

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 12:55:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068147.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_SRR6068147 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068147.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 12:55:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068147.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,584,358
Mapped reads	4,390,705 / 95.78%
Unmapped reads	193,653 / 4.22%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	31,629 / 0.69%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	511,921 / 11.17%
Duplication rate	9.99%
Clipped reads	1,990,842 / 43.43%

2.2. ACGT Content

Number/percentage of A's	78,144,203 / 26.95%
Number/percentage of C's	52,283,027 / 18.03%
Number/percentage of T's	94,015,063 / 32.43%
Number/percentage of G's	65,430,889 / 22.57%
Number/percentage of N's	34,311 / 0.01%
GC Percentage	40.6%

2.3. Coverage

Mean	0.0937

Standard Deviation	0.8814
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2.4. Mapping Quality

Mean Mapping Quality	46.83
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2.5. Mismatches and indels

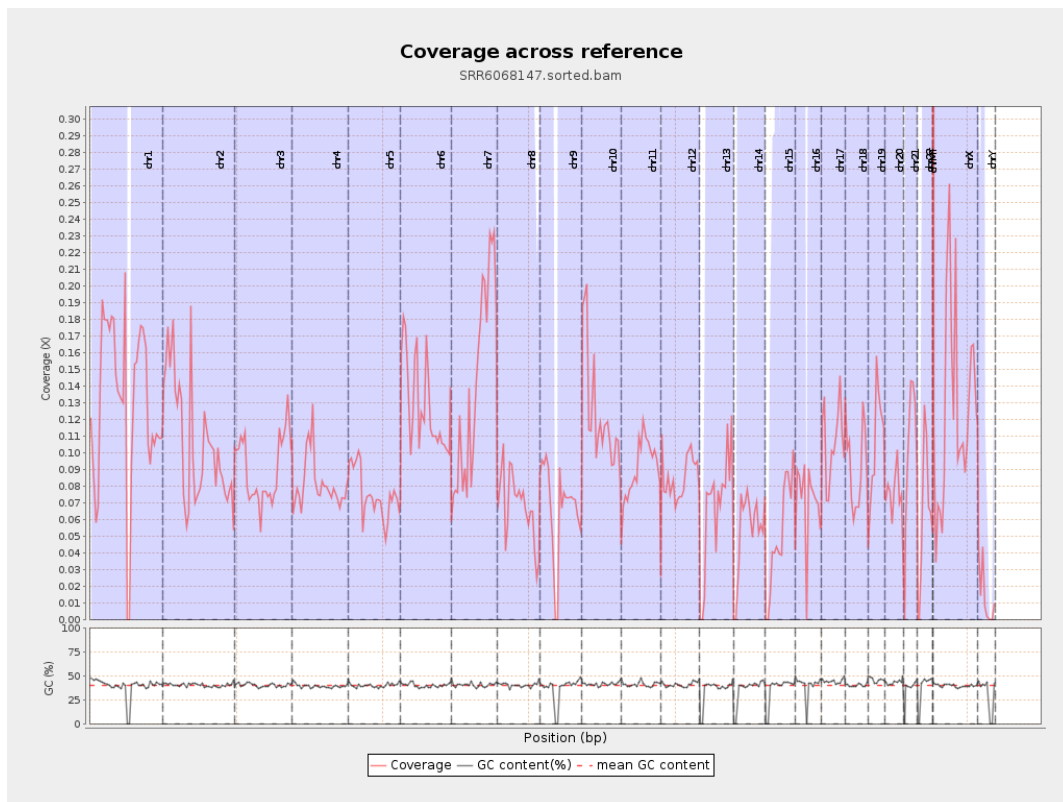
General error rate	0.56%
Mismatches	1,591,156
Insertions	19,047
Mapped reads with at least one insertion	0.43%
Deletions	75,731
Mapped reads with at least one deletion	1.71%
Homopolymer indels	45.62%

