

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 17:16:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068956.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_SRR6068956 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068956.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 17:16:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068956.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,360,808
Mapped reads	1,990,263 / 84.3%
Unmapped reads	370,545 / 15.7%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,318 / 0.48%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	81,036 / 3.43%
Duplication rate	3.17%
Clipped reads	1,038,325 / 43.98%

2.2. ACGT Content

Number/percentage of A's	34,674,329 / 26.88%
Number/percentage of C's	22,045,569 / 17.09%
Number/percentage of T's	42,770,991 / 33.16%
Number/percentage of G's	29,181,342 / 22.62%
Number/percentage of N's	311,162 / 0.24%
GC Percentage	39.72%

2.3. Coverage

Mean	0.0417

Standard Deviation	0.3734
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2.4. Mapping Quality

Mean Mapping Quality	46.31
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2.5. Mismatches and indels

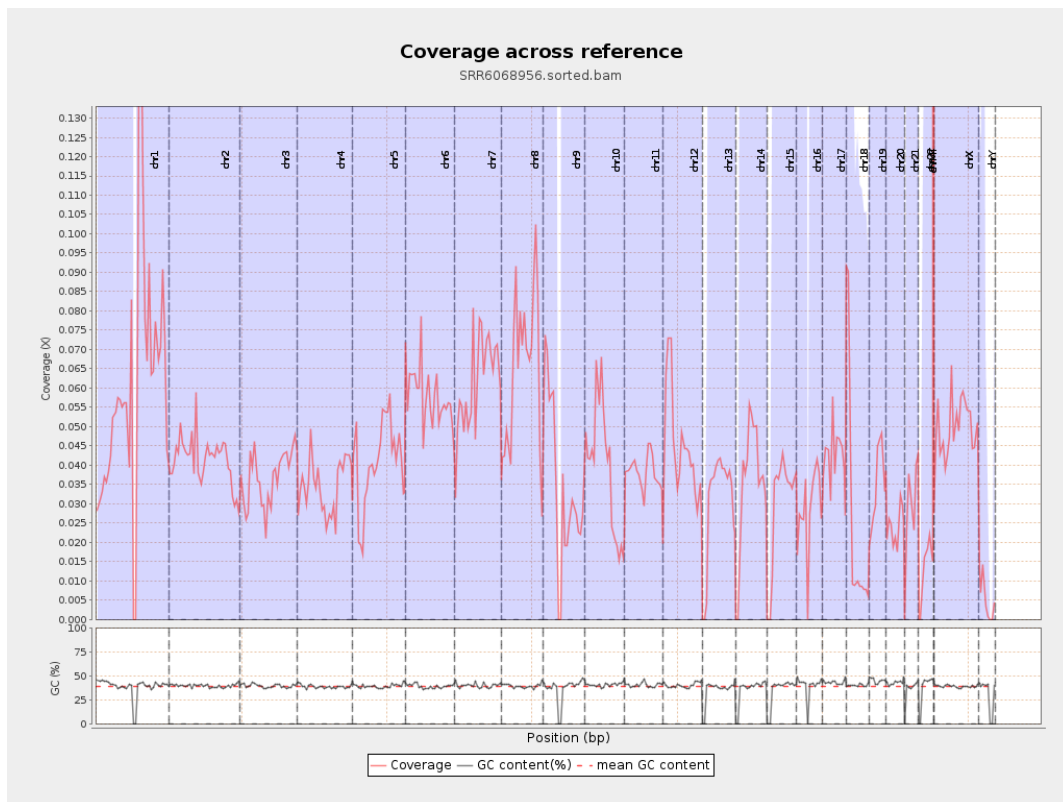
General error rate	0.95%
Mismatches	1,206,349
Insertions	11,071
Mapped reads with at least one insertion	0.55%
Deletions	36,518
Mapped reads with at least one deletion	1.82%
Homopolymer indels	48.79%

