

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 13:39:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068156.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_SRR6068156 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068156.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 13:39:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068156.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,451,888
Mapped reads	4,199,419 / 94.33%
Unmapped reads	252,469 / 5.67%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	43,083 / 0.97%
Read min/max/mean length	30 / 76 / 76.34
Duplicated reads (estimated)	542,374 / 12.18%
Duplication rate	10.8%
Clipped reads	2,351,747 / 52.83%

2.2. ACGT Content

Number/percentage of A's	70,939,901 / 26.48%
Number/percentage of C's	48,073,386 / 17.94%
Number/percentage of T's	87,283,879 / 32.58%
Number/percentage of G's	61,594,110 / 22.99%
Number/percentage of N's	30,365 / 0.01%
GC Percentage	40.93%

2.3. Coverage

Mean	0.0866

Standard Deviation	0.9292
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2.4. Mapping Quality

Mean Mapping Quality	45.41
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2.5. Mismatches and indels

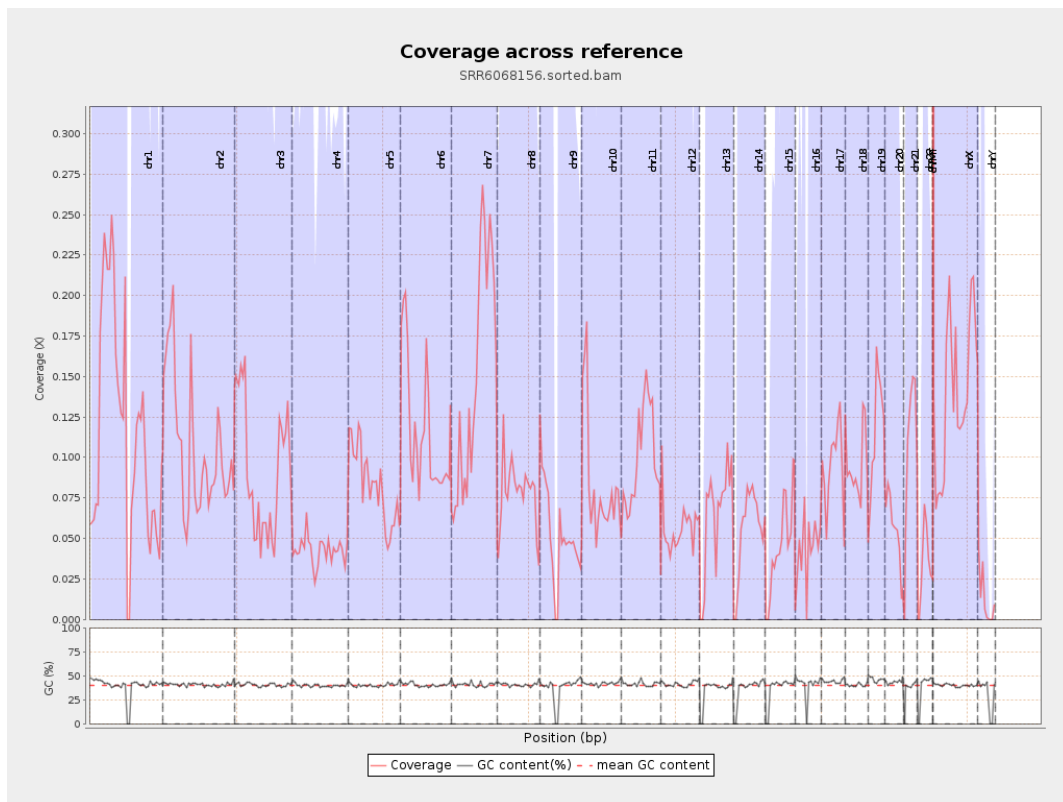
General error rate	0.57%
Mismatches	1,505,010
Insertions	16,716
Mapped reads with at least one insertion	0.4%
Deletions	66,549
Mapped reads with at least one deletion	1.57%
Homopolymer indels	43.88%

