

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 14:00:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068160.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_SRR6068160 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068160.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 14:00:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068160.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,954,178
Mapped reads	3,742,716 / 94.65%
Unmapped reads	211,462 / 5.35%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	33,316 / 0.84%
Read min/max/mean length	30 / 76 / 76.29
Duplicated reads (estimated)	478,422 / 12.1%
Duplication rate	10.6%
Clipped reads	2,037,389 / 51.52%

2.2. ACGT Content

Number/percentage of A's	61,967,176 / 25.87%
Number/percentage of C's	43,414,137 / 18.12%
Number/percentage of T's	77,657,379 / 32.42%
Number/percentage of G's	56,487,047 / 23.58%
Number/percentage of N's	27,370 / 0.01%
GC Percentage	41.7%

2.3. Coverage

Mean	0.0774

Standard Deviation	0.7822
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2.4. Mapping Quality

Mean Mapping Quality	43.94
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2.5. Mismatches and indels

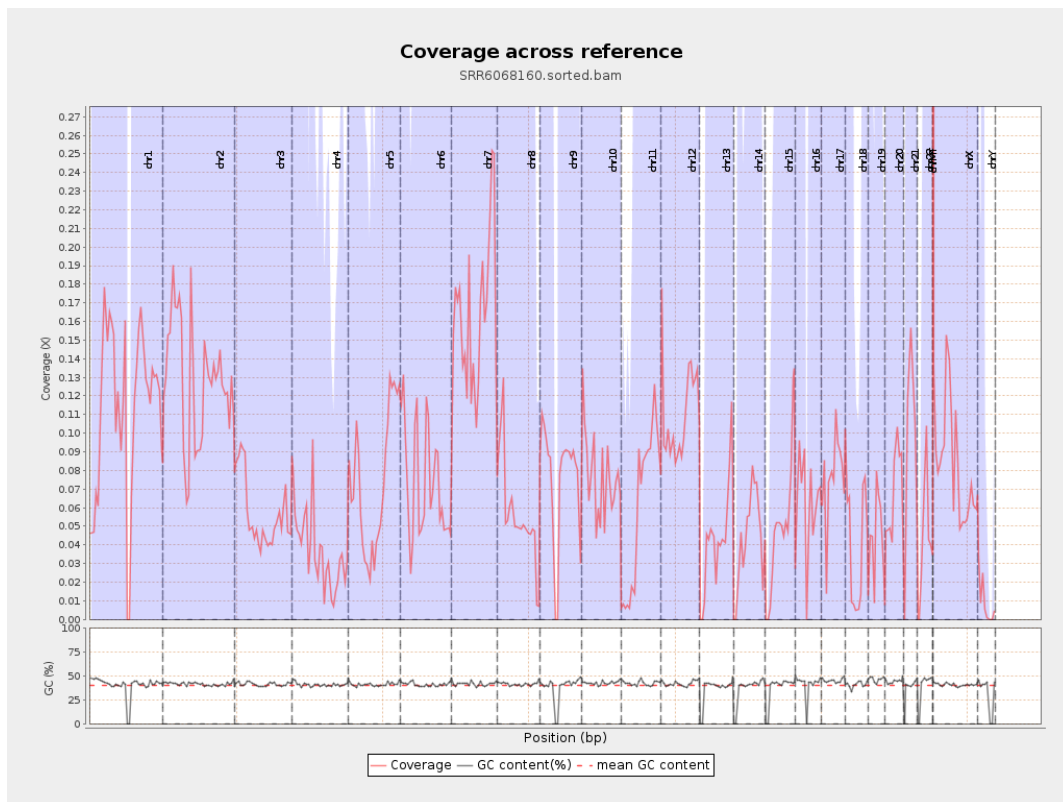
General error rate	0.56%
Mismatches	1,305,833
Insertions	14,540
Mapped reads with at least one insertion	0.39%
Deletions	56,994
Mapped reads with at least one deletion	1.51%
Homopolymer indels	44.25%

