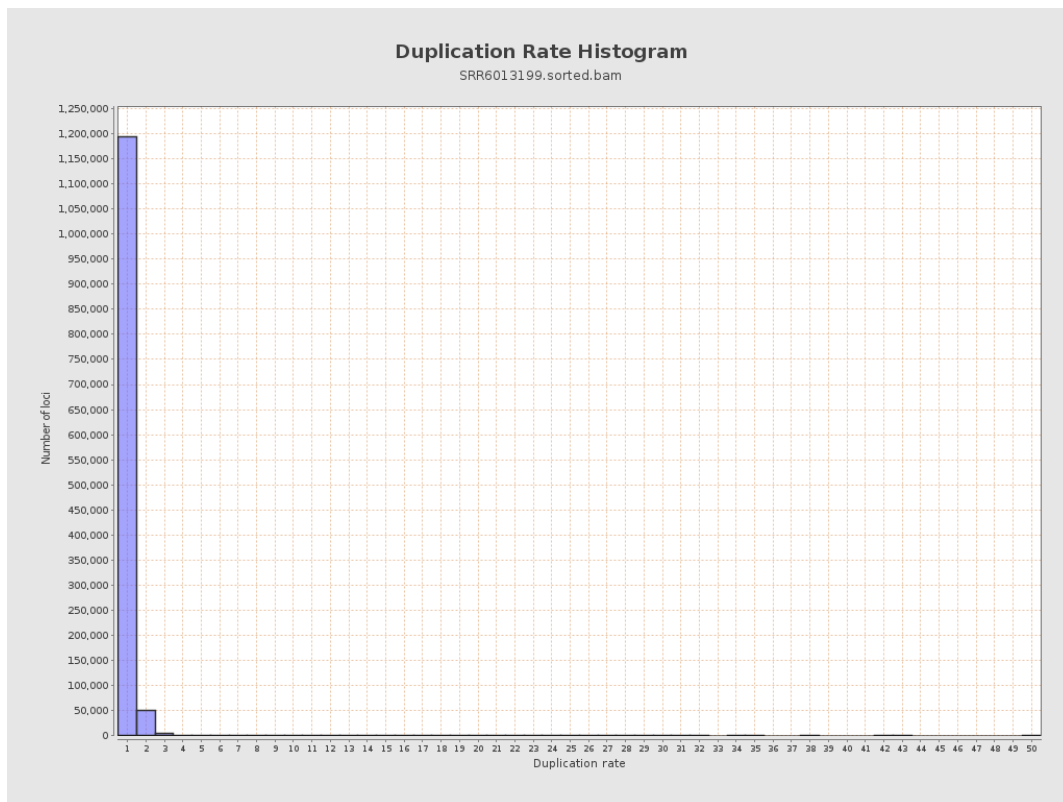
5. Results : Coverage Histogram (0-50X)



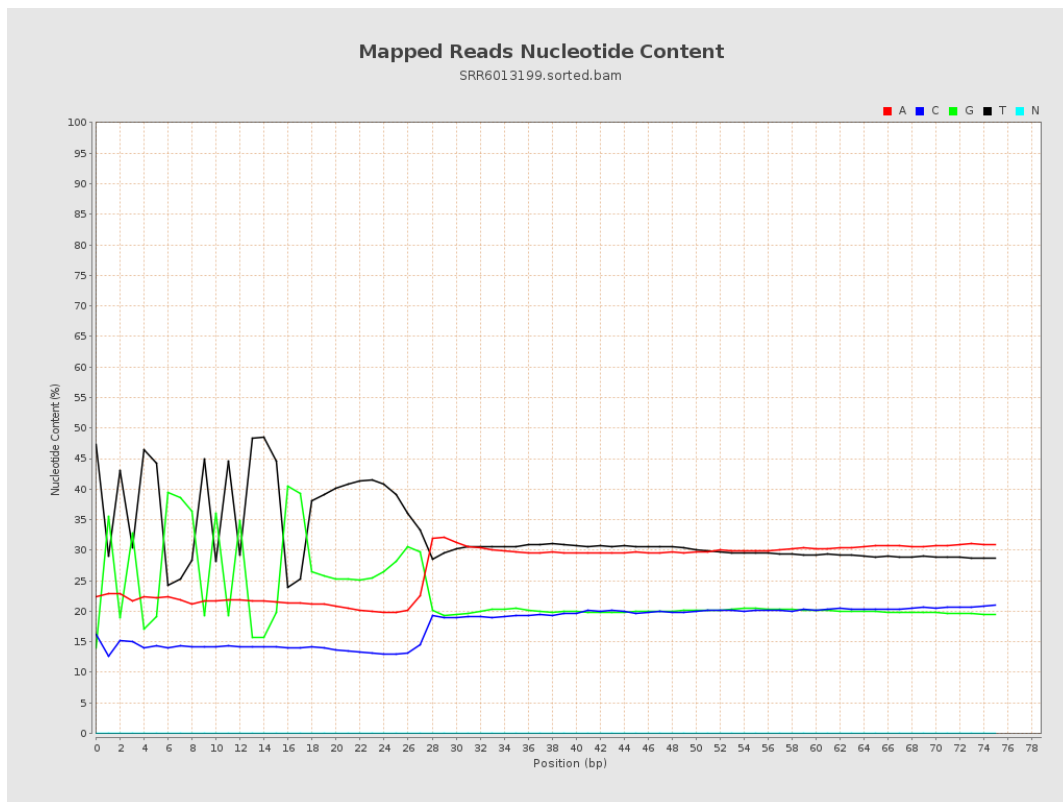