2.6. Chromosome stats

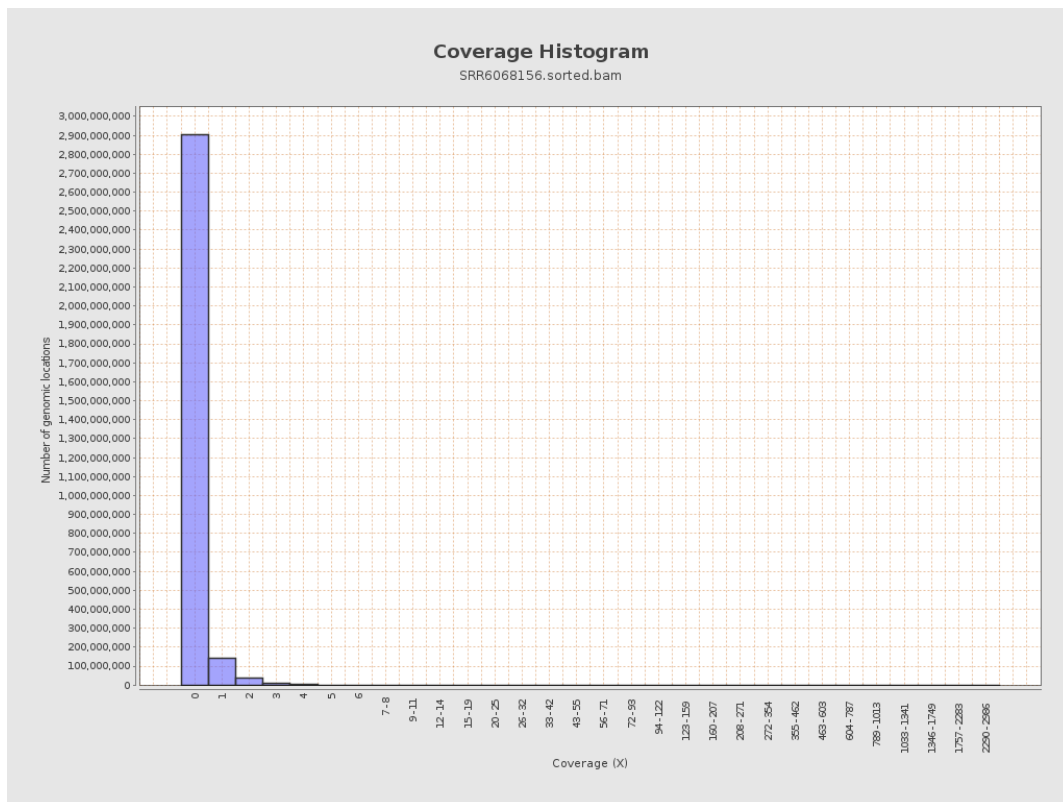
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	29084812	0.1167	2.3305
chr2	243199373	25926768	0.1066	1.392
chr3	198022430	18170732	0.0918	0.4014
chr4	191154276	8190975	0.0429	0.3004
chr5	180915260	14824402	0.0819	0.3837
chr6	171115067	19811592	0.1158	0.5995
chr7	159138663	23903723	0.1502	0.9321

chr8	146364022	11443005	0.0782	0.8308
chr9	141213431	7142029	0.0506	0.4869
chr10	135534747	11445843	0.0844	0.4854
chr11	135006516	13479877	0.0998	0.5226
chr12	133851895	7570172	0.0566	0.333
chr13	115169878	7406963	0.0643	0.3837
chr14	107349540	5967750	0.0556	0.3518
chr15	102531392	4665214	0.0455	0.3193
chr16	90354753	3861812	0.0427	0.3147
chr17	81195210	7802682	0.0961	0.4384
chr18	78077248	7444736	0.0954	0.9667
chr19	59128983	6941361	0.1174	1.4762
chr20	63025520	3470094	0.0551	0.33
chr21	48129895	5155200	0.1071	0.4457
chr22	51304566	1727350	0.0337	0.2342
chrMT	16571	279098	16.8426	10.5461
chrX	155270560	21574716	0.1389	0.5758
chrY	59373566	745493	0.0126	0.3341