2.6. Chromosome stats

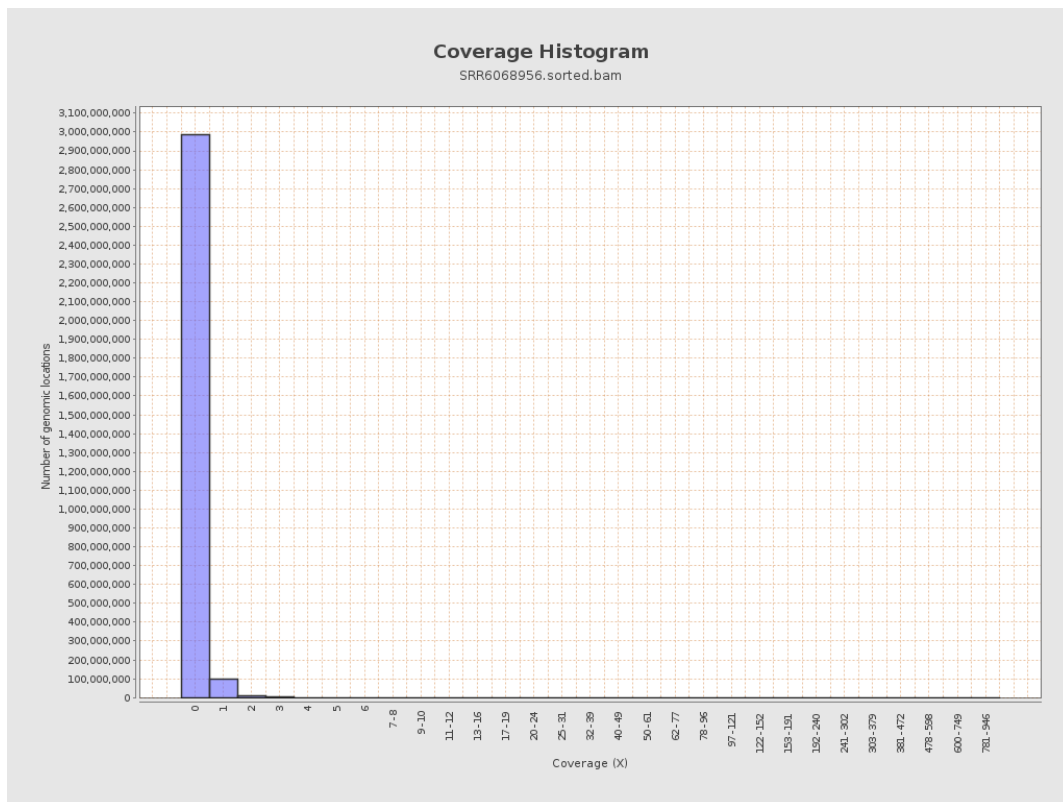
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	15023046	0.0603	0.7126
chr2	243199373	10106658	0.0416	0.3119
chr3	198022430	7266333	0.0367	0.2164
chr4	191154276	6605708	0.0346	0.2251
chr5	180915260	7327955	0.0405	0.2242
chr6	171115067	9882809	0.0578	0.35
chr7	159138663	9886204	0.0621	0.5728

chr8	146364022	9543237	0.0652	0.6655
chr9	141213431	4799046	0.034	0.2788
chr10	135534747	5400968	0.0398	0.3335
chr11	135006516	5110385	0.0379	0.2945
chr12	133851895	5944968	0.0444	0.2373
chr13	115169878	3493678	0.0303	0.1922
chr14	107349540	3815703	0.0355	0.2183
chr15	102531392	3064822	0.0299	0.1914
chr16	90354753	2593940	0.0287	0.2058
chr17	81195210	3428719	0.0422	0.2479
chr18	78077248	1871055	0.024	0.4332
chr19	59128983	2085118	0.0353	0.4533
chr20	63025520	1518808	0.0241	0.1838
chr21	48129895	1422532	0.0296	0.2009
chr22	51304566	665944	0.013	0.1286
chrMT	16571	211589	12.7686	6.3482
chrX	155270560	7675195	0.0494	0.2755
chrY	59373566	297990	0.005	0.1138