2.6. Chromosome stats

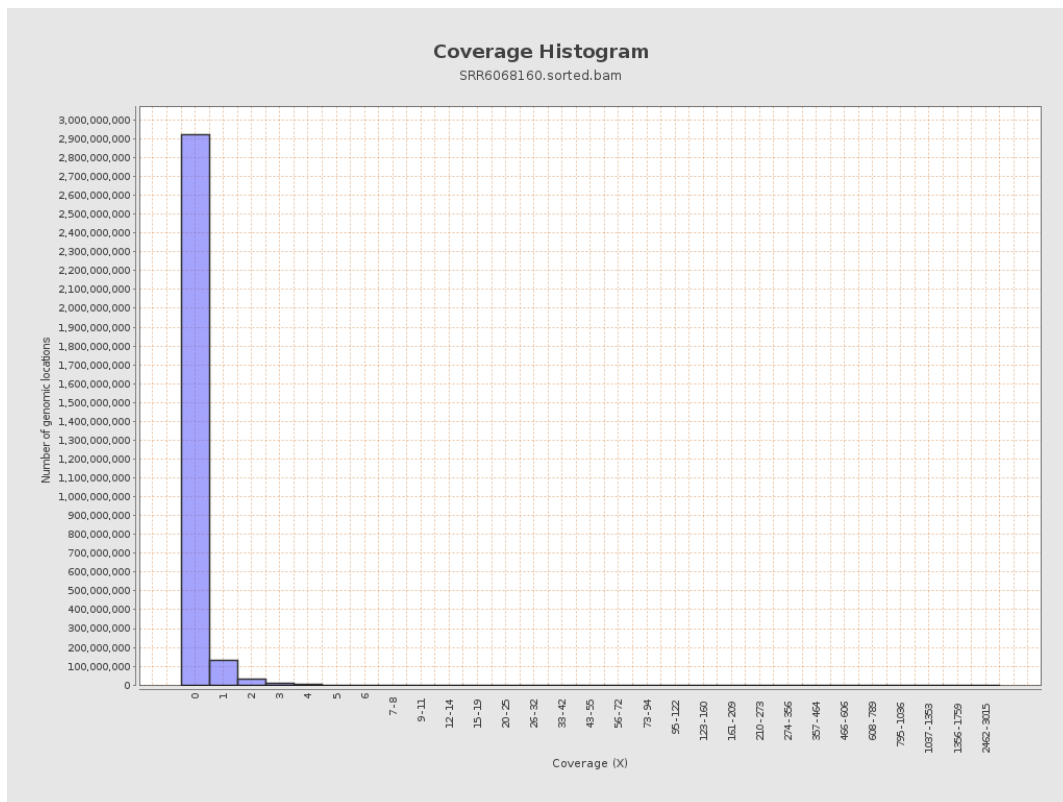
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	28329043	0.1137	1.4749
chr2	243199373	31531795	0.1297	1.434
chr3	198022430	11333478	0.0572	0.3159
chr4	191154276	6989221	0.0366	0.2897
chr5	180915260	13393297	0.074	0.3614
chr6	171115067	12630976	0.0738	0.5579
chr7	159138663	25838113	0.1624	1.3892

chr8	146364022	8202119	0.056	0.4701
chr9	141213431	10662252	0.0755	0.5331
chr10	135534747	10343155	0.0763	0.5615
chr11	135006516	8220607	0.0609	0.3766
chr12	133851895	14801053	0.1106	0.4572
chr13	115169878	5107461	0.0443	0.3222
chr14	107349540	4690610	0.0437	0.3239
chr15	102531392	4923208	0.048	0.3184
chr16	90354753	5554822	0.0615	0.3684
chr17	81195210	6216752	0.0766	0.3776
chr18	78077248	3082605	0.0395	0.9396
chr19	59128983	2611656	0.0442	1.0401
chr20	63025520	4357696	0.0691	0.3719
chr21	48129895	4516736	0.0938	0.4193
chr22	51304566	2277265	0.0444	0.2718
chrMT	16571	530246	31.9984	17.7823
chrX	155270560	12983788	0.0836	0.4353
chrY	59373566	524677	0.0088	0.2222

