

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 06:35:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6063601.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_SRR6063601 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6063601.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 06:35:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6063601.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,169,061
Mapped reads	3,065,792 / 96.74%
Unmapped reads	103,269 / 3.26%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	27,257 / 0.86%
Read min/max/mean length	30 / 76 / 76.3
Duplicated reads (estimated)	225,673 / 7.12%
Duplication rate	6.17%
Clipped reads	869,930 / 27.45%

2.2. ACGT Content

Number/percentage of A's	63,707,767 / 29.52%
Number/percentage of C's	40,155,815 / 18.61%
Number/percentage of T's	66,197,522 / 30.68%
Number/percentage of G's	45,689,361 / 21.17%
Number/percentage of N's	27,315 / 0.01%
GC Percentage	39.78%

2.3. Coverage

Mean	0.0697

Standard Deviation	0.685
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2.4. Mapping Quality

Mean Mapping Quality	47.9
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2.5. Mismatches and indels

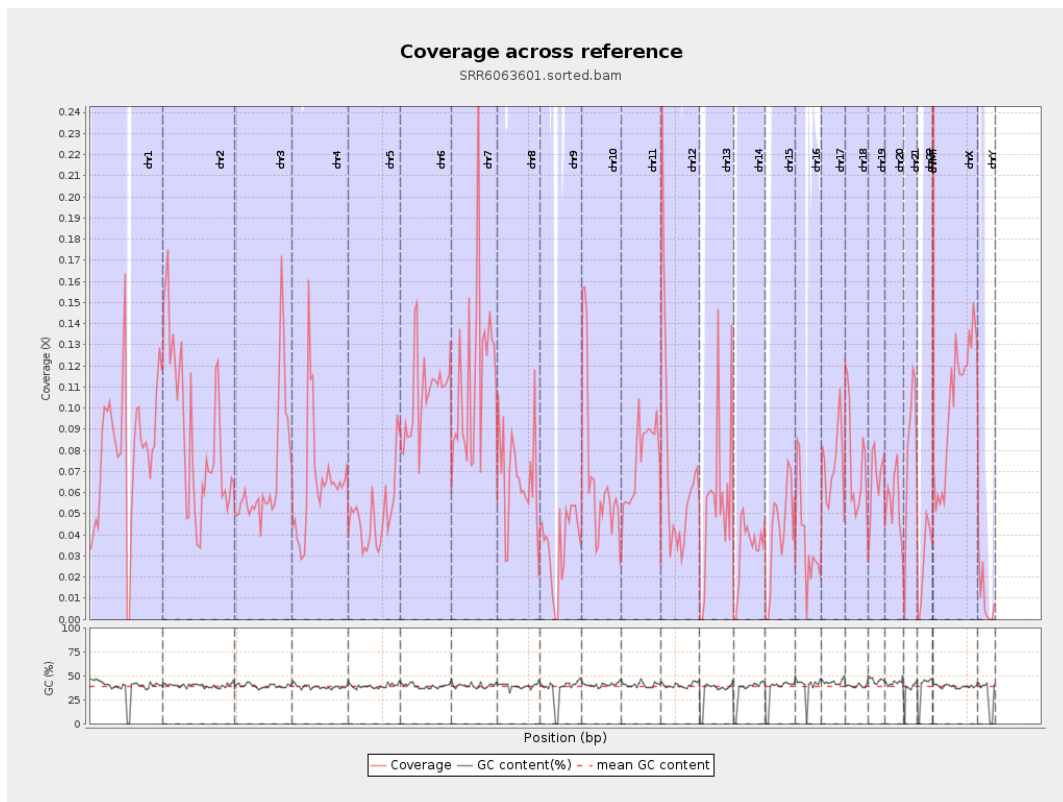
General error rate	0.5%
Mismatches	1,055,208
Insertions	14,330
Mapped reads with at least one insertion	0.46%
Deletions	49,249
Mapped reads with at least one deletion	1.59%
Homopolymer indels	45.63%