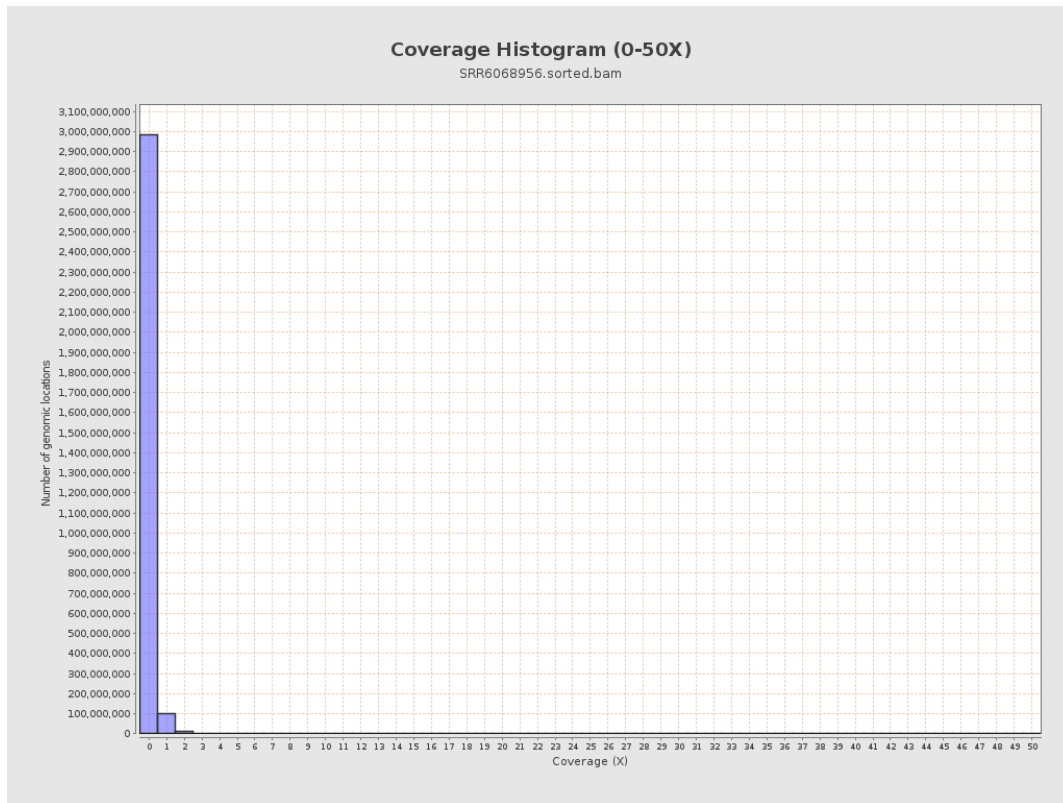
3. Results : Coverage across reference



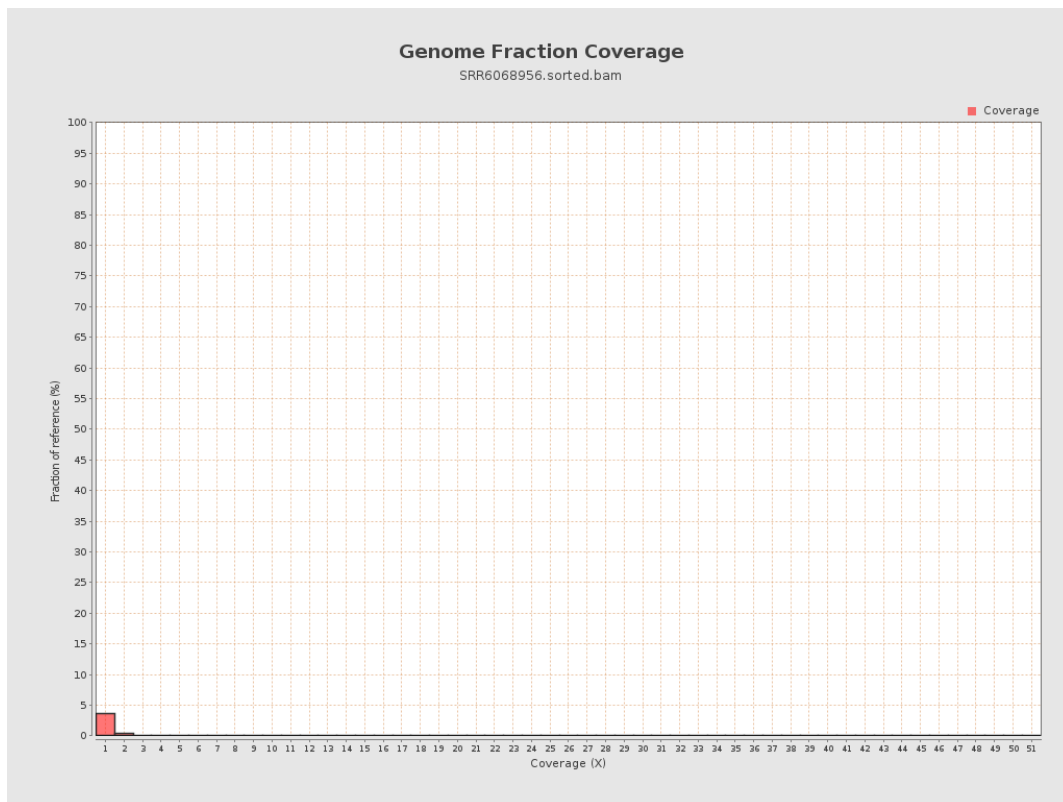