2.6. Chromosome stats

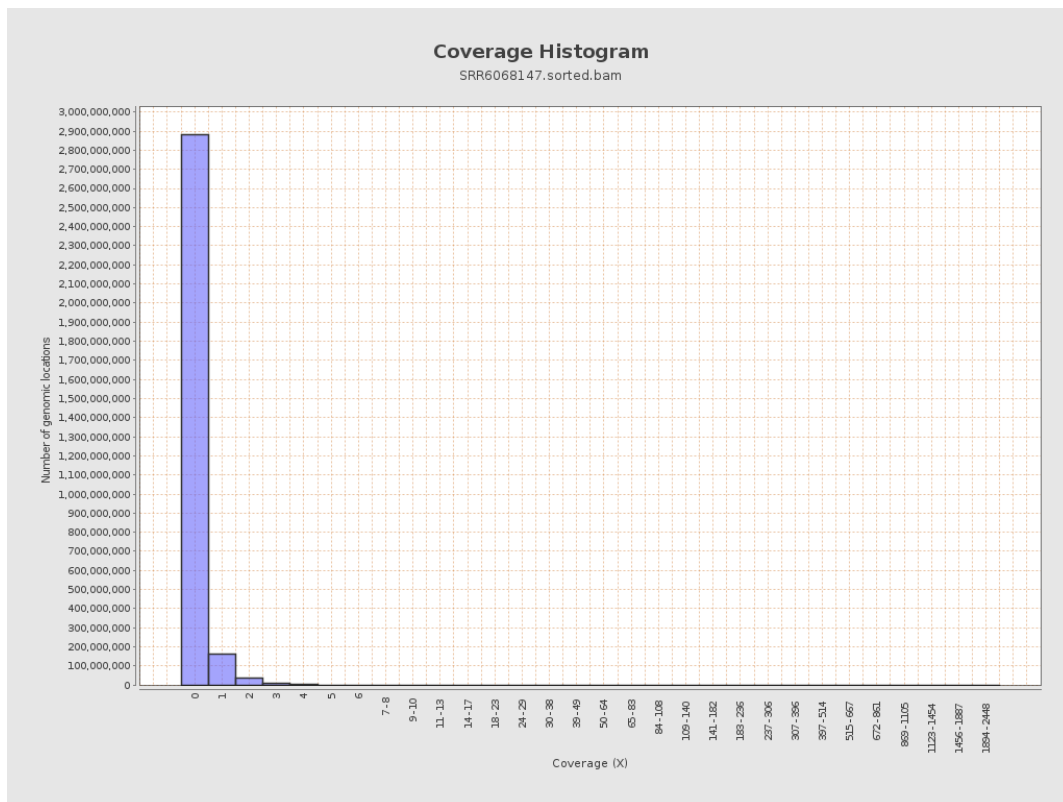
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	32195893	0.1292	2.1057
chr2	243199373	25914179	0.1066	1.0349
chr3	198022430	17856800	0.0902	0.3849
chr4	191154276	15592555	0.0816	0.4037
chr5	180915260	13541743	0.0749	0.3513
chr6	171115067	22071894	0.129	0.5932
chr7	159138663	22395460	0.1407	0.9521

chr8	146364022	9862922	0.0674	1.1249
chr9	141213431	9529430	0.0675	0.6496
chr10	135534747	16838056	0.1242	0.6987
chr11	135006516	12270566	0.0909	0.5411
chr12	133851895	11460918	0.0856	0.4014
chr13	115169878	7817698	0.0679	0.3509
chr14	107349540	5769871	0.0537	0.3521
chr15	102531392	5287437	0.0516	0.3344
chr16	90354753	6312775	0.0699	0.3877
chr17	81195210	8747023	0.1077	0.4571
chr18	78077248	7133171	0.0914	1.2133
chr19	59128983	6288852	0.1064	1.3522
chr20	63025520	4750626	0.0754	0.385
chr21	48129895	4860144	0.101	0.4418
chr22	51304566	3263838	0.0636	0.3165
chrMT	16571	186597	11.2605	6.5388
chrX	155270560	19275418	0.1241	0.5585
chrY	59373566	818698	0.0138	0.409

