

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 13:24:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068153.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_SRR6068153 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068153.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 13:24:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068153.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,049,545
Mapped reads	3,846,319 / 94.98%
Unmapped reads	203,226 / 5.02%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	39,656 / 0.98%
Read min/max/mean length	30 / 76 / 76.34
Duplicated reads (estimated)	510,583 / 12.61%
Duplication rate	10.86%
Clipped reads	2,125,190 / 52.48%

2.2. ACGT Content

Number/percentage of A's	64,246,847 / 26.08%
Number/percentage of C's	45,069,509 / 18.29%
Number/percentage of T's	79,196,329 / 32.14%
Number/percentage of G's	57,844,000 / 23.48%
Number/percentage of N's	28,901 / 0.01%
GC Percentage	41.77%

2.3. Coverage

Mean	0.0796

Standard Deviation	0.8107
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2.4. Mapping Quality

Mean Mapping Quality	44.65
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2.5. Mismatches and indels

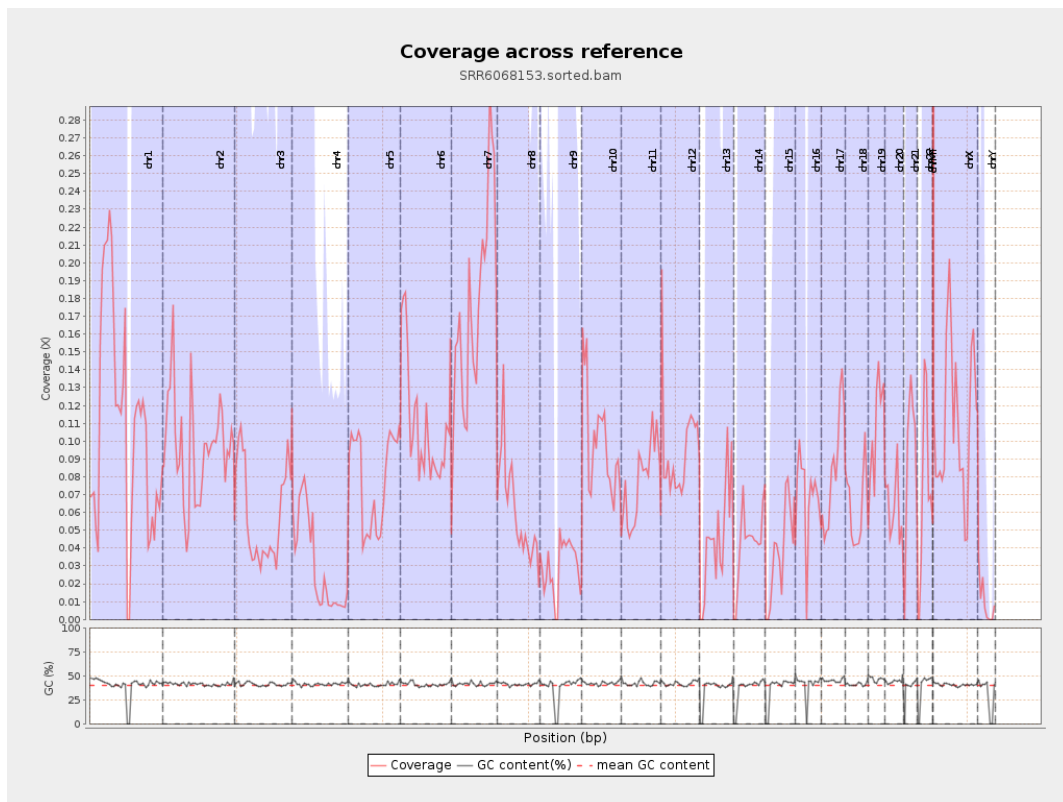
General error rate	0.56%
Mismatches	1,355,955
Insertions	14,990
Mapped reads with at least one insertion	0.39%
Deletions	56,690
Mapped reads with at least one deletion	1.46%
Homopolymer indels	43.83%