2.6. Chromosome stats

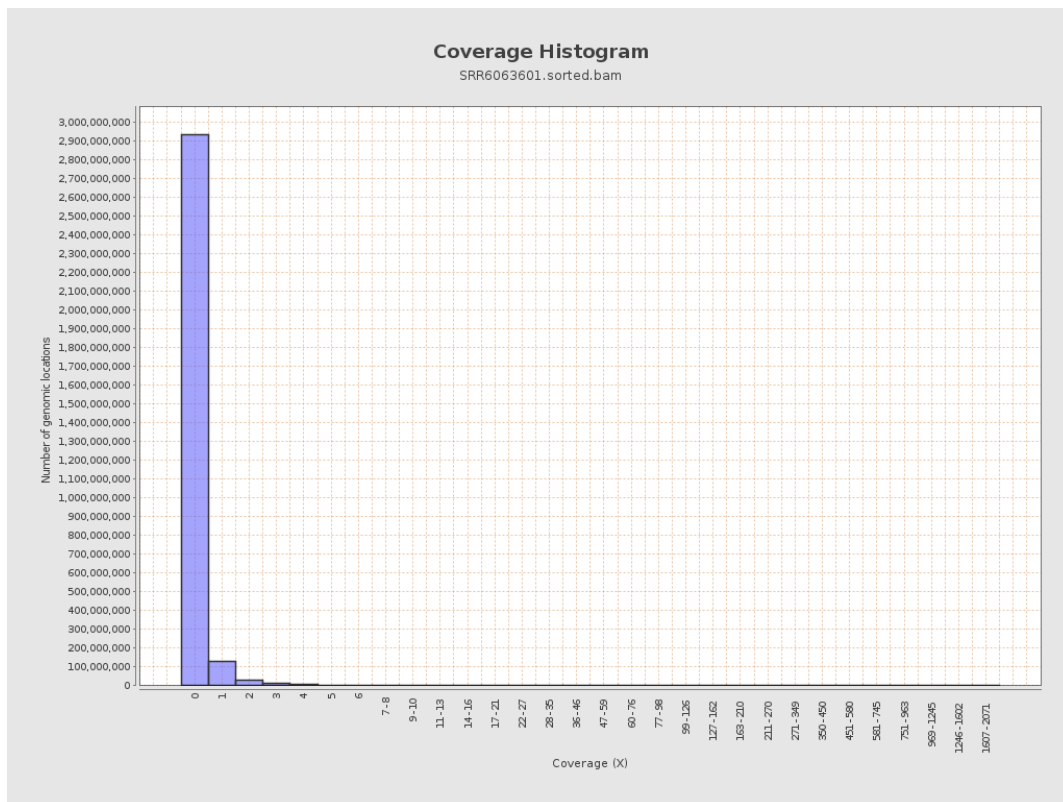
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	20167051	0.0809	1.3795
chr2	243199373	21401267	0.088	0.6043
chr3	198022430	13659843	0.069	0.3313
chr4	191154276	12570243	0.0658	0.3324
chr5	180915260	9085049	0.0502	0.2806
chr6	171115067	18211203	0.1064	0.461
chr7	159138663	18297239	0.115	1.2525

chr8	146364022	9693720	0.0662	1.2614
chr9	141213431	4997810	0.0354	0.5025
chr10	135534747	9307857	0.0687	0.4321
chr11	135006516	10193396	0.0755	0.4614
chr12	133851895	9666417	0.0722	0.3656
chr13	115169878	6532819	0.0567	0.3054
chr14	107349540	3592134	0.0335	0.282
chr15	102531392	4159592	0.0406	0.2494
chr16	90354753	3308204	0.0366	0.2692
chr17	81195210	6096456	0.0751	0.3787
chr18	78077248	5817632	0.0745	0.8843
chr19	59128983	3901889	0.066	0.8671
chr20	63025520	3445802	0.0547	0.3334
chr21	48129895	3790629	0.0788	0.3666
chr22	51304566	1463887	0.0285	0.2052
chrMT	16571	127489	7.6935	5.5755
chrX	155270560	15812286	0.1018	0.4525
chrY	59373566	567598	0.0096	0.3174