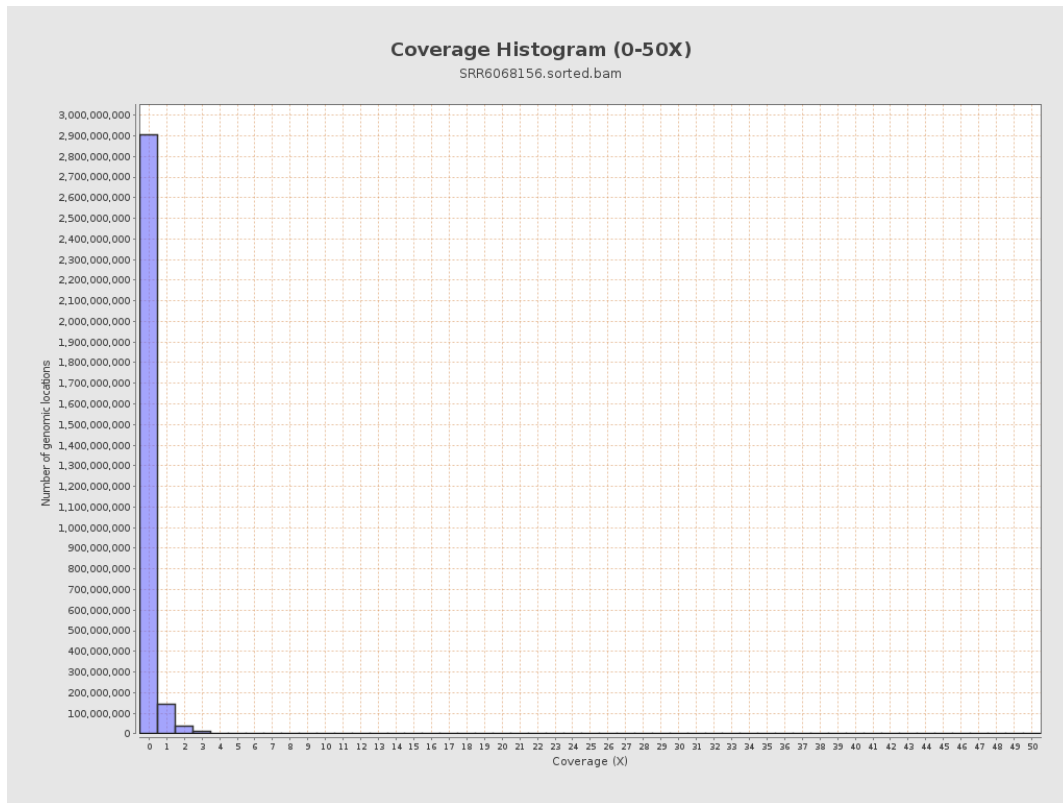
3. Results : Coverage across reference



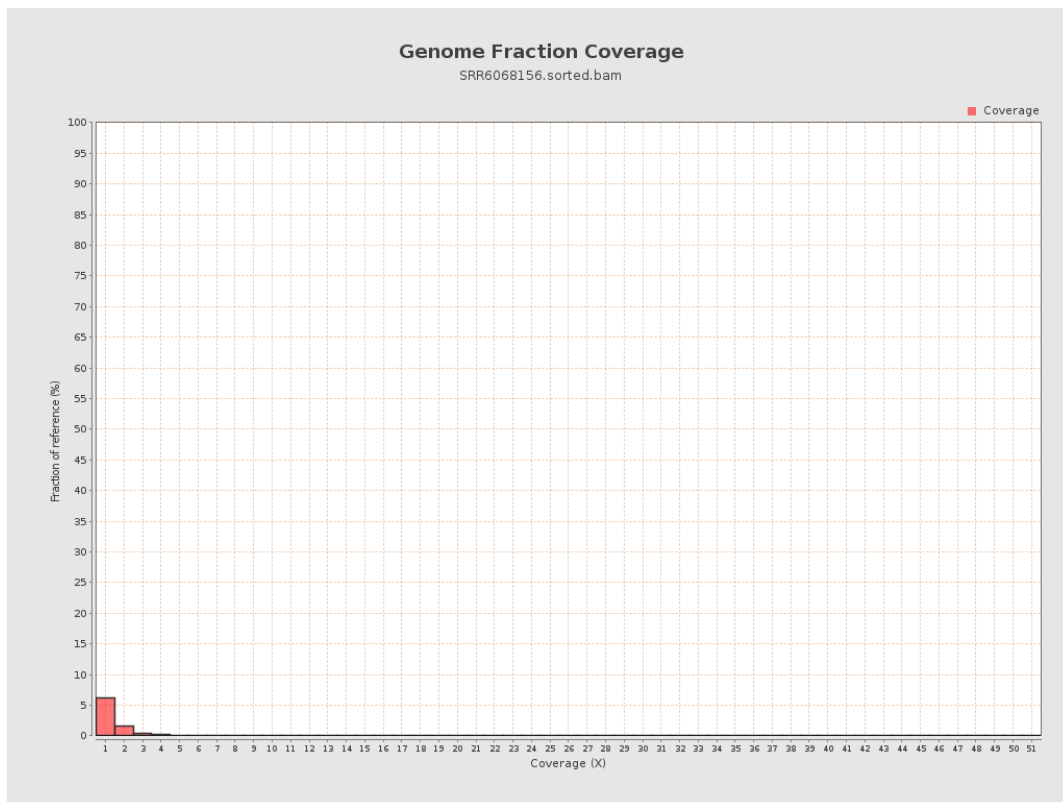
