

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 12:08:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068133.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_SRR6068133 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068133.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 12:08:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068133.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,754,755
Mapped reads	1,253,815 / 71.45%
Unmapped reads	500,940 / 28.55%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,301 / 0.64%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	129,691 / 7.39%
Duplication rate	8.1%
Clipped reads	571,915 / 32.59%

2.2. ACGT Content

Number/percentage of A's	22,983,049 / 27.74%
Number/percentage of C's	14,761,769 / 17.81%
Number/percentage of T's	26,942,239 / 32.51%
Number/percentage of G's	18,115,937 / 21.86%
Number/percentage of N's	62,156 / 0.08%
GC Percentage	39.68%

2.3. Coverage

Mean	0.0268

Standard Deviation	0.3389
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2.4. Mapping Quality

Mean Mapping Quality	47.01
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2.5. Mismatches and indels

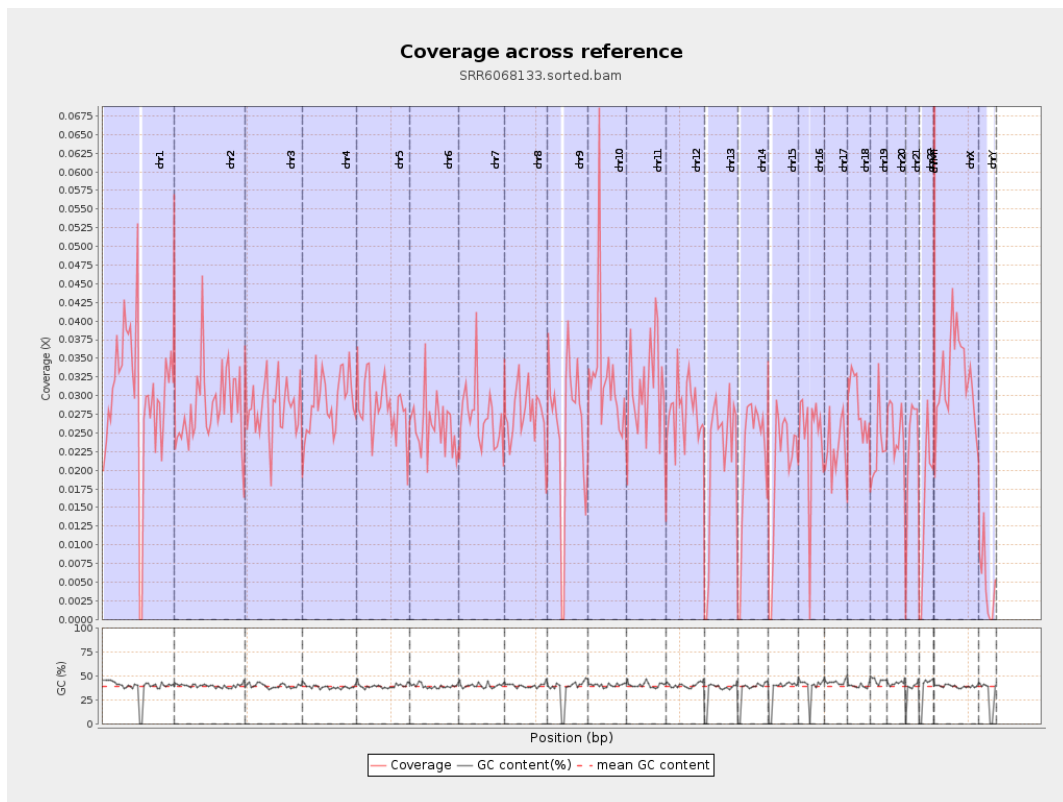
General error rate	0.9%
Mismatches	734,974
Insertions	6,509
Mapped reads with at least one insertion	0.51%
Deletions	20,726
Mapped reads with at least one deletion	1.64%
Homopolymer indels	47.45%