4. Results : Coverage Histogram



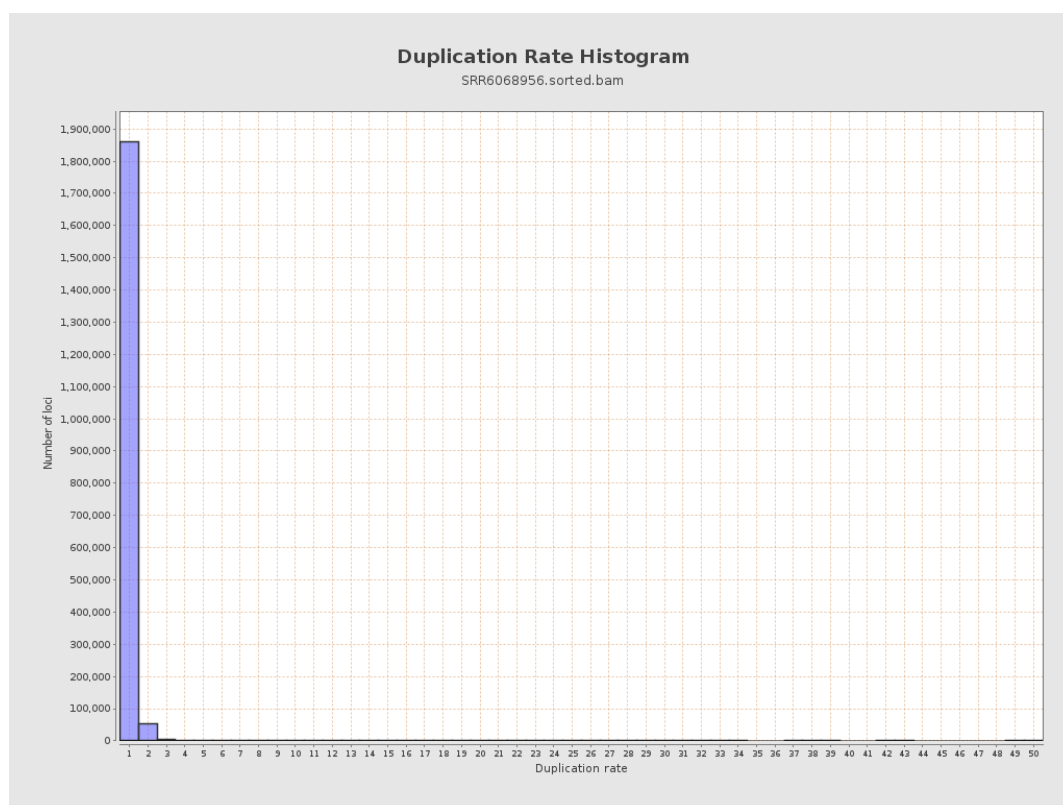
5. Results : Coverage Histogram (0-50X)