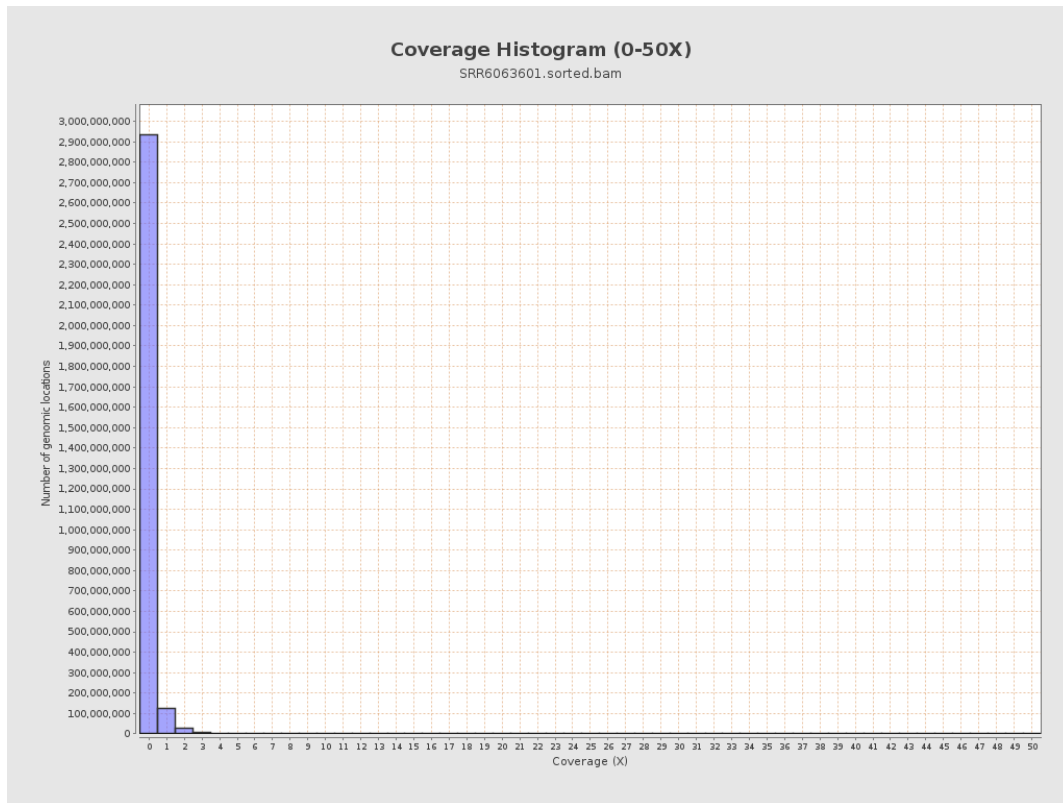
3. Results : Coverage across reference



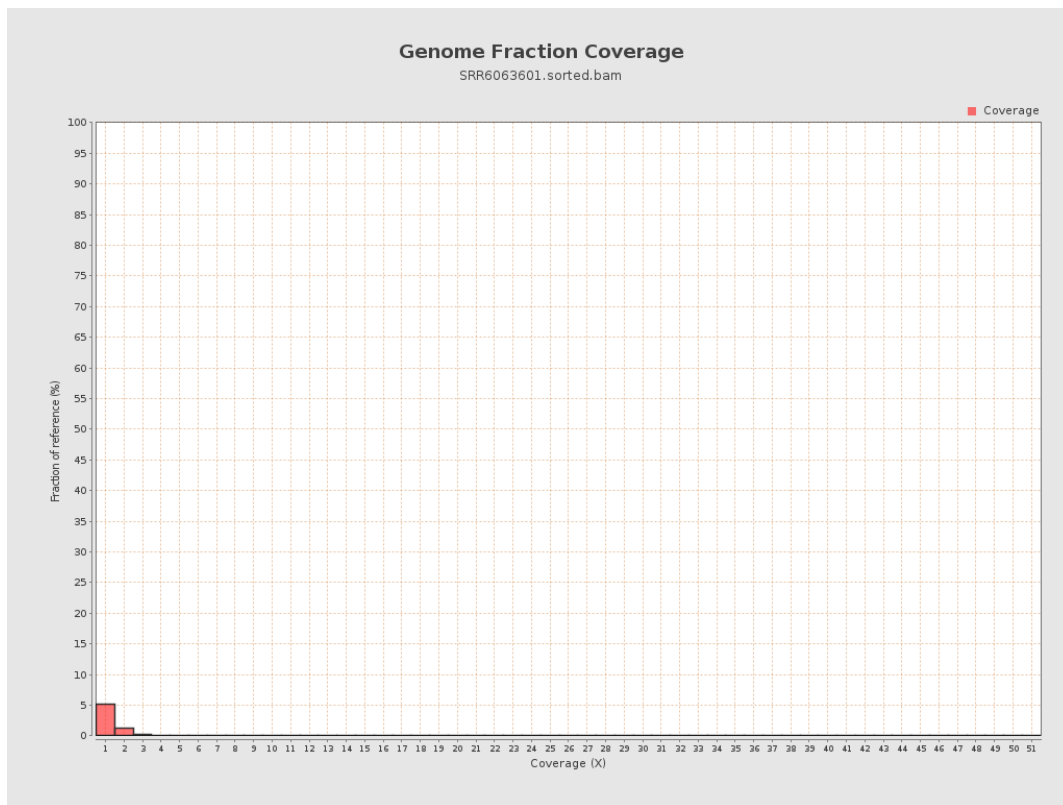