2.6. Chromosome stats

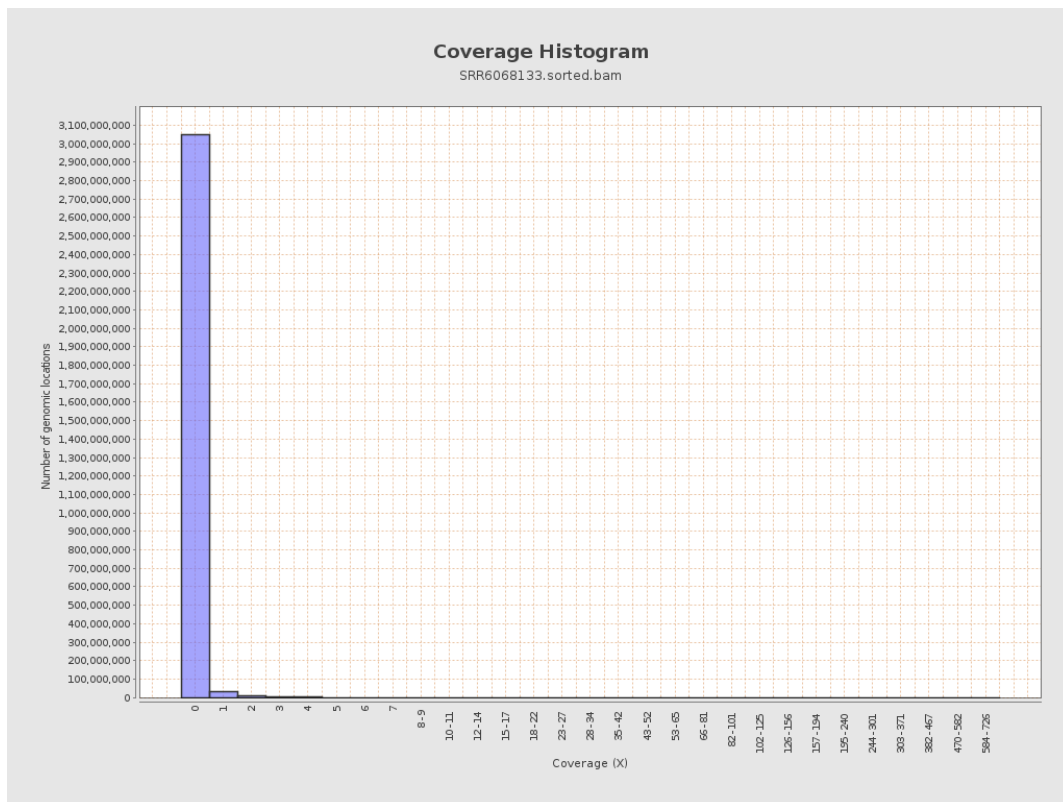
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	7459144	0.0299	0.6302
chr2	243199373	6914063	0.0284	0.3213
chr3	198022430	5629236	0.0284	0.2694
chr4	191154276	5545485	0.029	0.2711
chr5	180915260	5102553	0.0282	0.2668
chr6	171115067	4430659	0.0259	0.2757
chr7	159138663	4295951	0.027	0.3563

chr8	146364022	4024829	0.0275	0.3633
chr9	141213431	3642967	0.0258	0.2891
chr10	135534747	4406007	0.0325	0.4333
chr11	135006516	4250847	0.0315	0.315
chr12	133851895	3757988	0.0281	0.2673
chr13	115169878	2495588	0.0217	0.2384
chr14	107349540	2332681	0.0217	0.2347
chr15	102531392	2064252	0.0201	0.2213
chr16	90354753	2179275	0.0241	0.2587
chr17	81195210	1855838	0.0229	0.245
chr18	78077248	2242081	0.0287	0.4474
chr19	59128983	1362134	0.023	0.3794
chr20	63025520	1598166	0.0254	0.2664
chr21	48129895	1122349	0.0233	0.2545
chr22	51304566	833310	0.0162	0.201
chrMT	16571	30709	1.8532	2.1755
chrX	155270560	5043267	0.0325	0.3037
chrY	59373566	280152	0.0047	0.1132