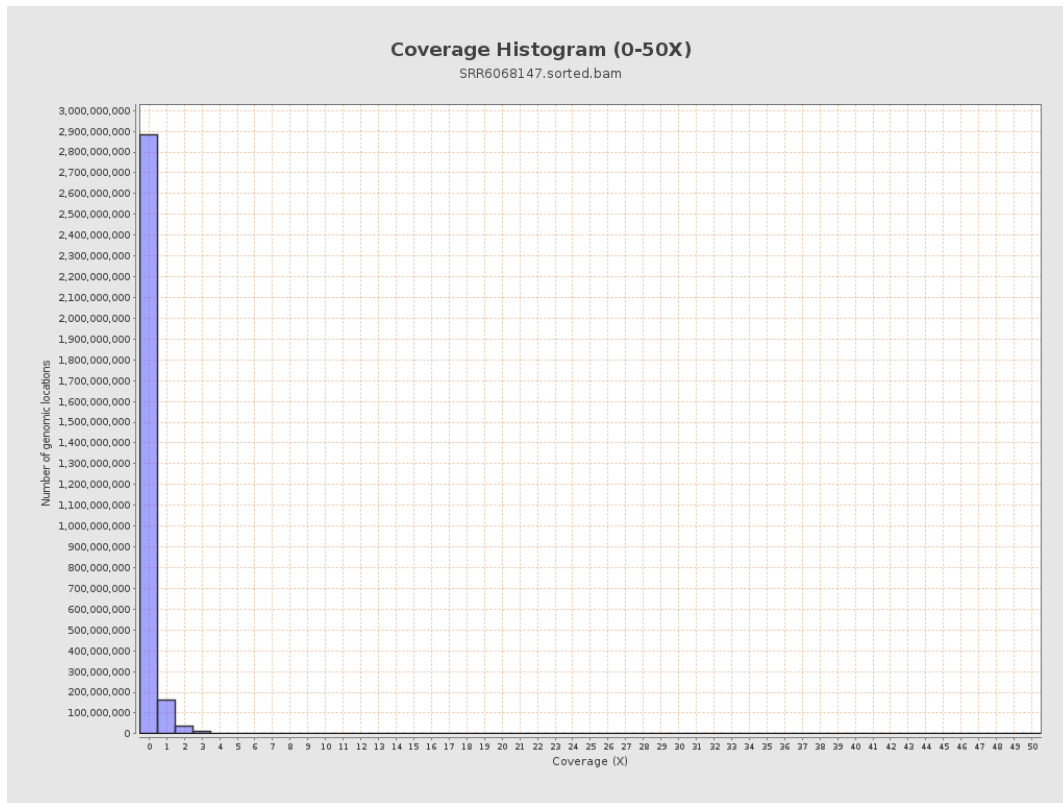
3. Results : Coverage across reference



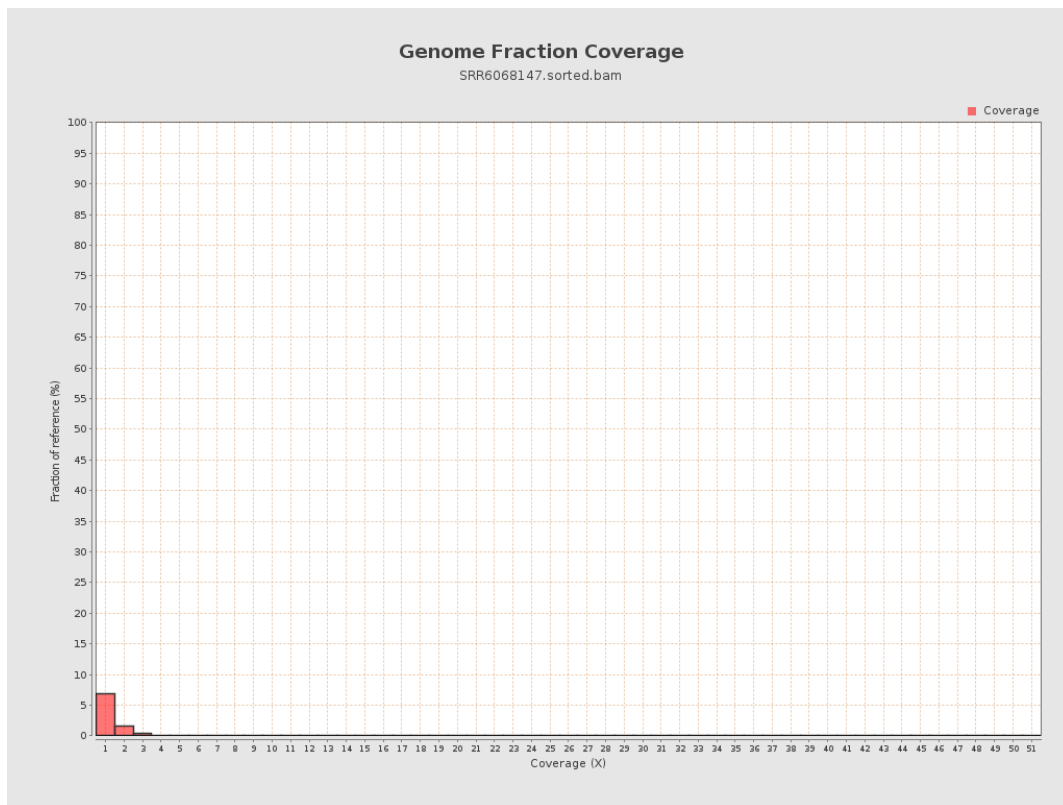