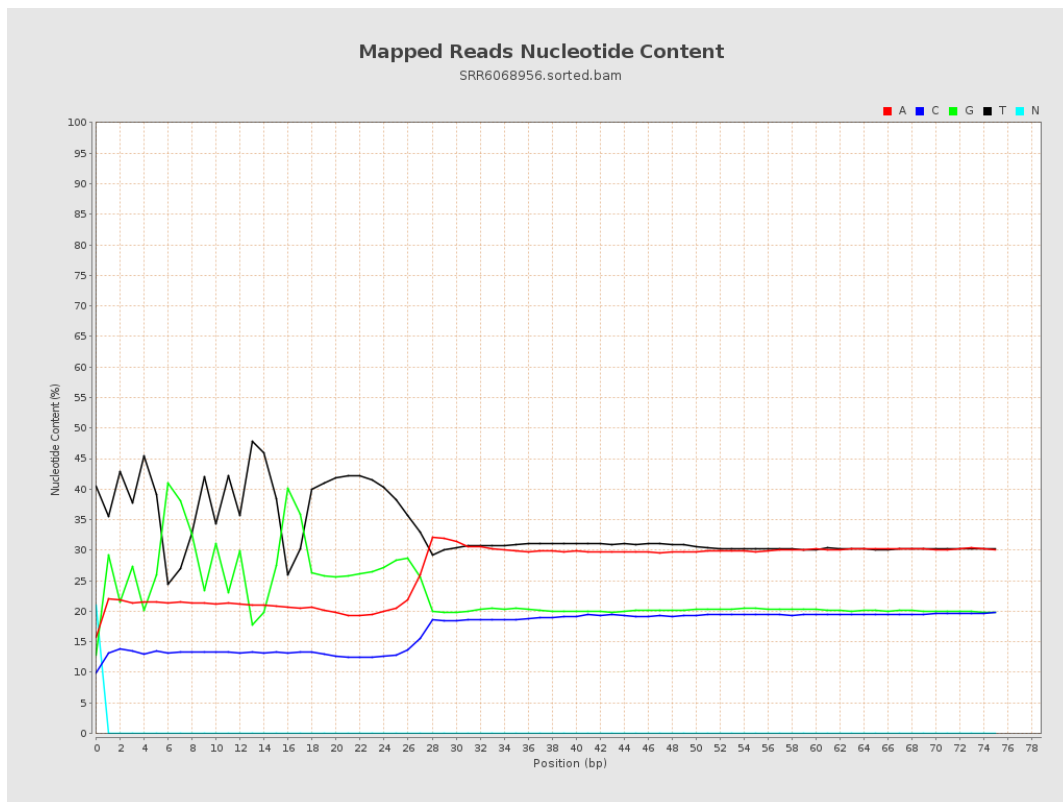
6. Results : Genome Fraction Coverage



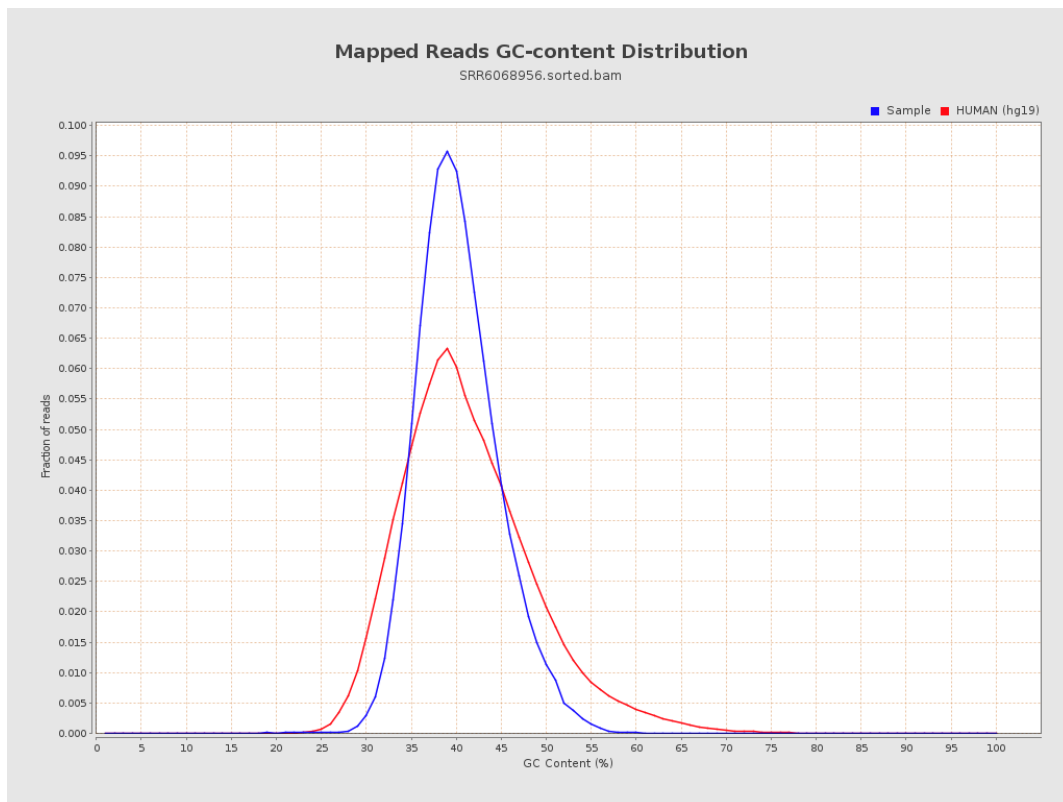