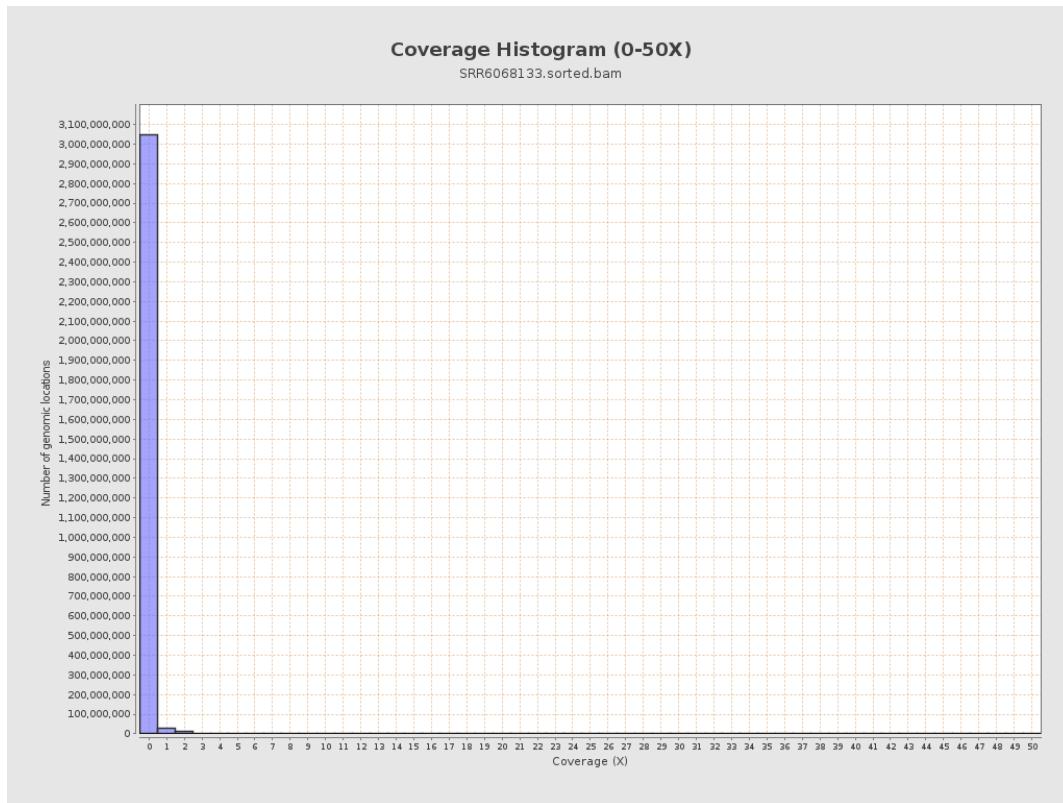
3. Results : Coverage across reference



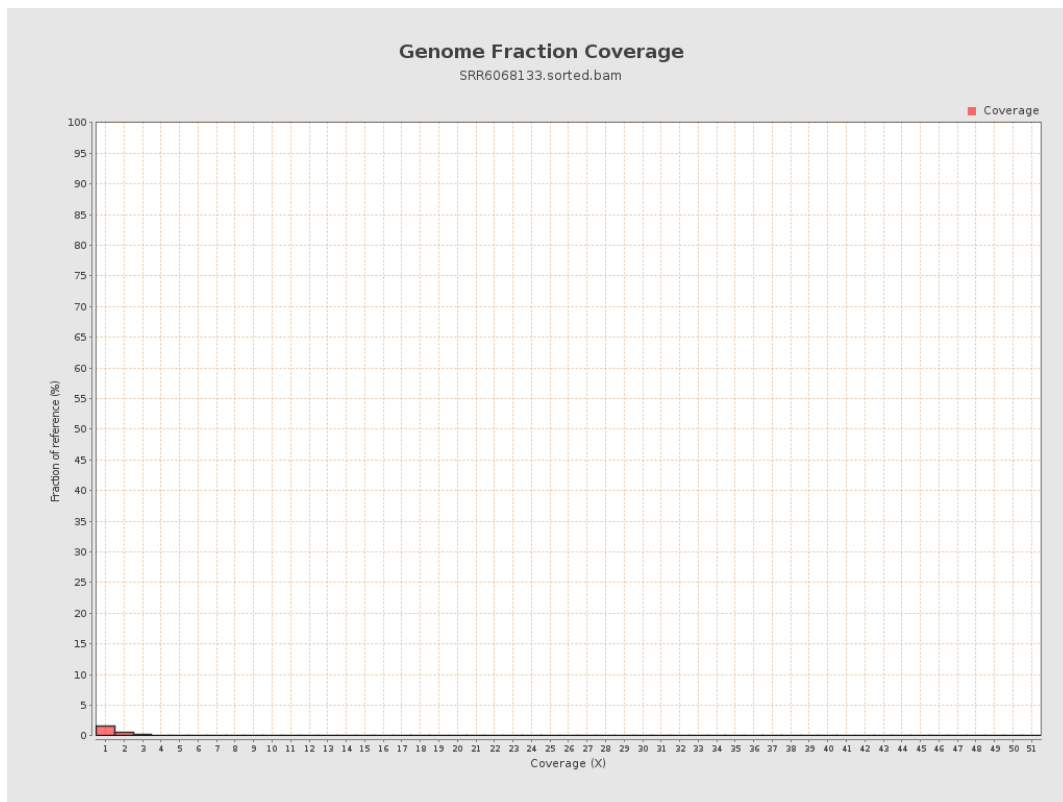