6. Results : Genome Fraction Coverage



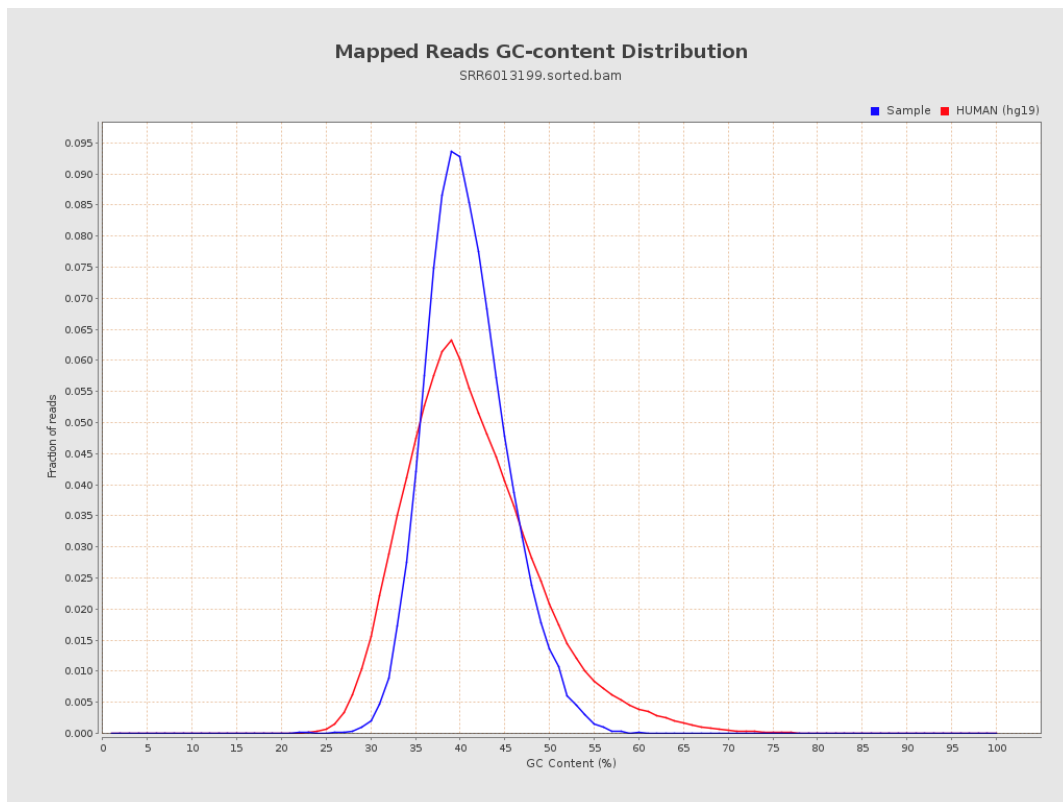
7. Results : Duplication Rate Histogram



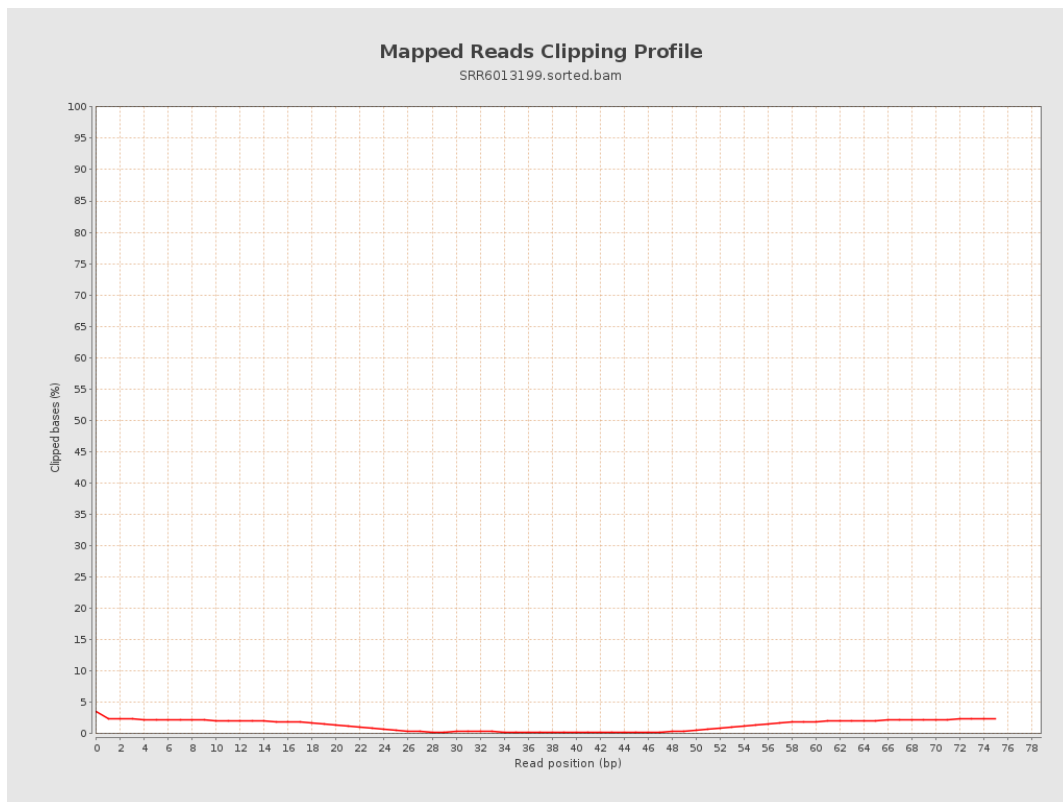