4. Results : Coverage Histogram



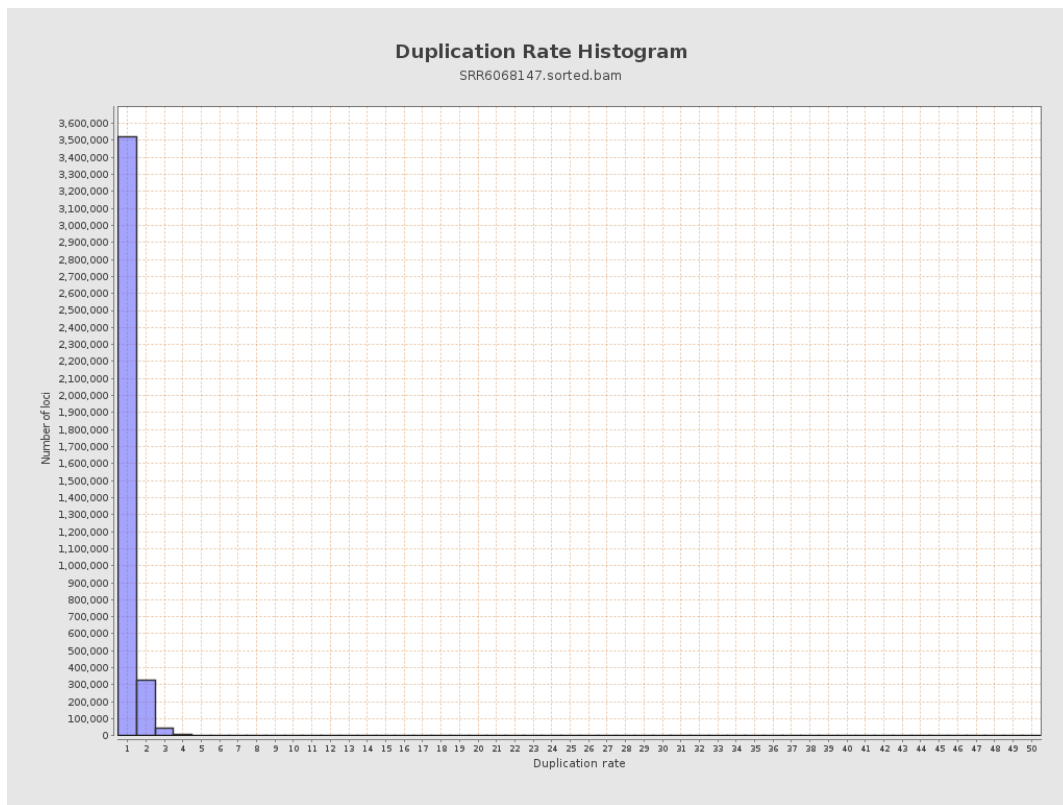
5. Results : Coverage Histogram (0-50X)