4. Results : Coverage Histogram



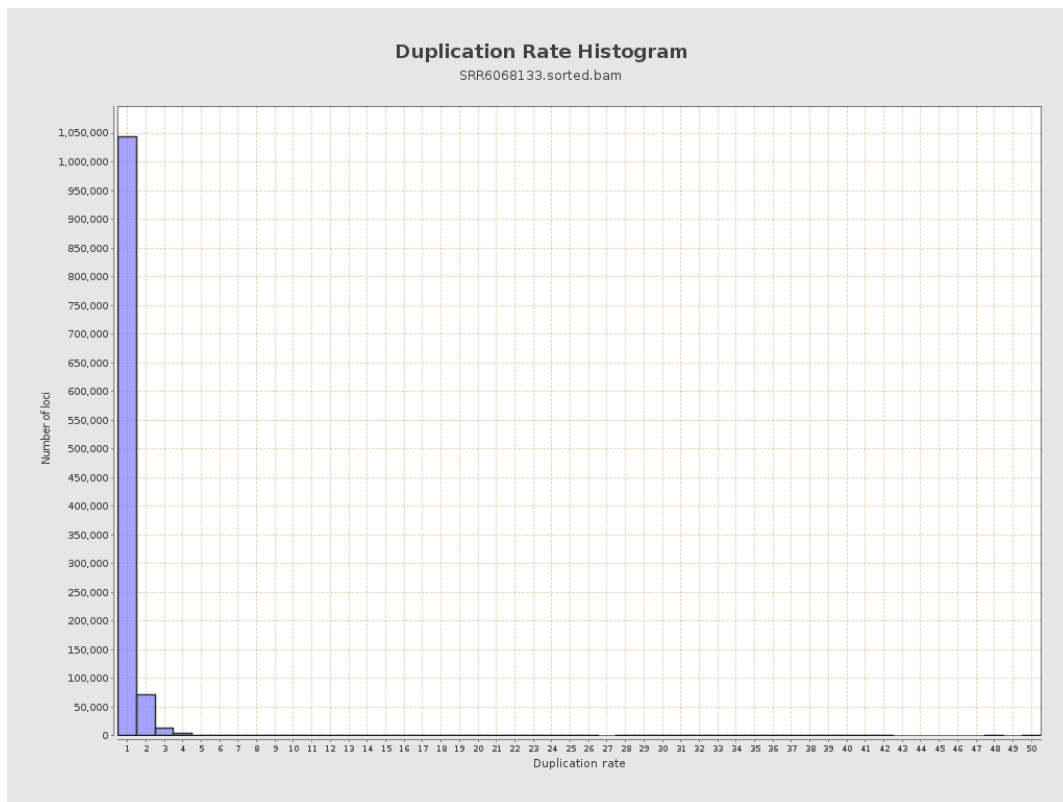
5. Results : Coverage Histogram (0-50X)



