

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 15:50:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068928.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_SRR6068928 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068928.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 15:50:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068928.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,435,137
Mapped reads	2,090,613 / 85.85%
Unmapped reads	344,524 / 14.15%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,090 / 0.46%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	78,590 / 3.23%
Duplication rate	2.61%
Clipped reads	1,047,634 / 43.02%

2.2. ACGT Content

Number/percentage of A's	36,861,739 / 27.01%
Number/percentage of C's	23,522,458 / 17.24%
Number/percentage of T's	45,179,678 / 33.11%
Number/percentage of G's	30,556,523 / 22.39%
Number/percentage of N's	331,642 / 0.24%
GC Percentage	39.63%

2.3. Coverage

Mean	0.0441

Standard Deviation	0.4285
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2.4. Mapping Quality

Mean Mapping Quality	46.04
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2.5. Mismatches and indels

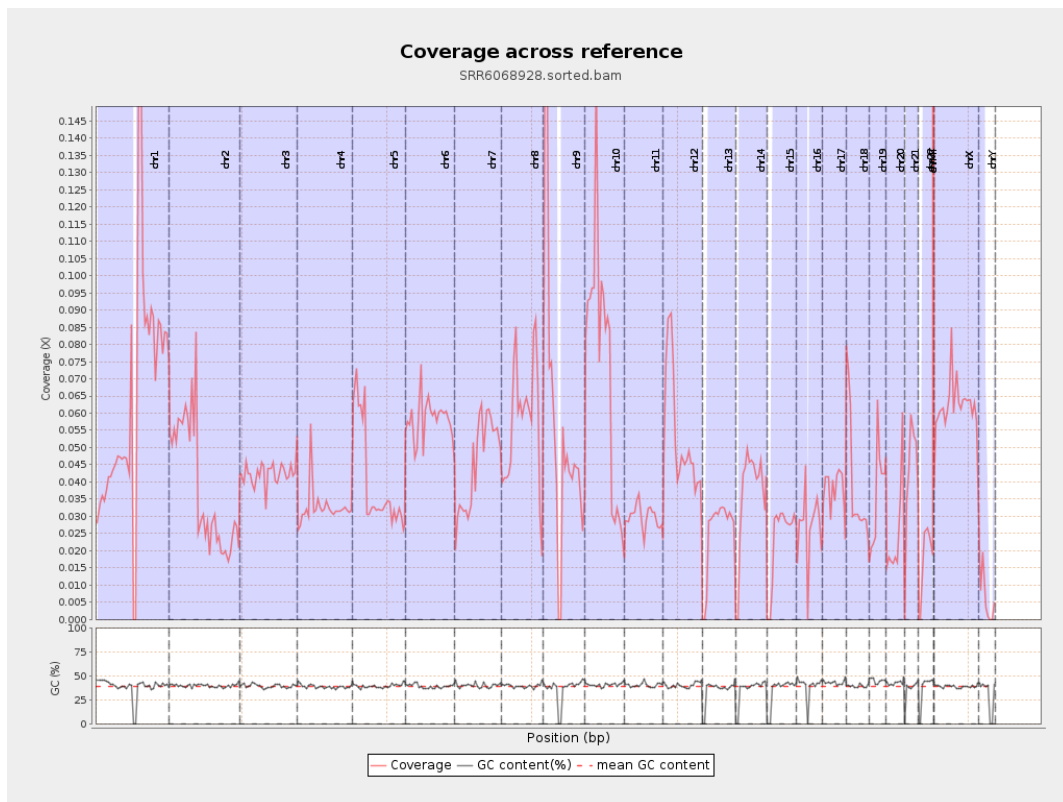
General error rate	0.98%
Mismatches	1,313,590
Insertions	12,544
Mapped reads with at least one insertion	0.59%
Deletions	37,361
Mapped reads with at least one deletion	1.77%
Homopolymer indels	48.06%