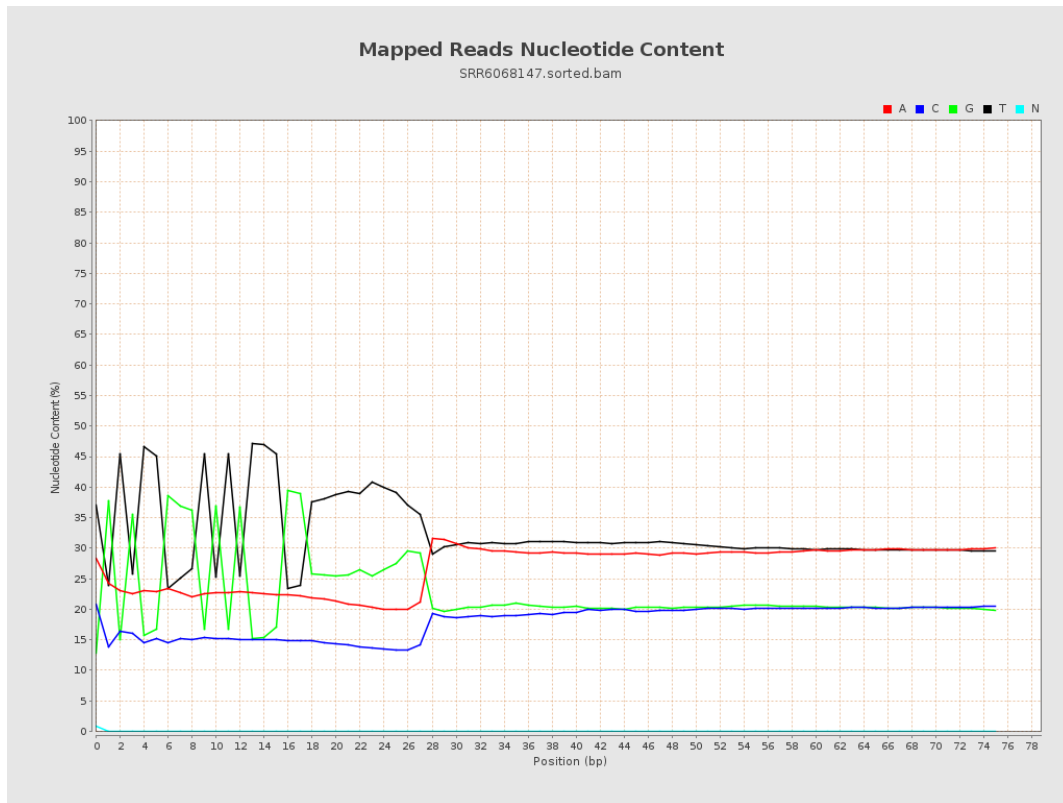
6. Results : Genome Fraction Coverage



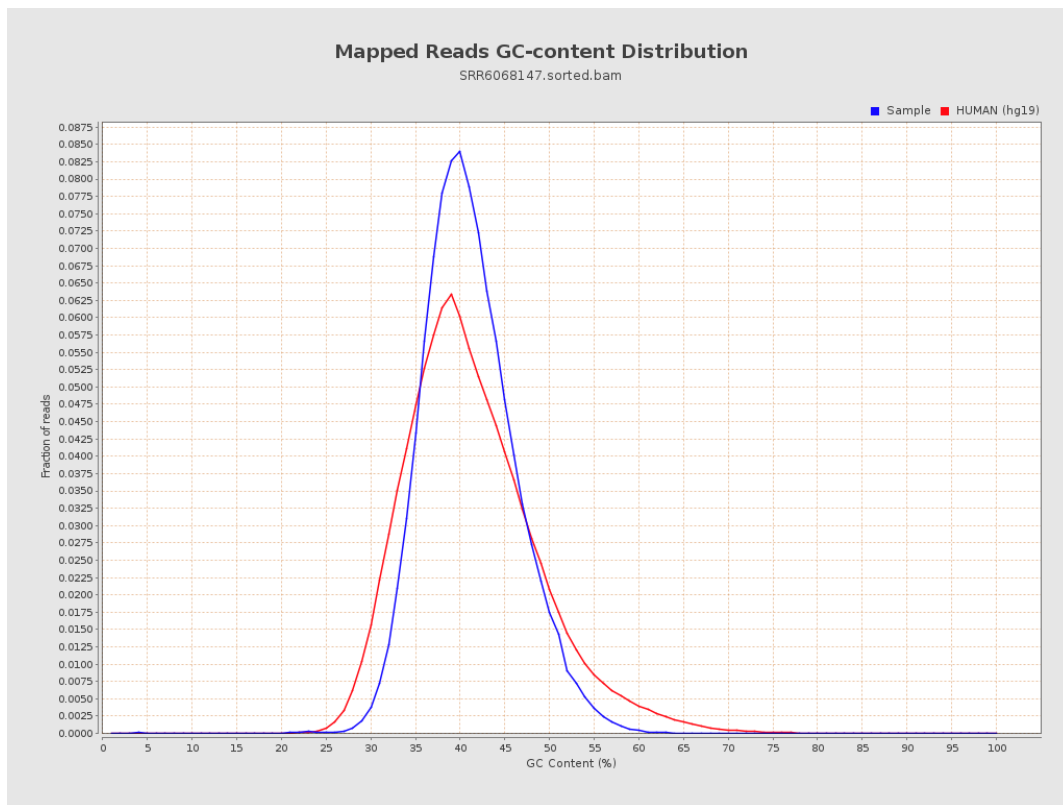