4. Results : Coverage Histogram



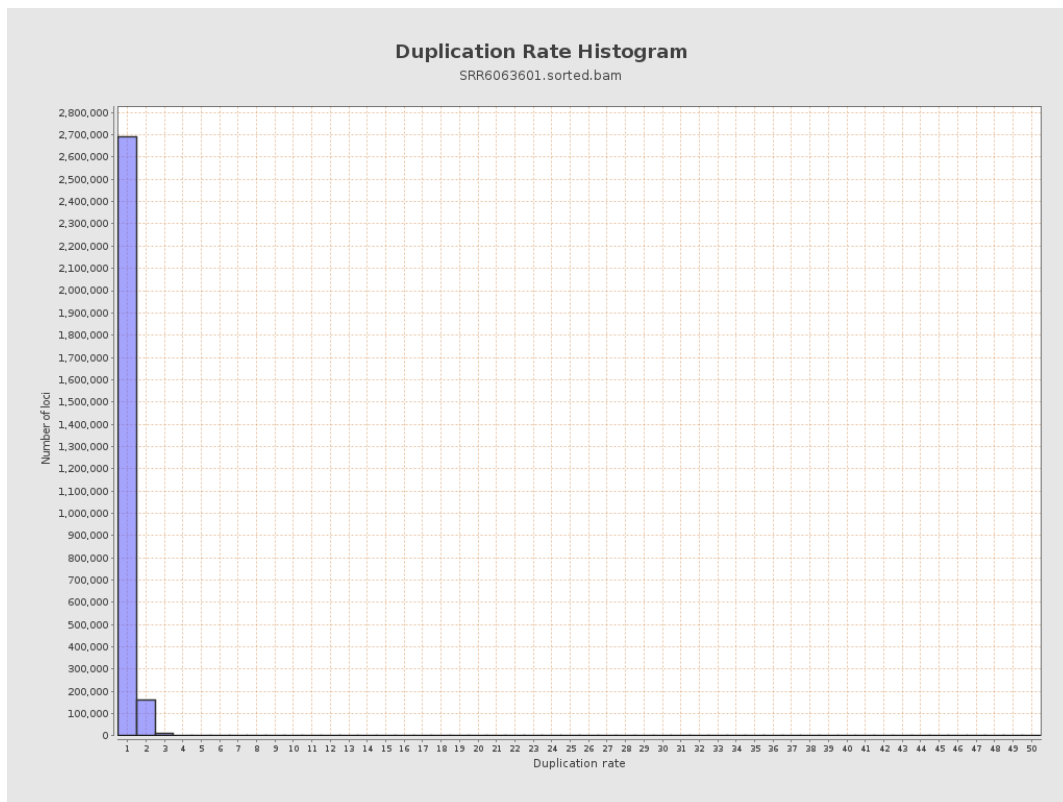
5. Results : Coverage Histogram (0-50X)