2.6. Chromosome stats

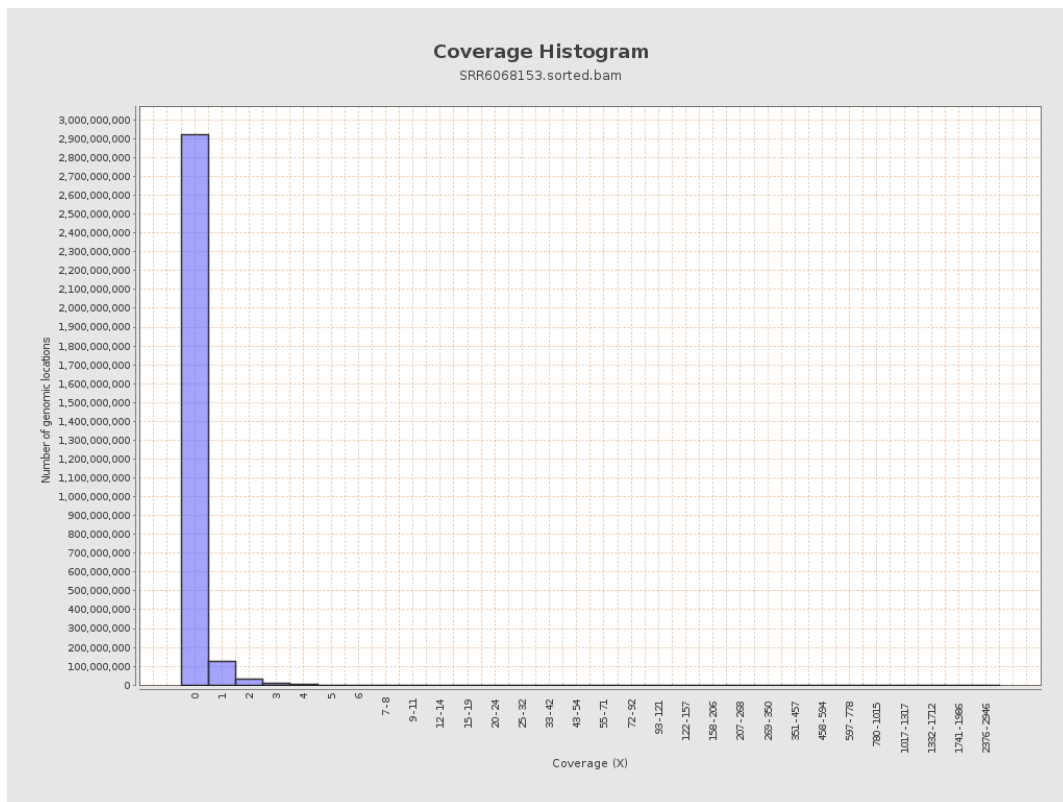
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	26711969	0.1072	1.6286
chr2	243199373	23628332	0.0972	1.3938
chr3	198022430	11719605	0.0592	0.3269
chr4	191154276	5794998	0.0303	0.2667
chr5	180915260	14313758	0.0791	0.3801
chr6	171115067	18716767	0.1094	0.5725
chr7	159138663	27925119	0.1755	1.3833

chr8	146364022	8723241	0.0596	0.8045
chr9	141213431	4198368	0.0297	0.3675
chr10	135534747	13577816	0.1002	0.5285
chr11	135006516	10517932	0.0779	0.4532
chr12	133851895	12779219	0.0955	0.4191
chr13	115169878	5338841	0.0464	0.3345
chr14	107349540	4578959	0.0427	0.2922
chr15	102531392	3757522	0.0366	0.2781
chr16	90354753	6140132	0.068	0.3631
chr17	81195210	6872498	0.0846	0.4098
chr18	78077248	4946874	0.0634	0.7919
chr19	59128983	6332815	0.1071	1.1252
chr20	63025520	3855103	0.0612	0.3544
chr21	48129895	4182802	0.0869	0.4002
chr22	51304566	3639704	0.0709	0.3541
chrMT	16571	555075	33.4968	20.0271
chrX	155270560	17109293	0.1102	0.5298
chrY	59373566	566131	0.0095	0.2147