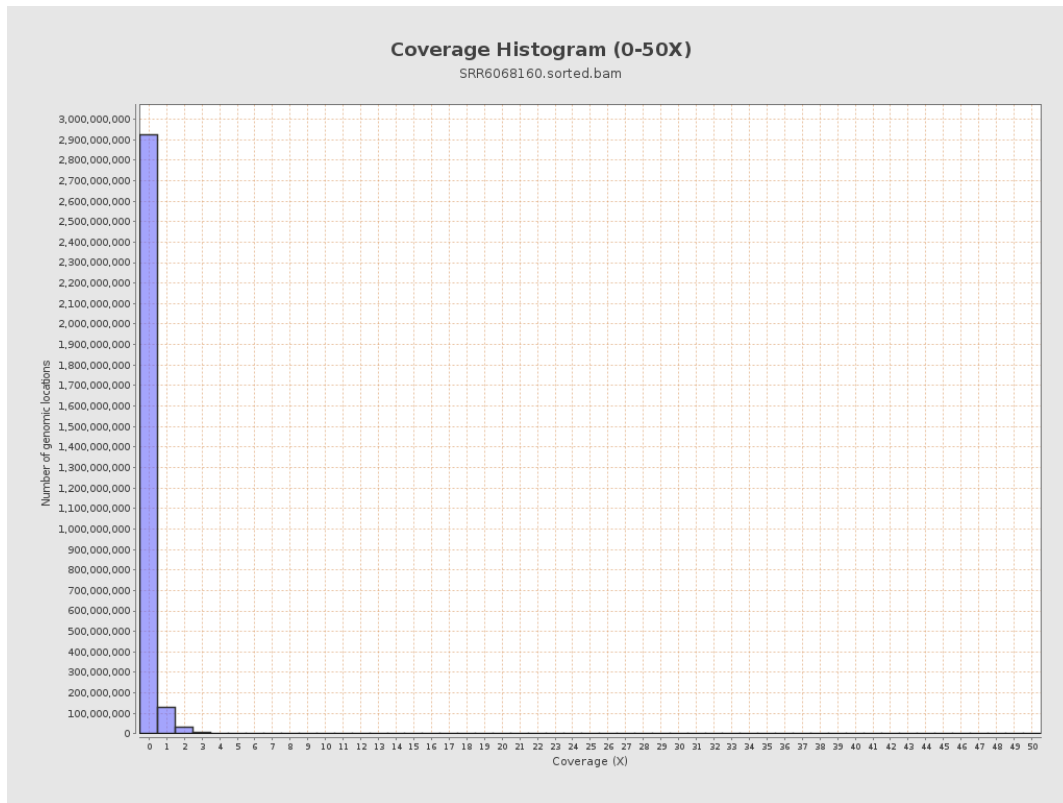
3. Results : Coverage across reference



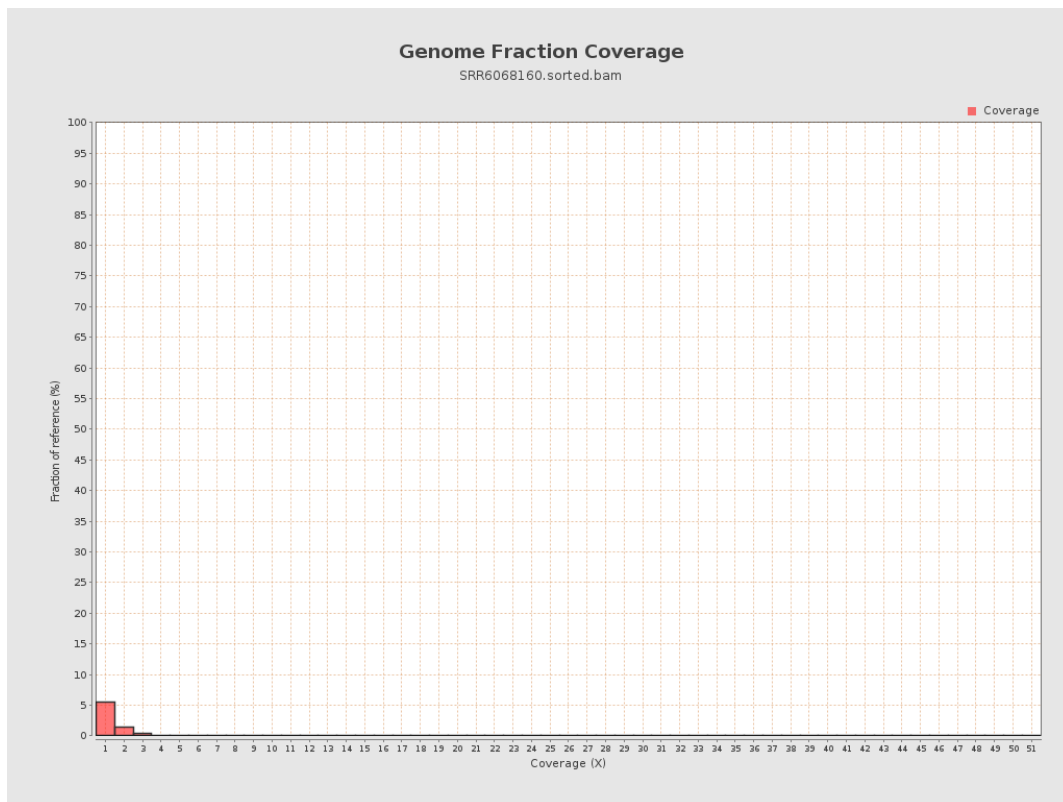