7. Results : Duplication Rate Histogram



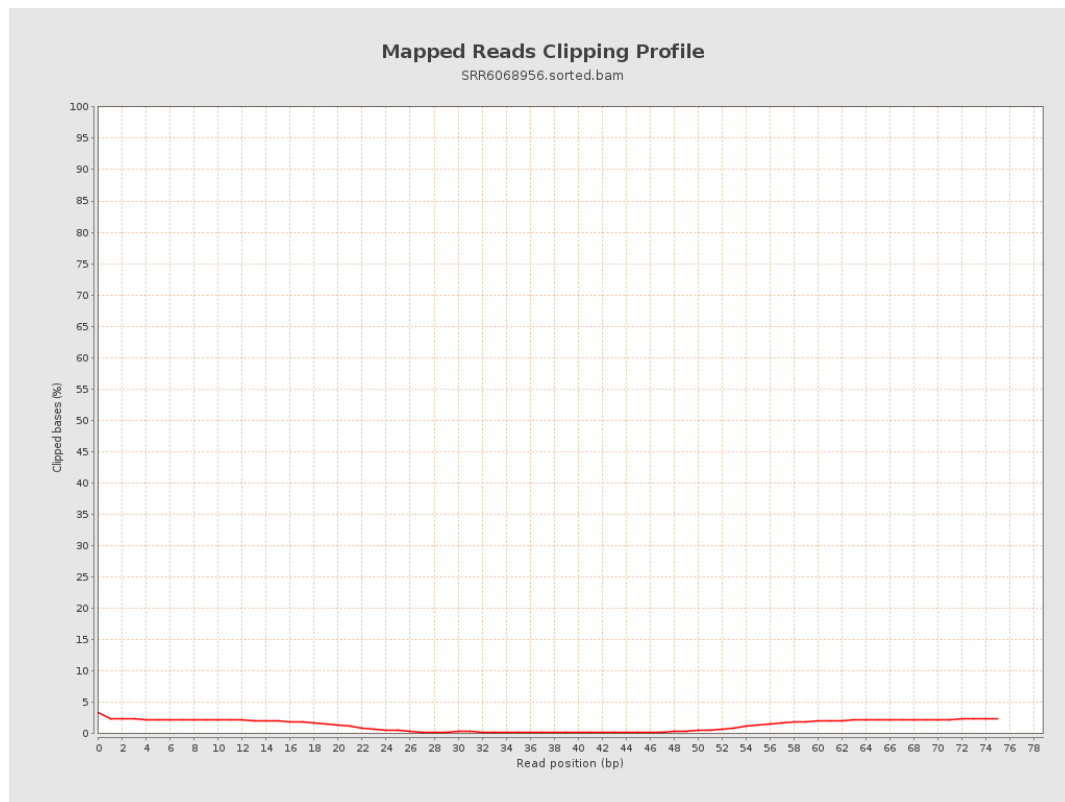
8. Results : Mapped Reads Nucleotide Content