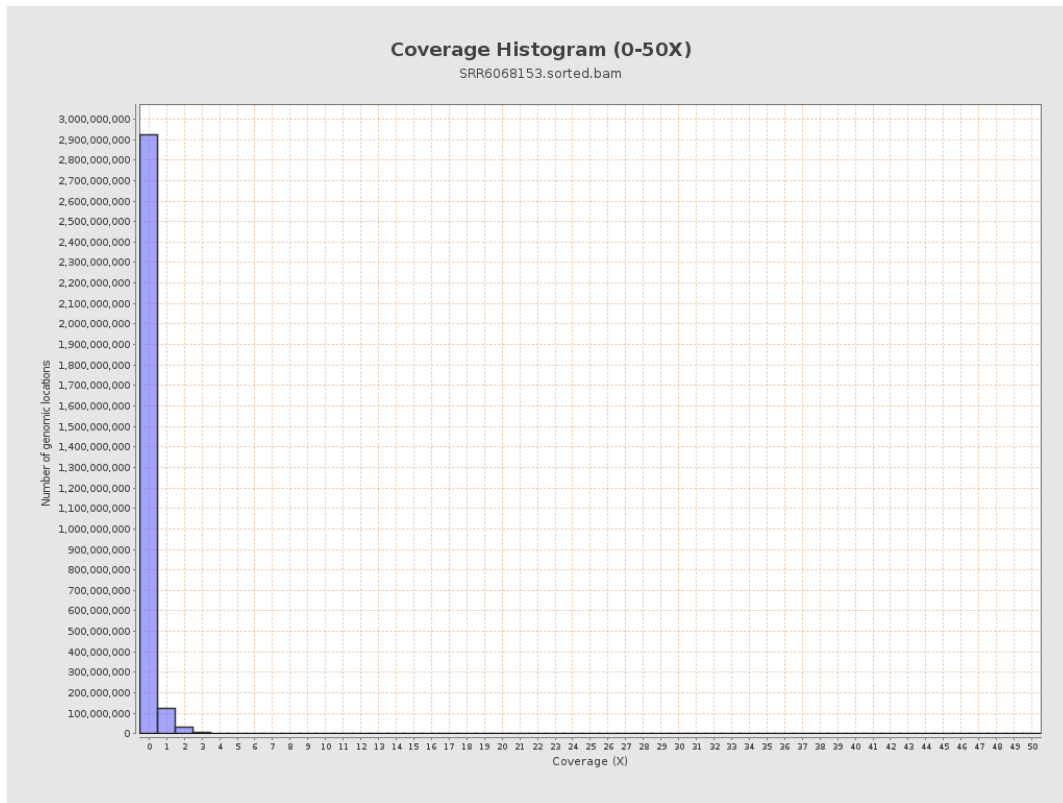
3. Results : Coverage across reference



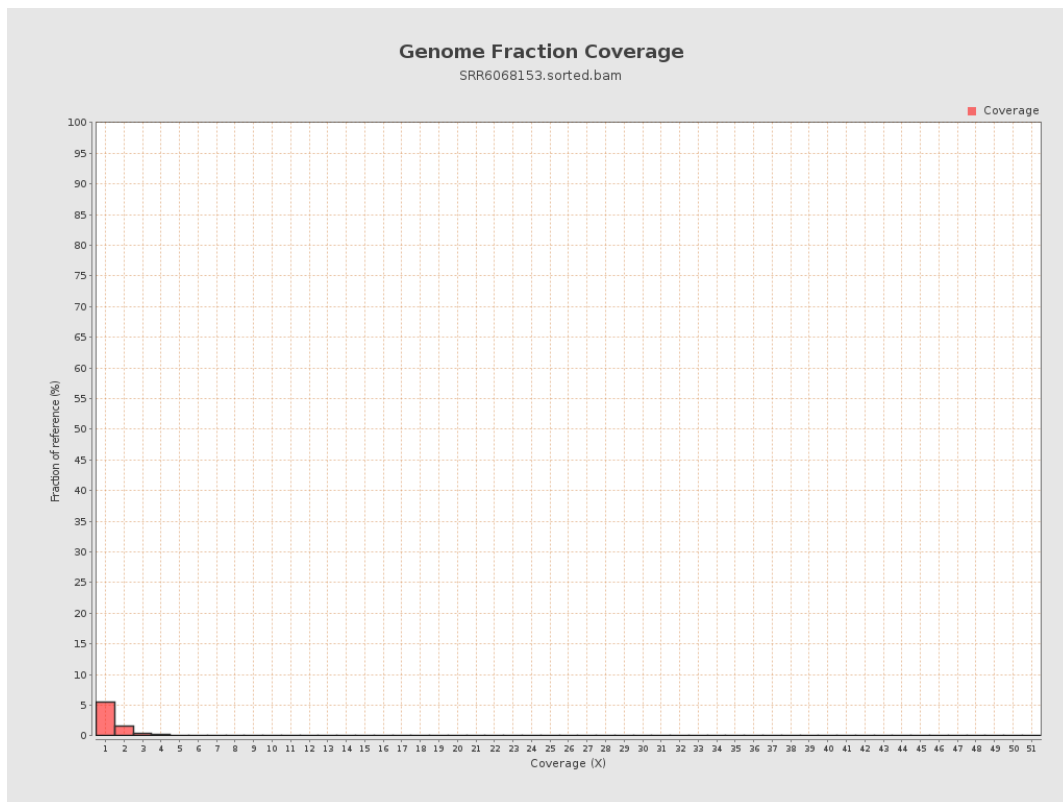