2.6. Chromosome stats

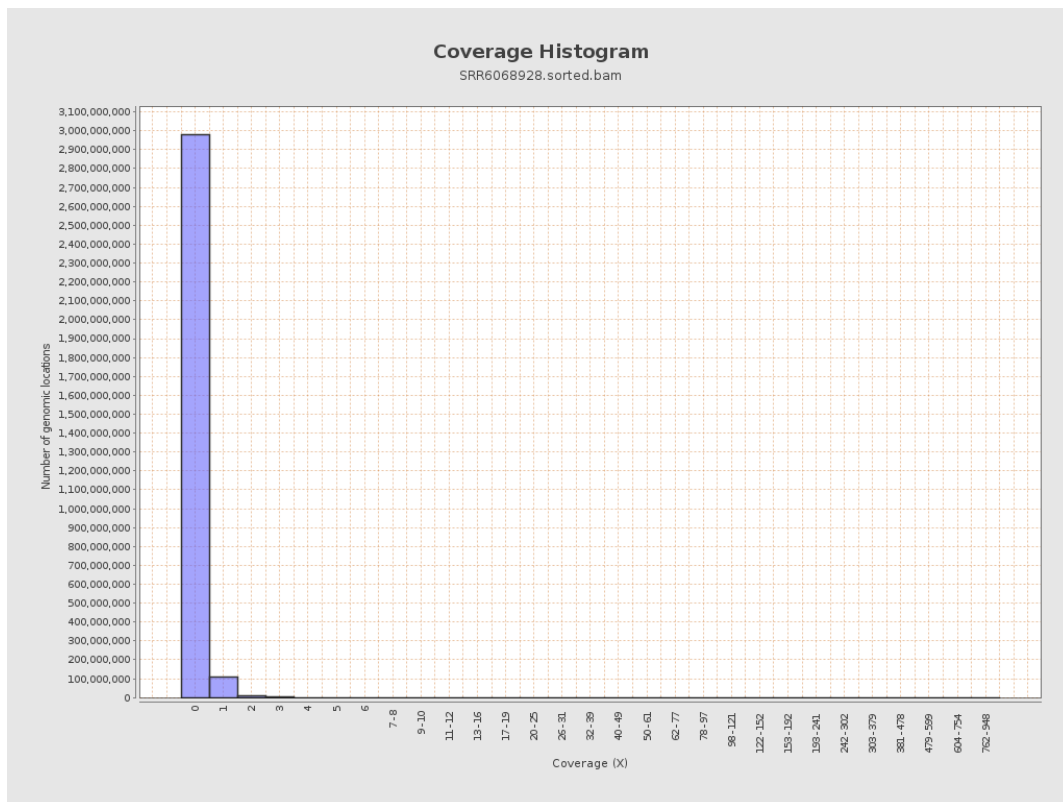
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	15975766	0.0641	0.8152
chr2	243199373	9310076	0.0383	0.3649
chr3	198022430	8369584	0.0423	0.2967
chr4	191154276	6203298	0.0325	0.228
chr5	180915260	7219012	0.0399	0.2213
chr6	171115067	9963854	0.0582	0.3527
chr7	159138663	7288549	0.0458	0.3412

chr8	146364022	8418389	0.0575	0.5539
chr9	141213431	8048654	0.057	0.4073
chr10	135534747	10027726	0.074	0.8679
chr11	135006516	3995293	0.0296	0.3002
chr12	133851895	7046885	0.0526	0.2645
chr13	115169878	2909120	0.0253	0.173
chr14	107349540	3895657	0.0363	0.2533
chr15	102531392	2418628	0.0236	0.1716
chr16	90354753	2456434	0.0272	0.25
chr17	81195210	3045560	0.0375	0.2328
chr18	78077248	3048053	0.039	0.682
chr19	59128983	2173701	0.0368	0.5118
chr20	63025520	1597467	0.0253	0.2
chr21	48129895	2058079	0.0428	0.2651
chr22	51304566	886002	0.0173	0.151
chrMT	16571	167051	10.0809	6.6342
chrX	155270560	9607455	0.0619	0.3169
chrY	59373566	383744	0.0065	0.1532