4. Results : Coverage Histogram



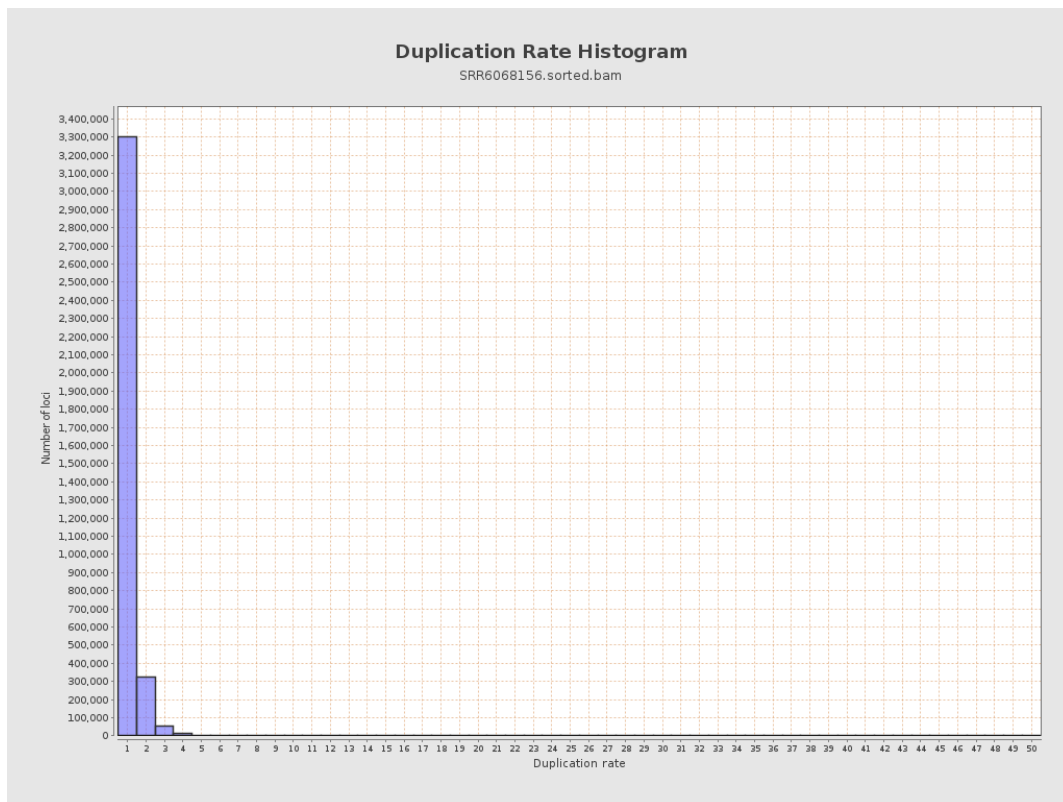
5. Results : Coverage Histogram (0-50X)