8. Results : Mapped Reads Nucleotide Content



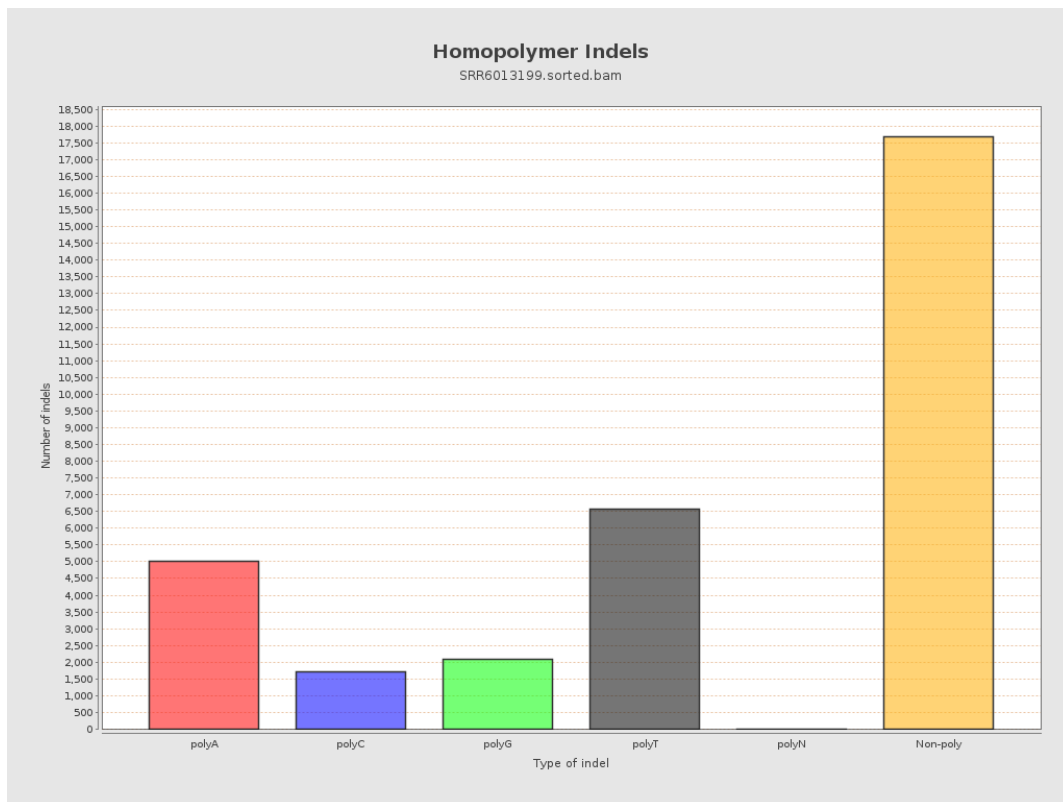
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