4. Results : Coverage Histogram



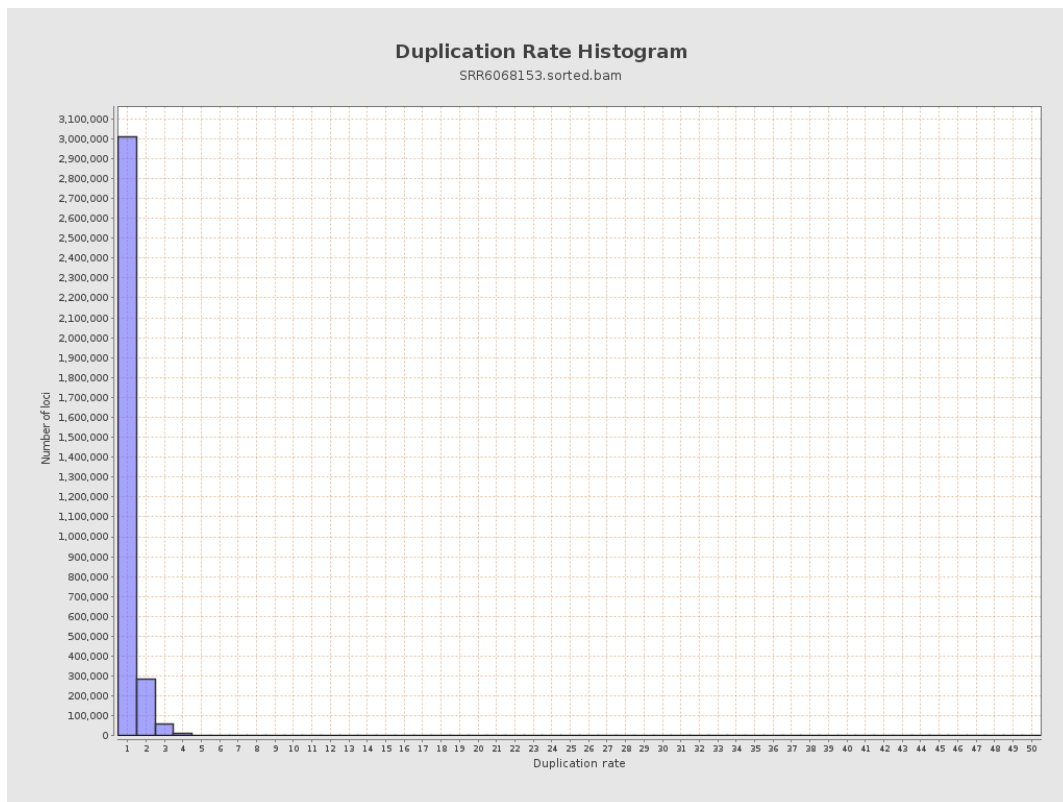
5. Results : Coverage Histogram (0-50X)