7. Results : Duplication Rate Histogram



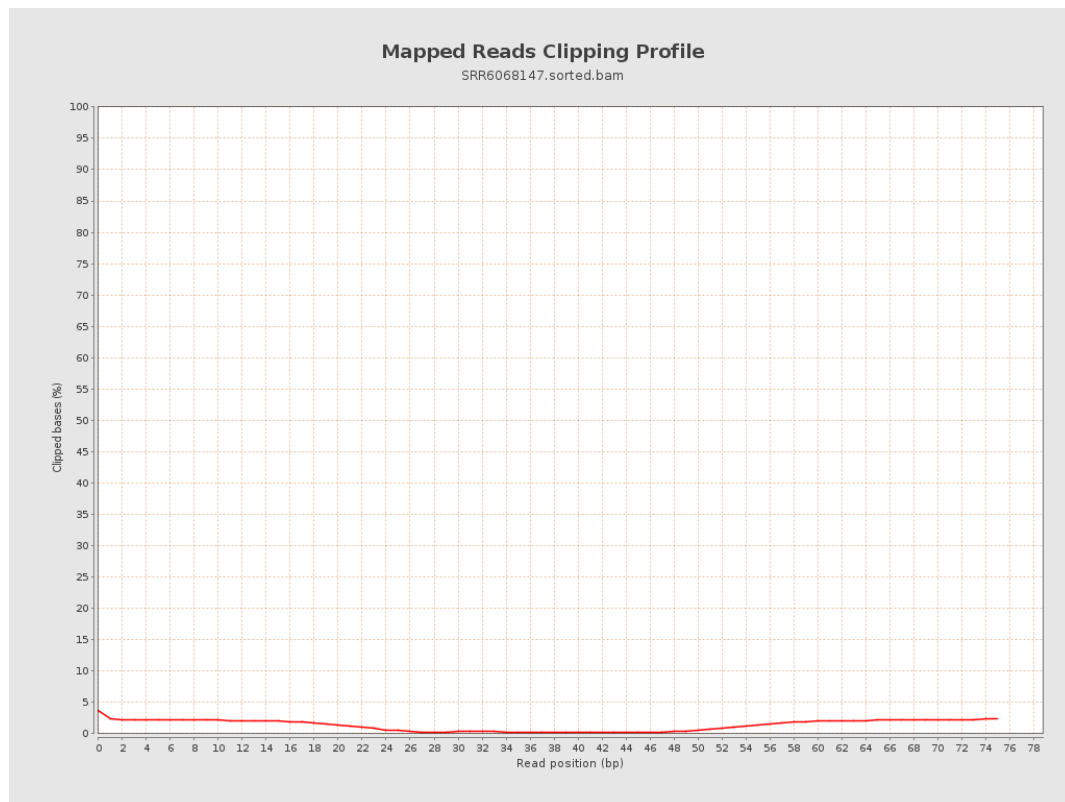
8. Results : Mapped Reads Nucleotide Content