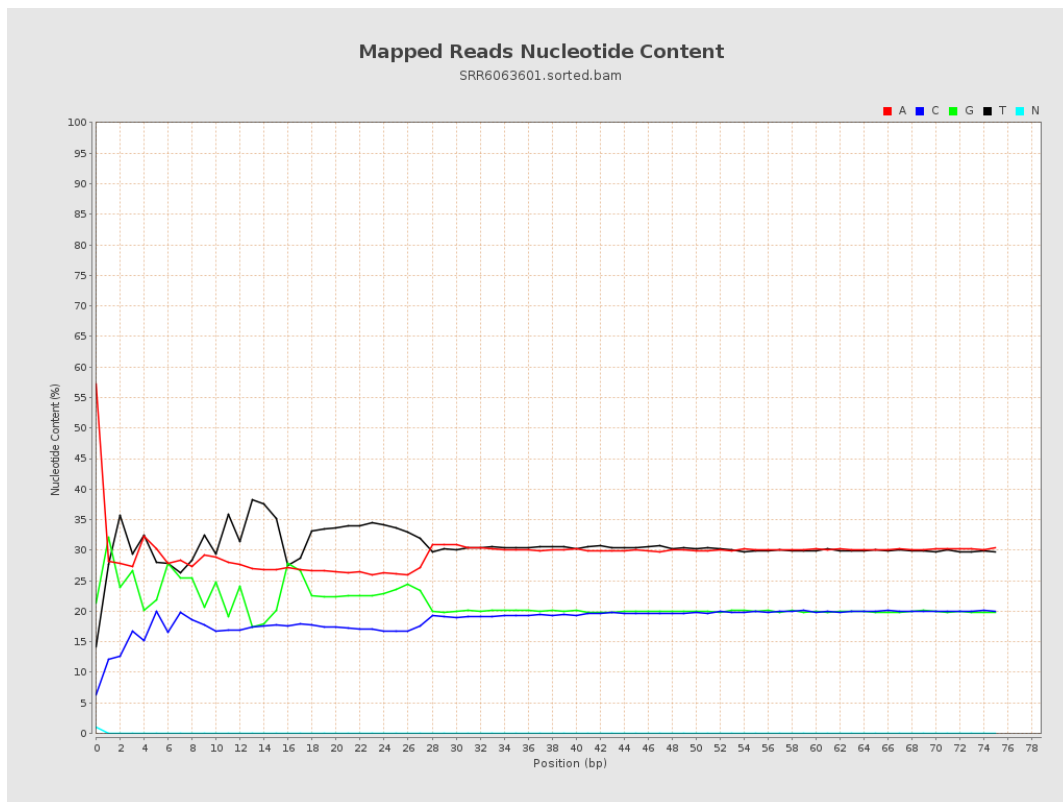
6. Results : Genome Fraction Coverage



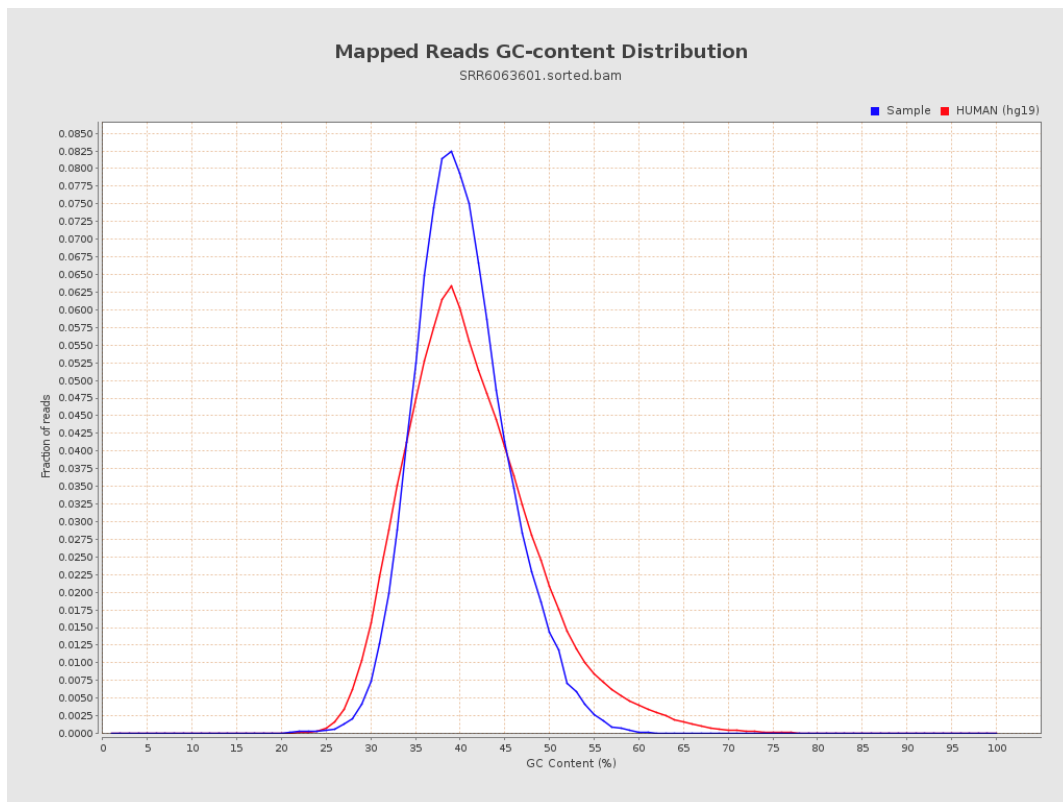