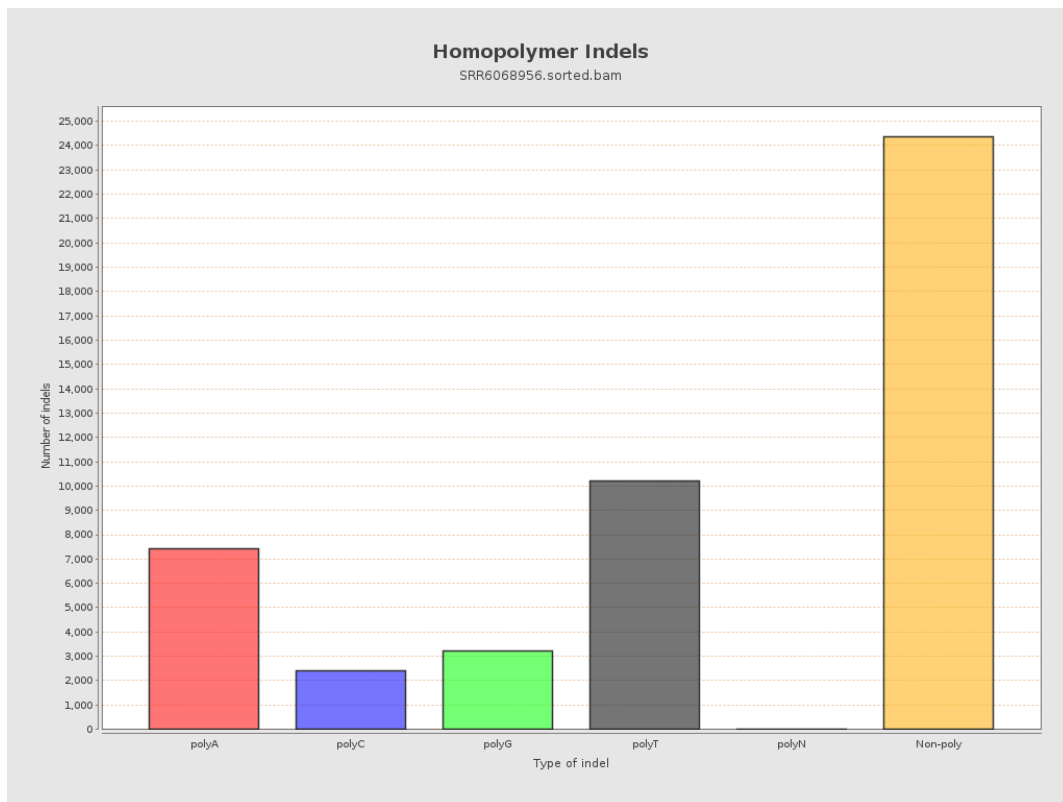
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