4. Results : Coverage Histogram



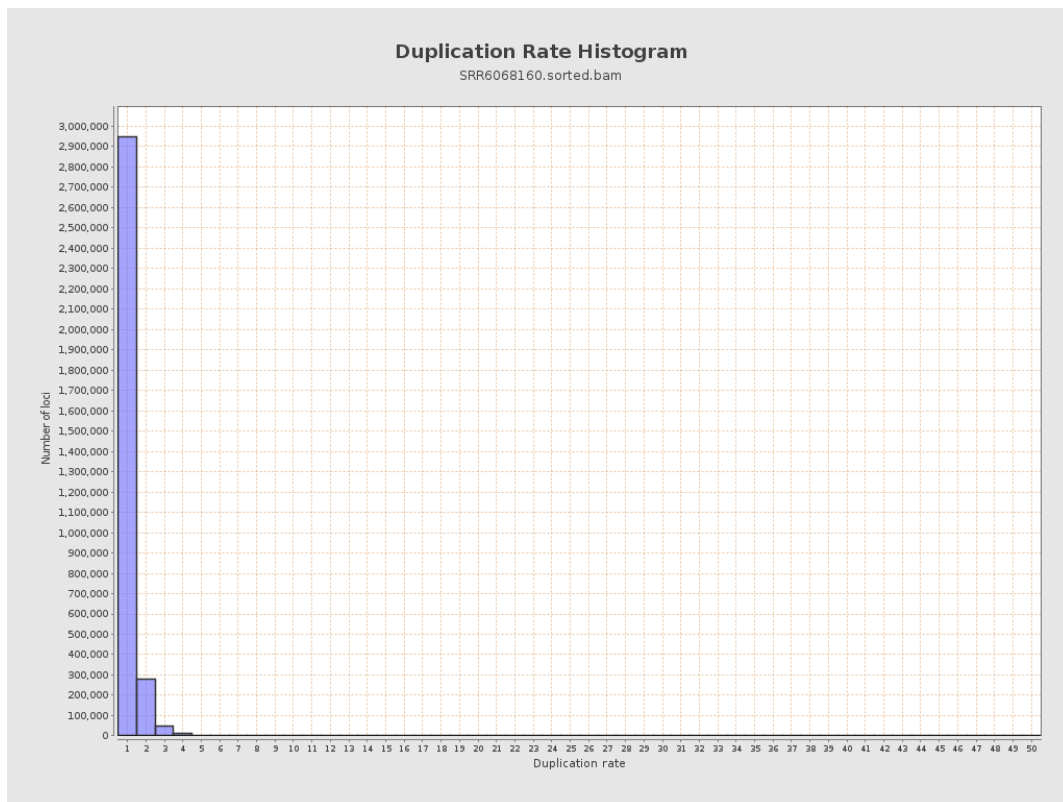
5. Results : Coverage Histogram (0-50X)