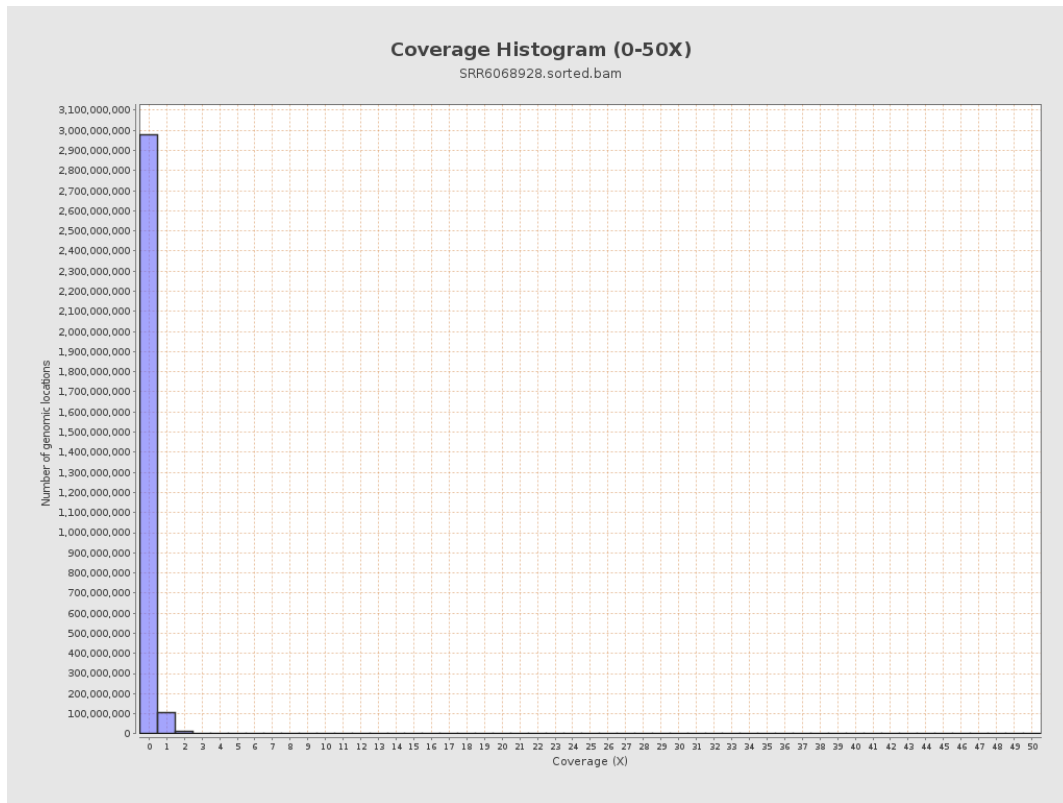
3. Results : Coverage across reference



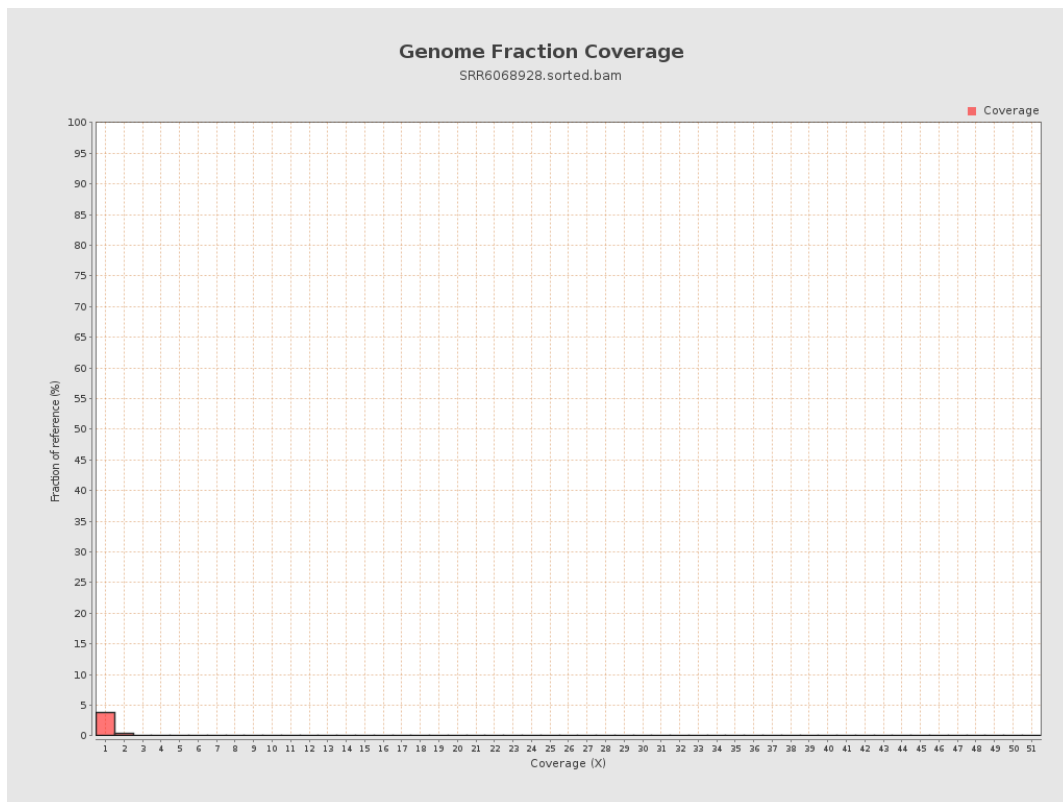
4. Results : Coverage Histogram