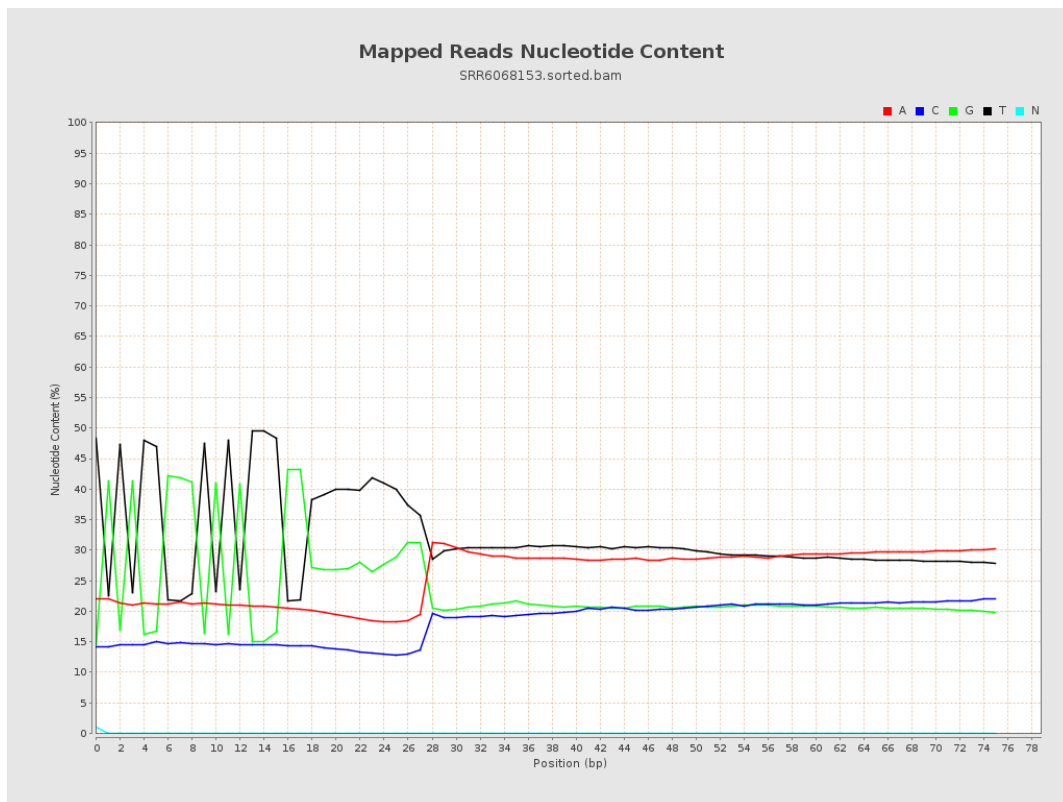
6. Results : Genome Fraction Coverage



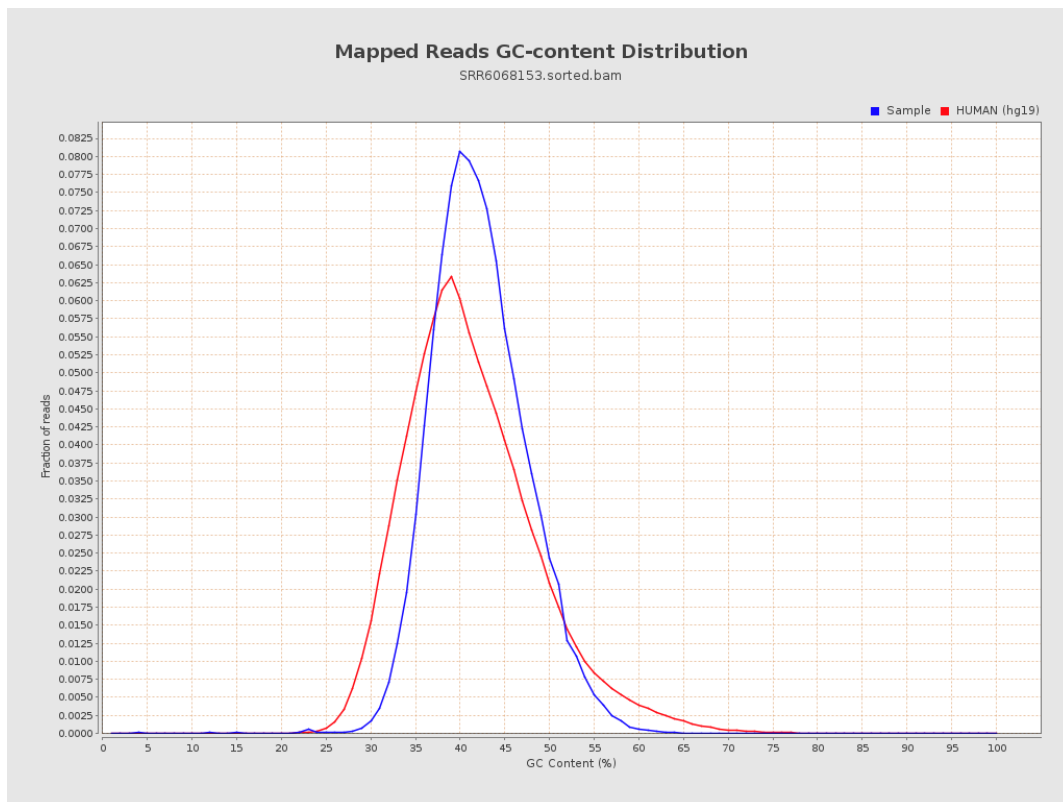