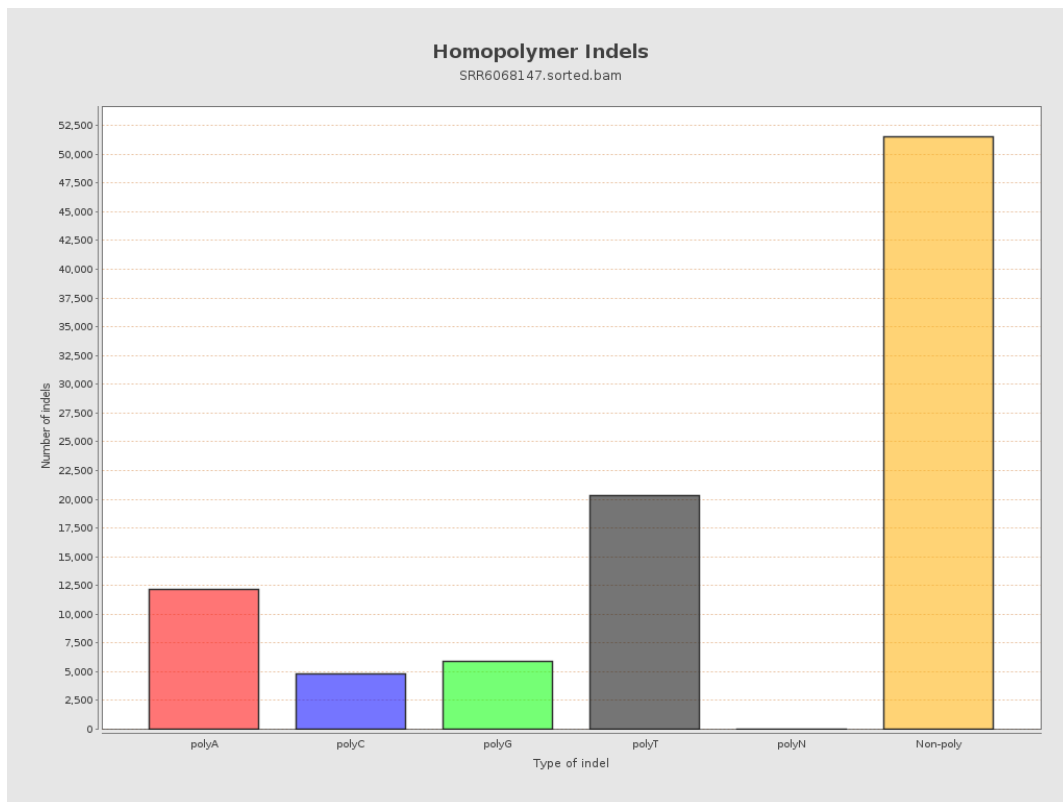
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