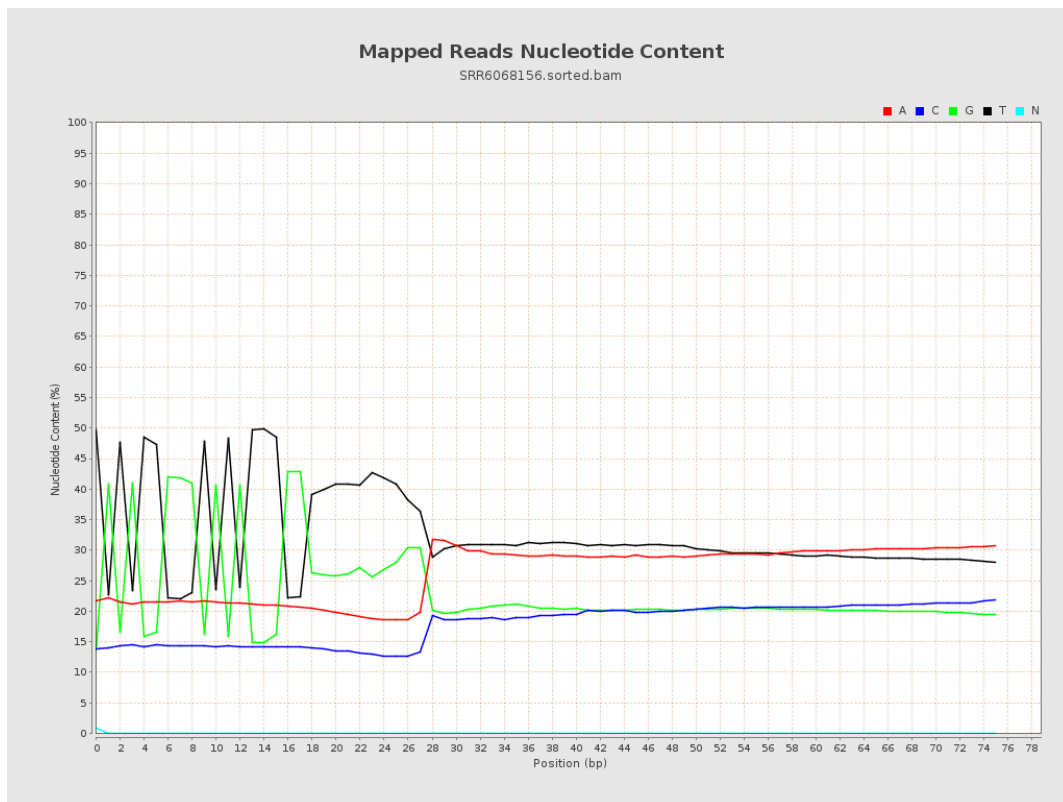
6. Results : Genome Fraction Coverage



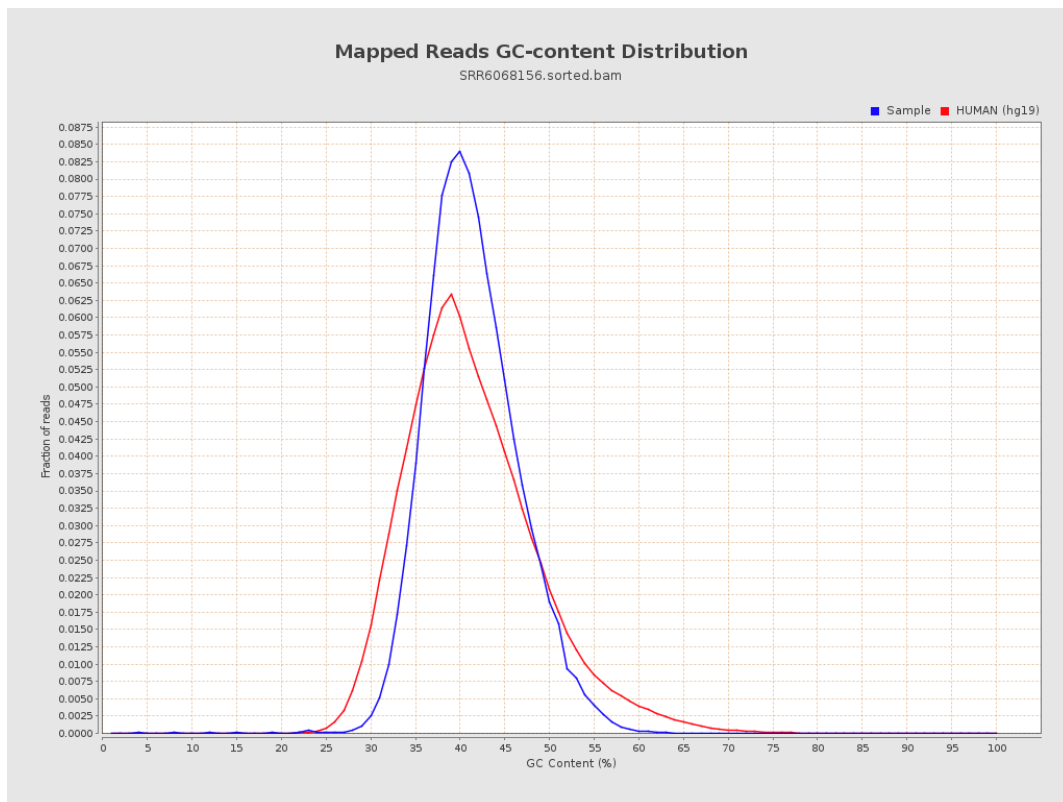