7. Results : Duplication Rate Histogram



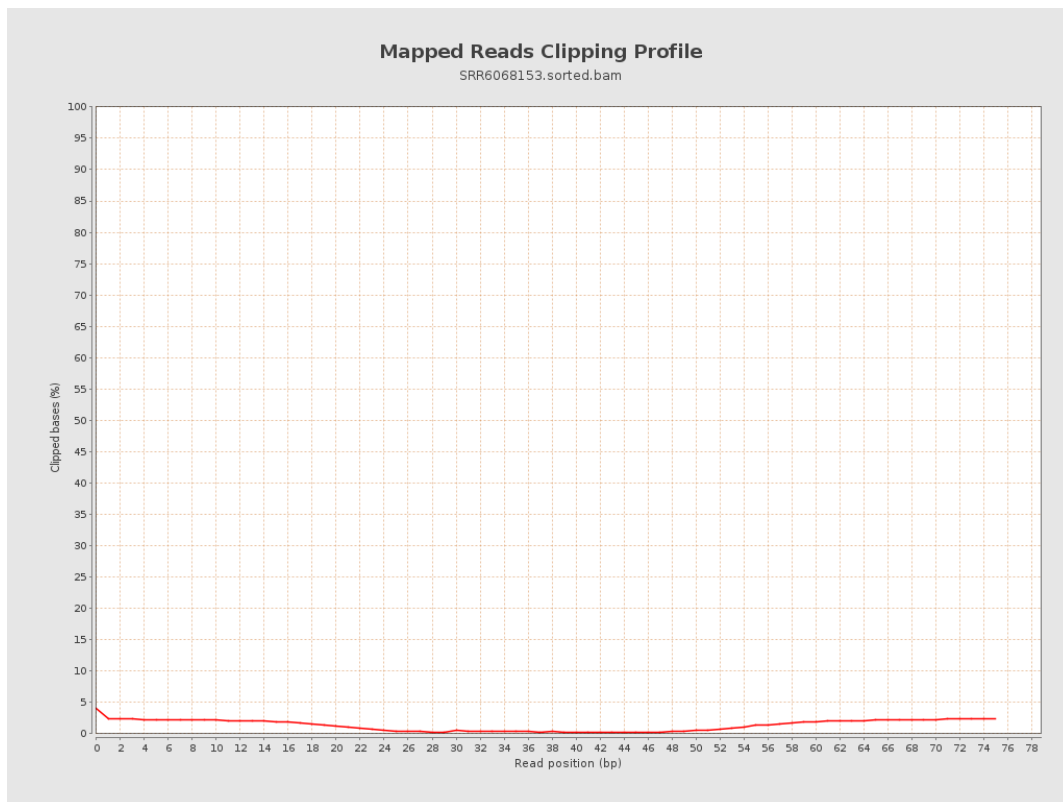
8. Results : Mapped Reads Nucleotide Content