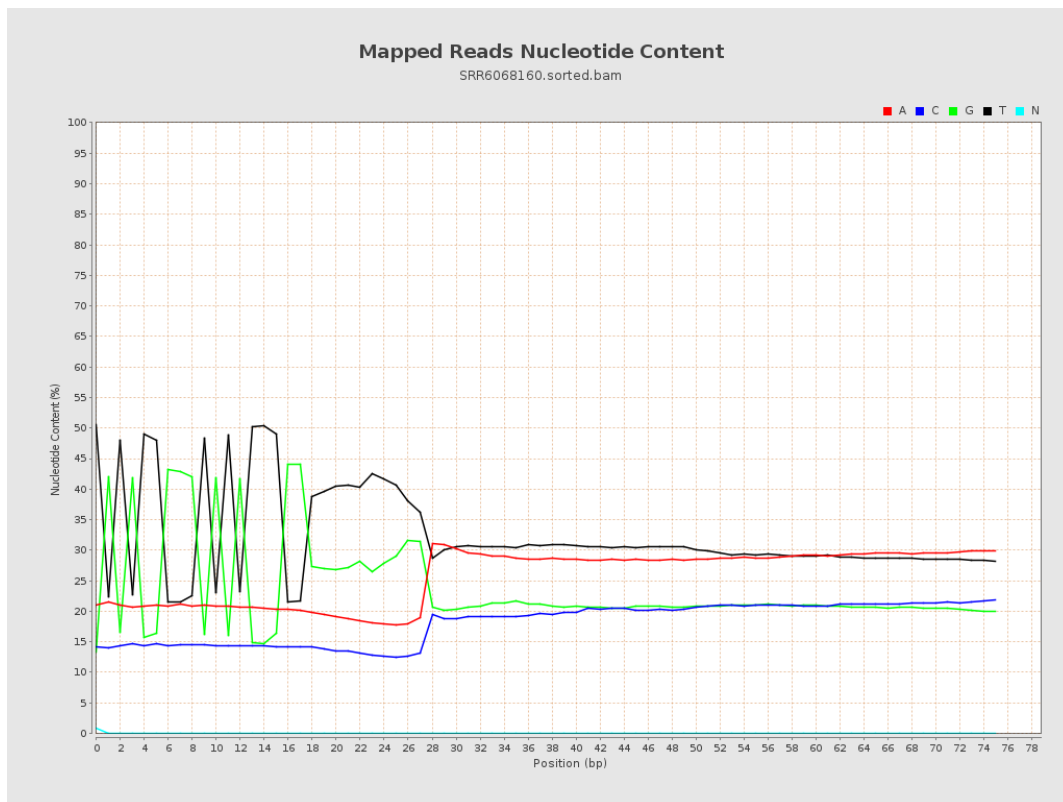
6. Results : Genome Fraction Coverage



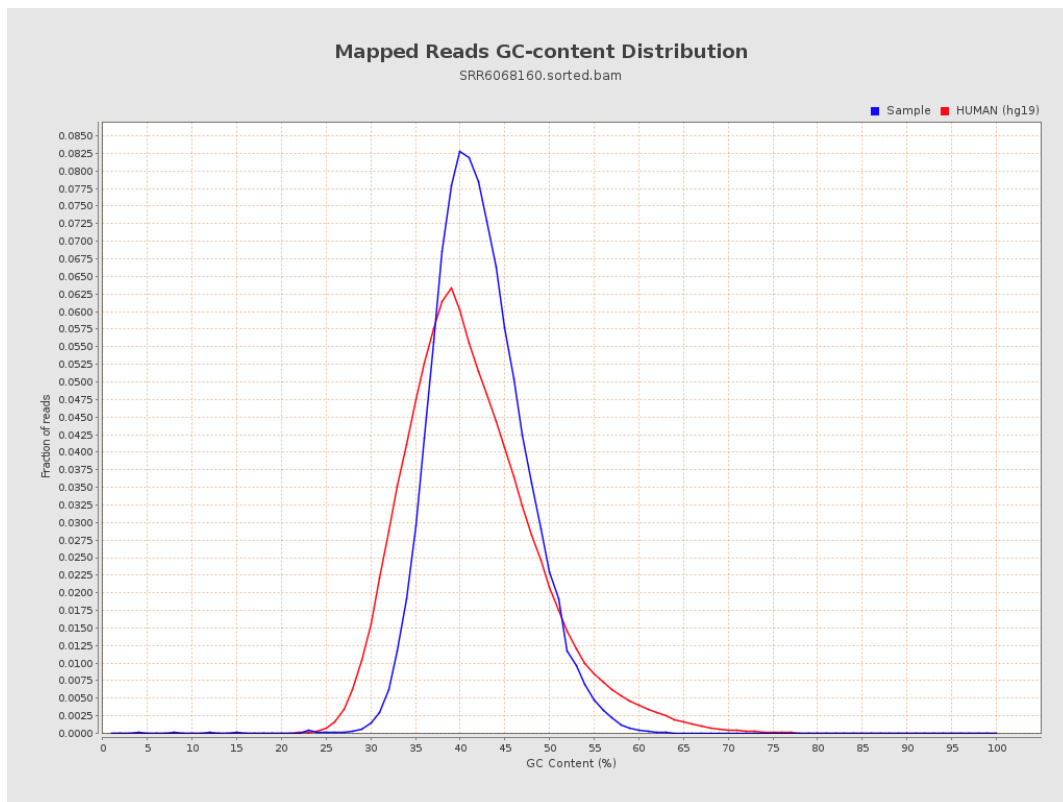