7. Results : Duplication Rate Histogram



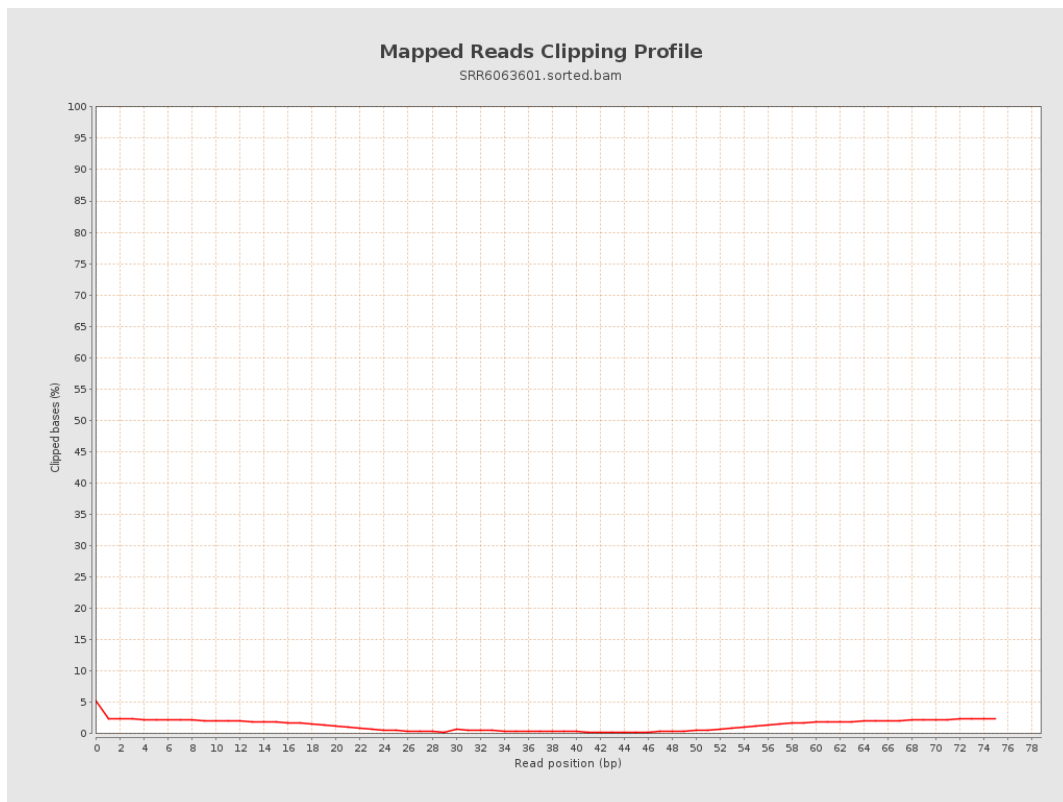
8. Results : Mapped Reads Nucleotide Content