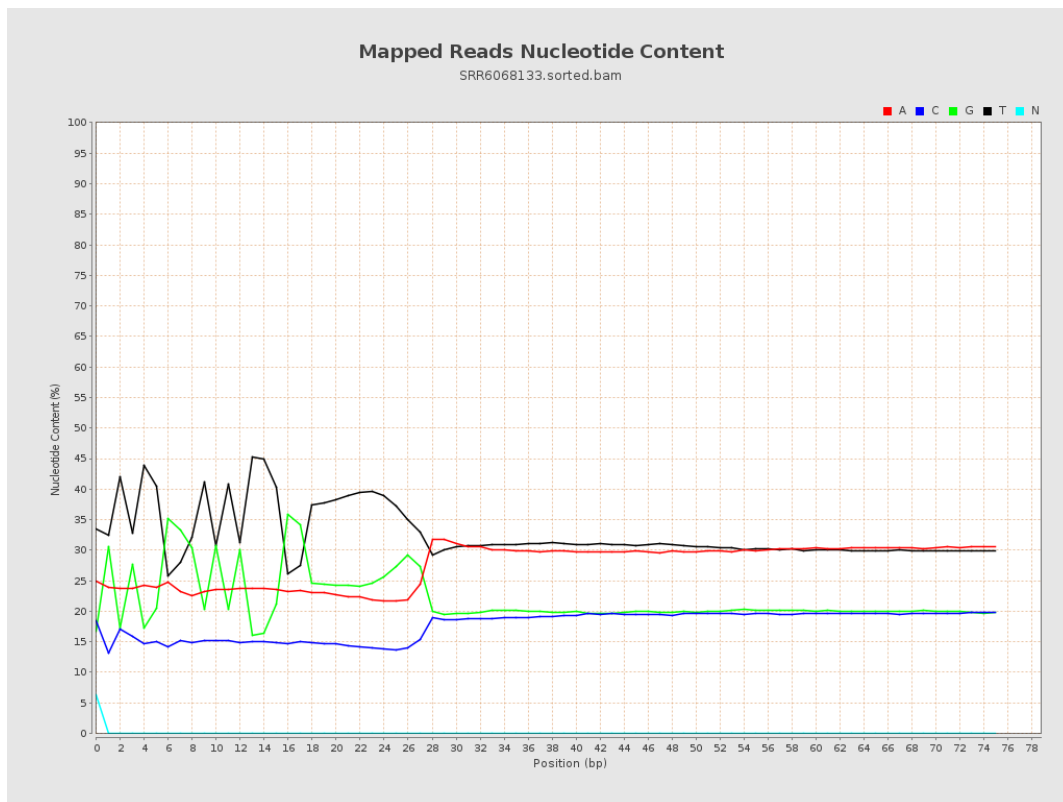
6. Results : Genome Fraction Coverage



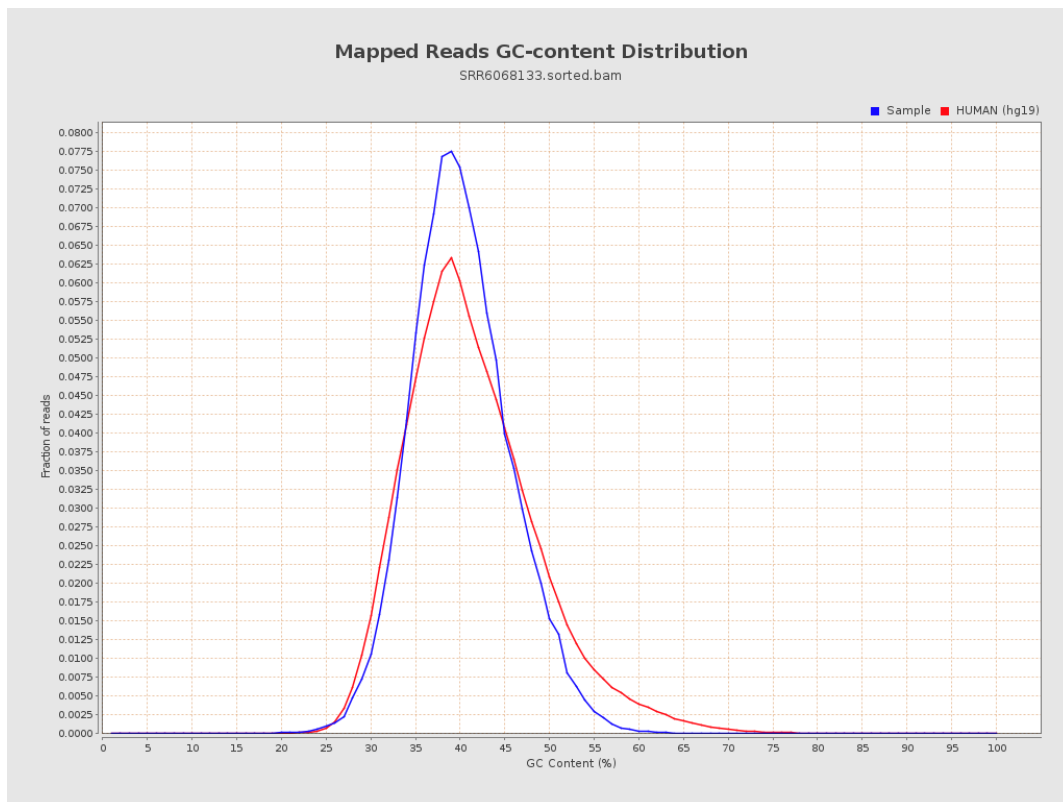