7. Results : Duplication Rate Histogram



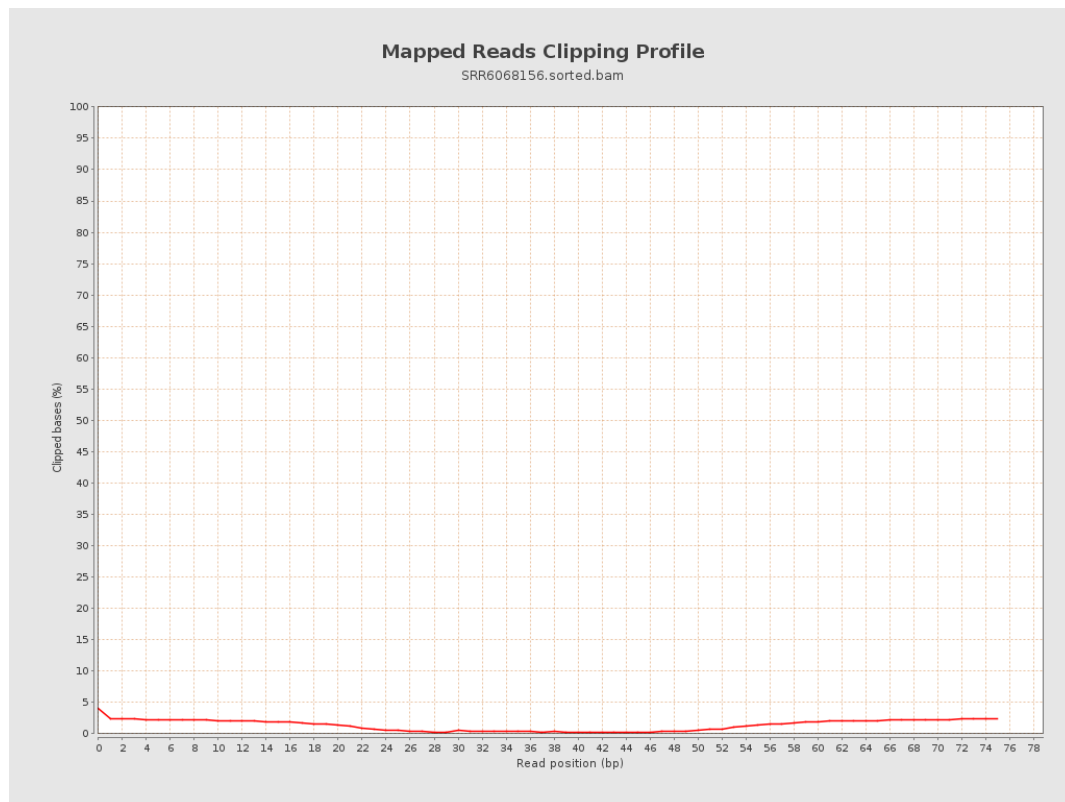
8. Results : Mapped Reads Nucleotide Content