7. Results : Duplication Rate Histogram



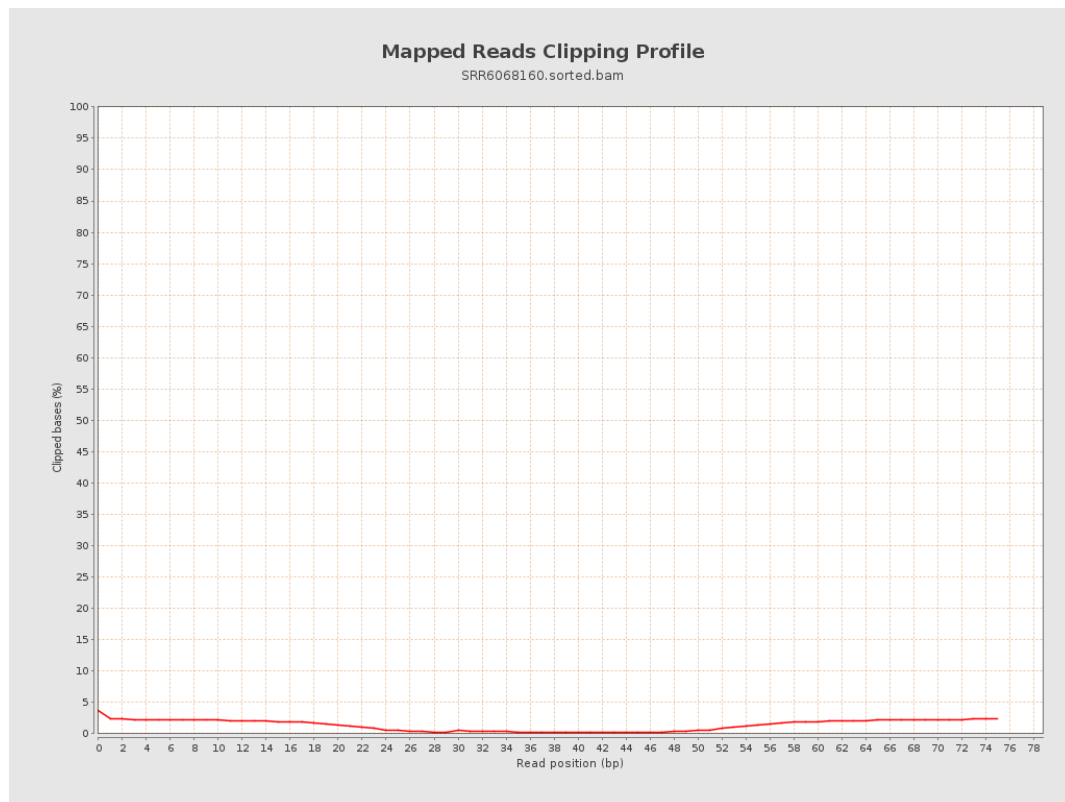
8. Results : Mapped Reads Nucleotide Content