7. Results : Duplication Rate Histogram



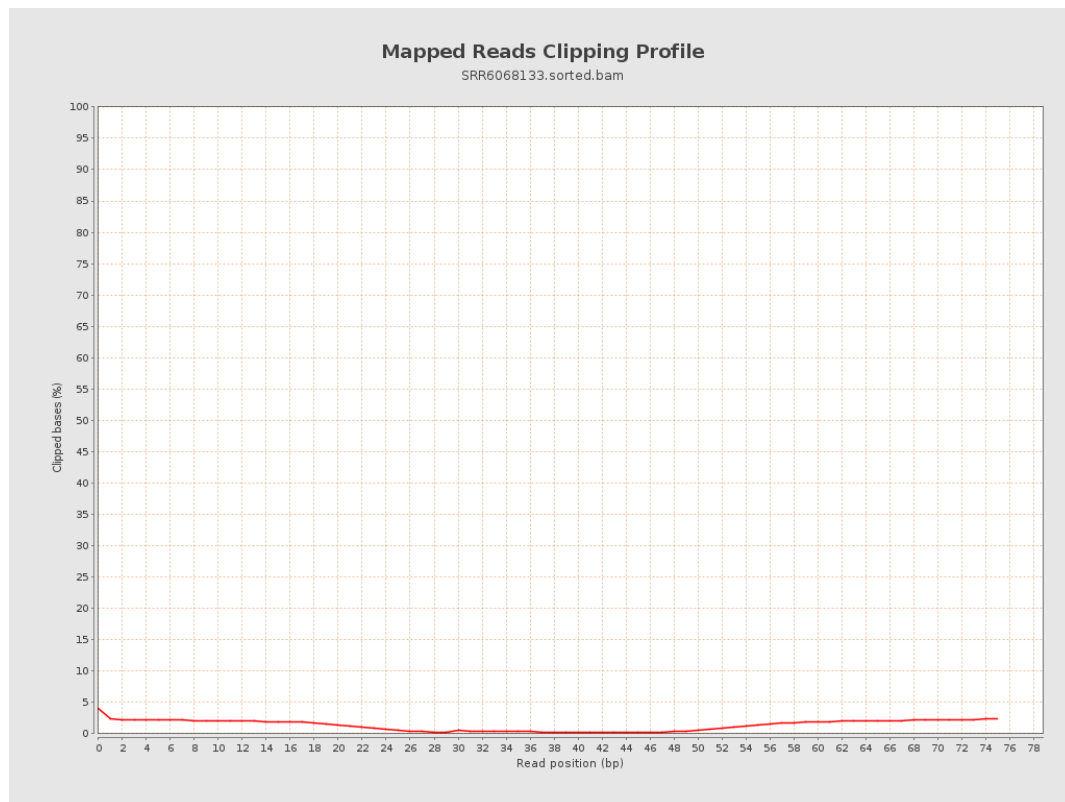
8. Results : Mapped Reads Nucleotide Content