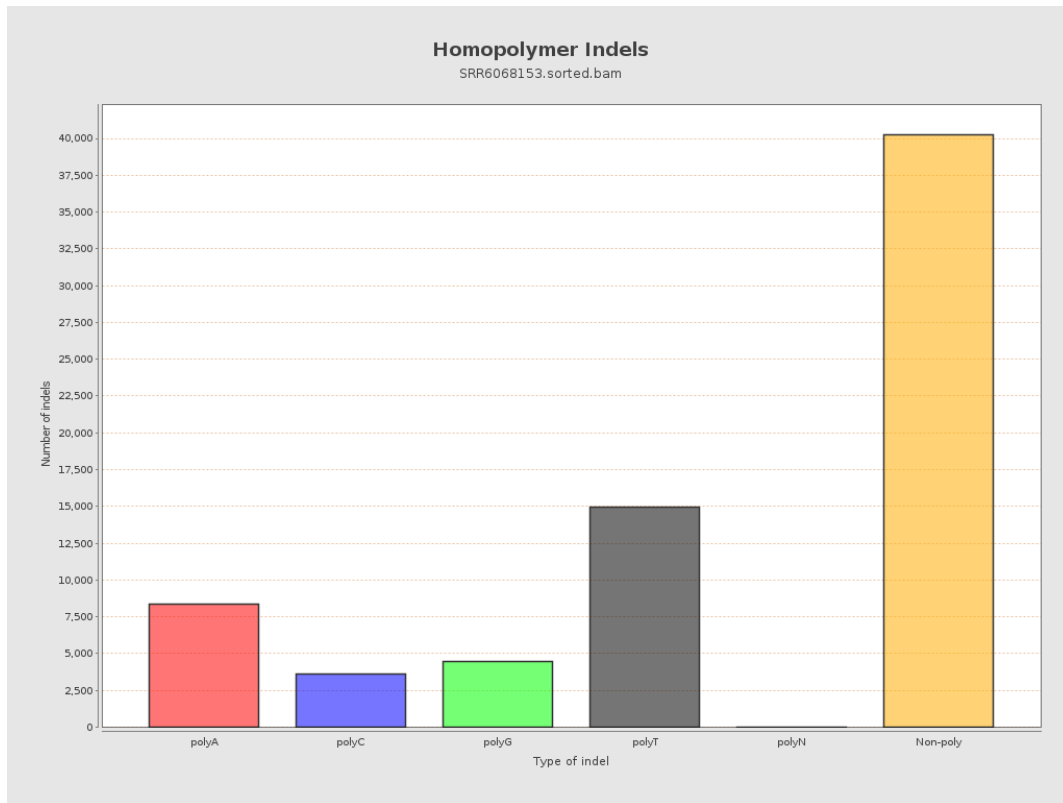
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