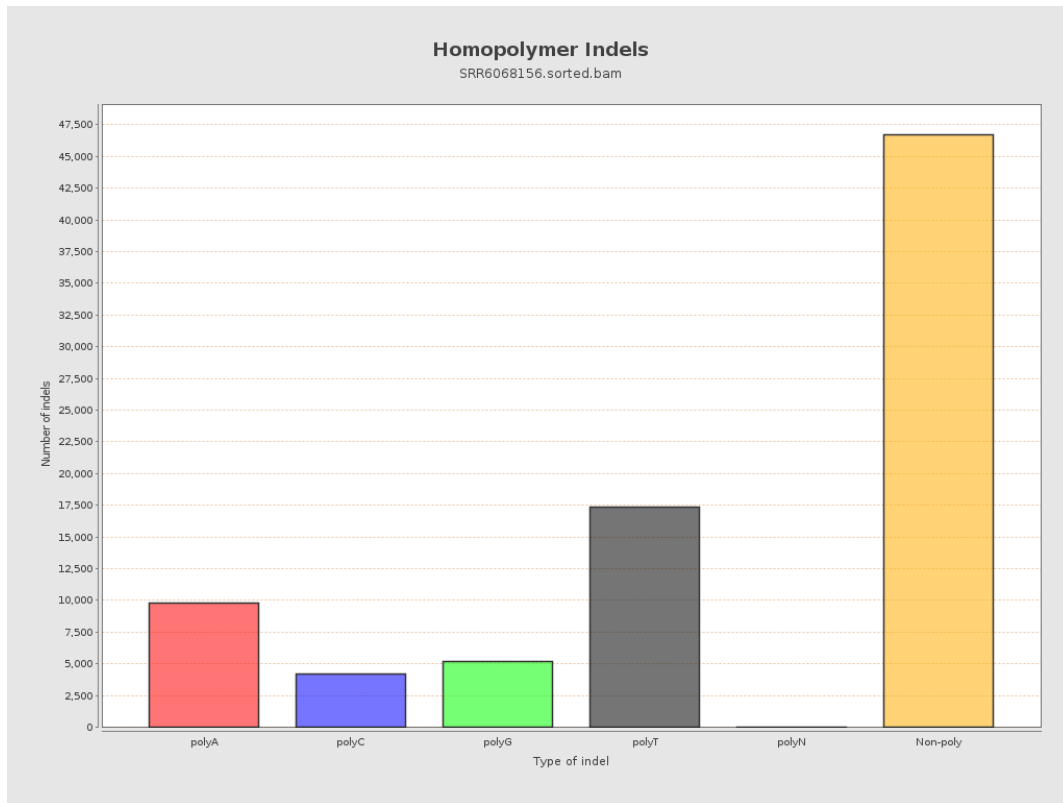
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