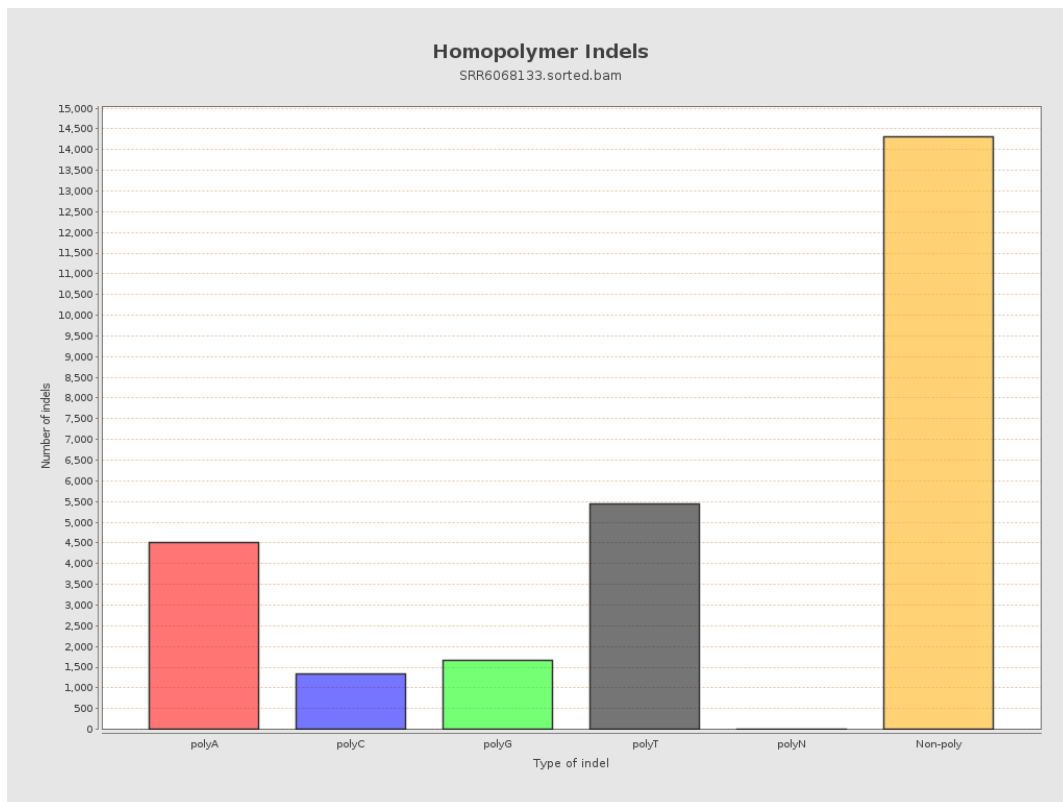
9. Results : Mapped Reads GC-content Distribution



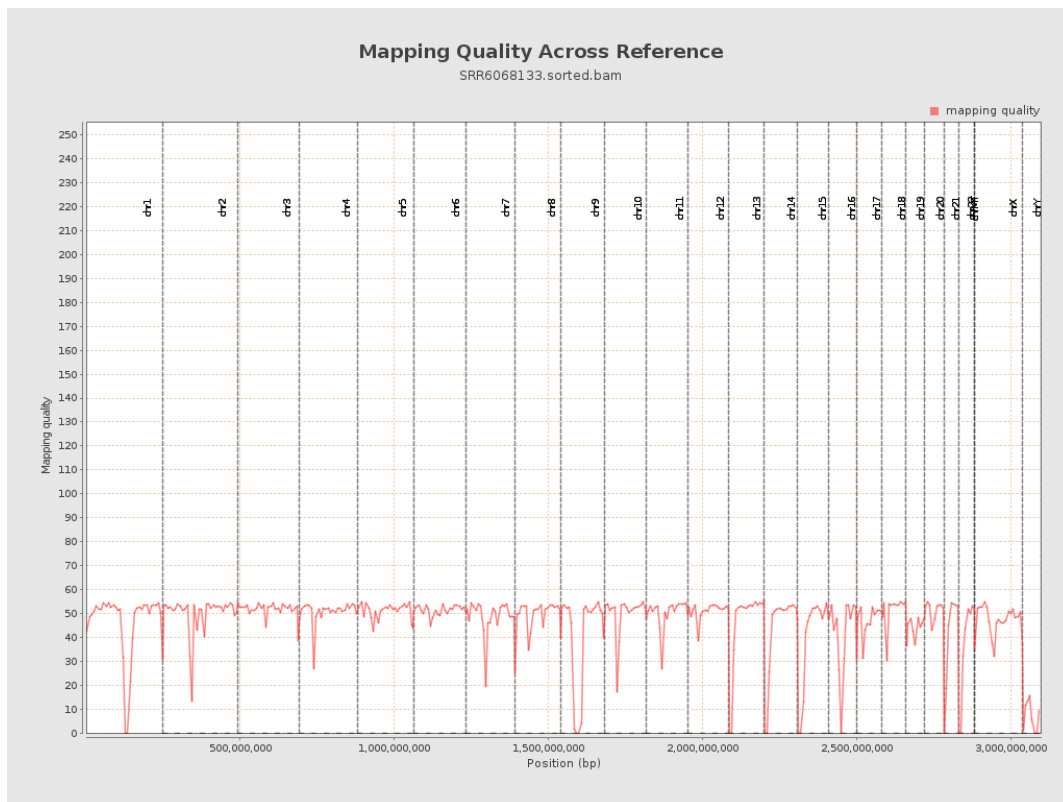
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