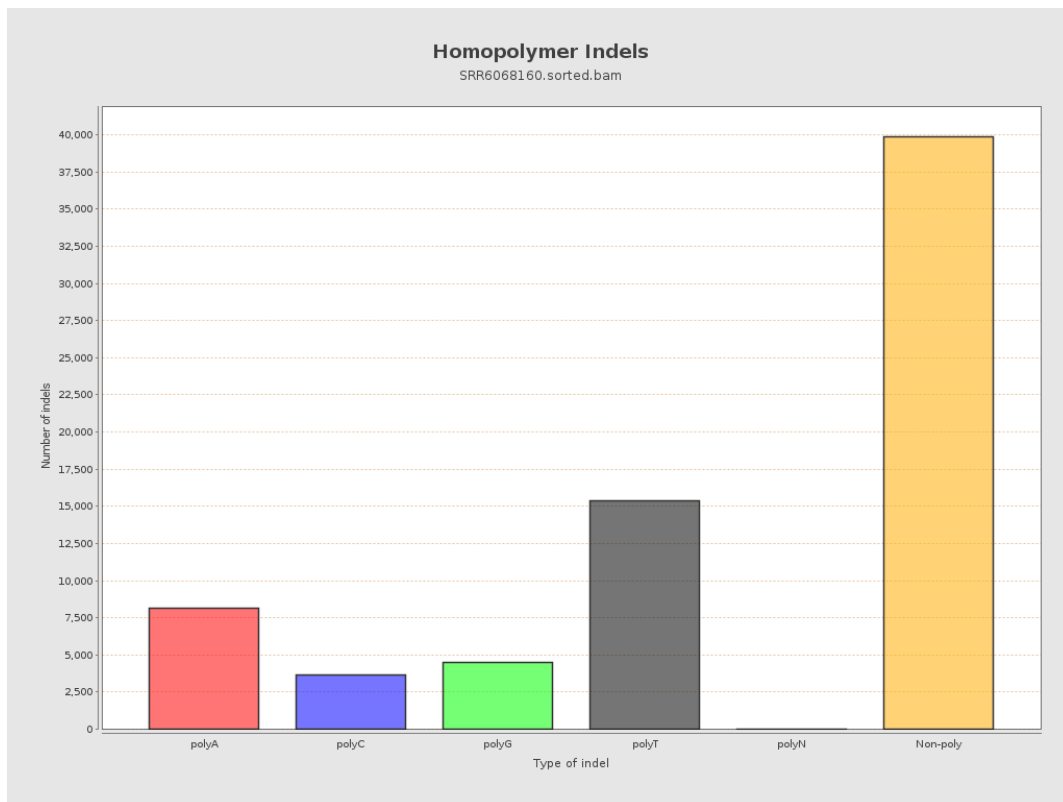
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