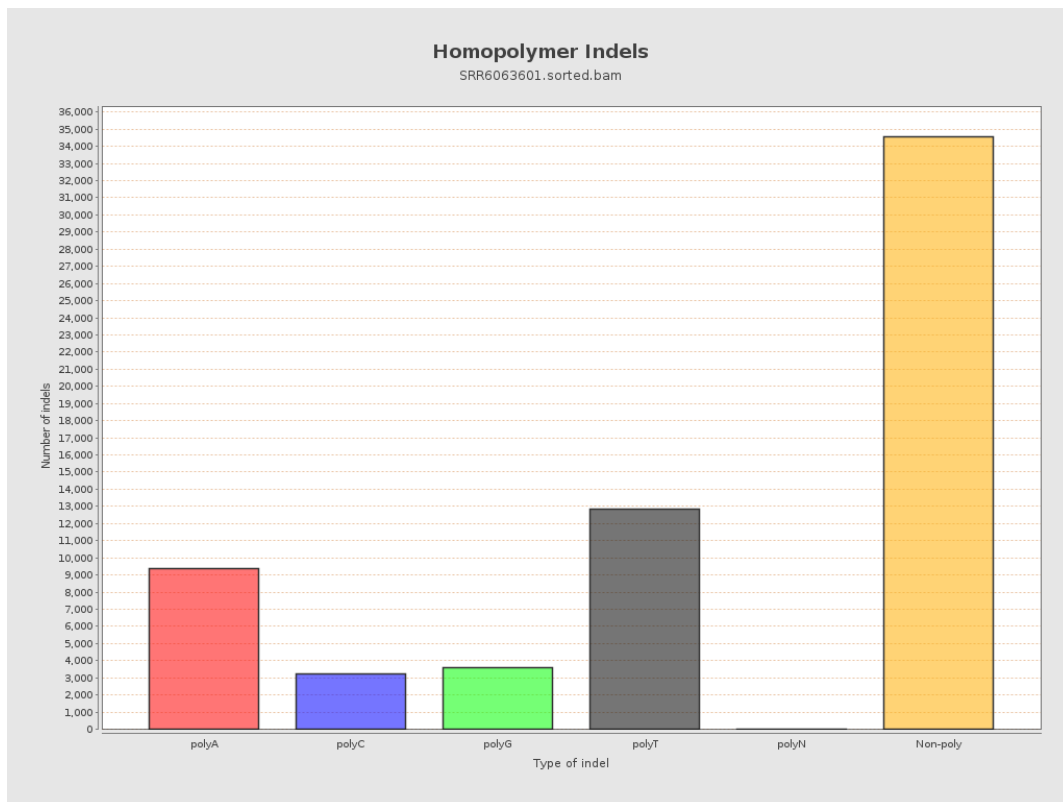
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