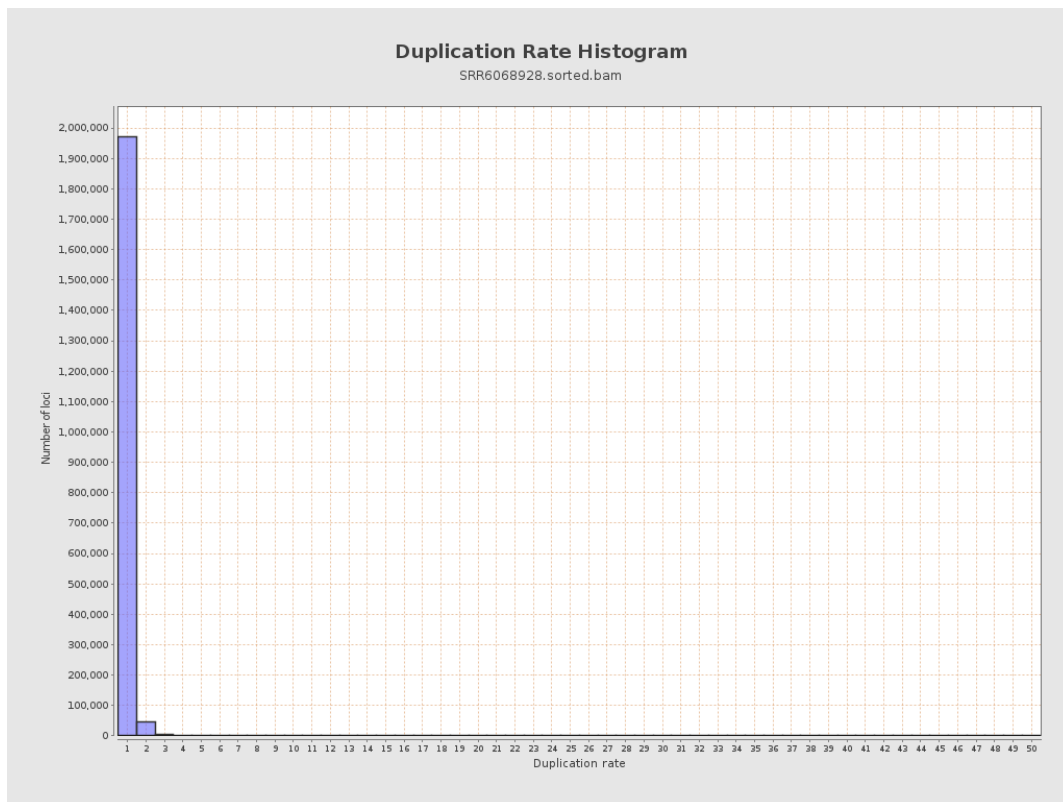
5. Results : Coverage Histogram (0-50X)



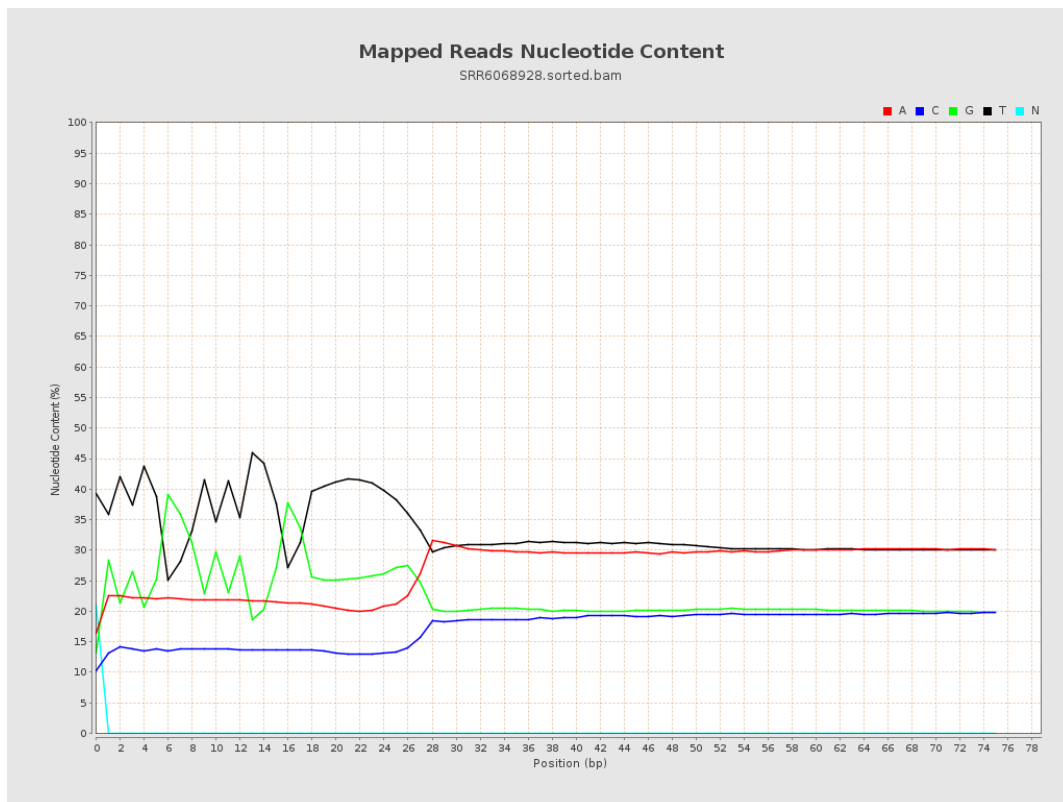
6. Results : Genome Fraction Coverage



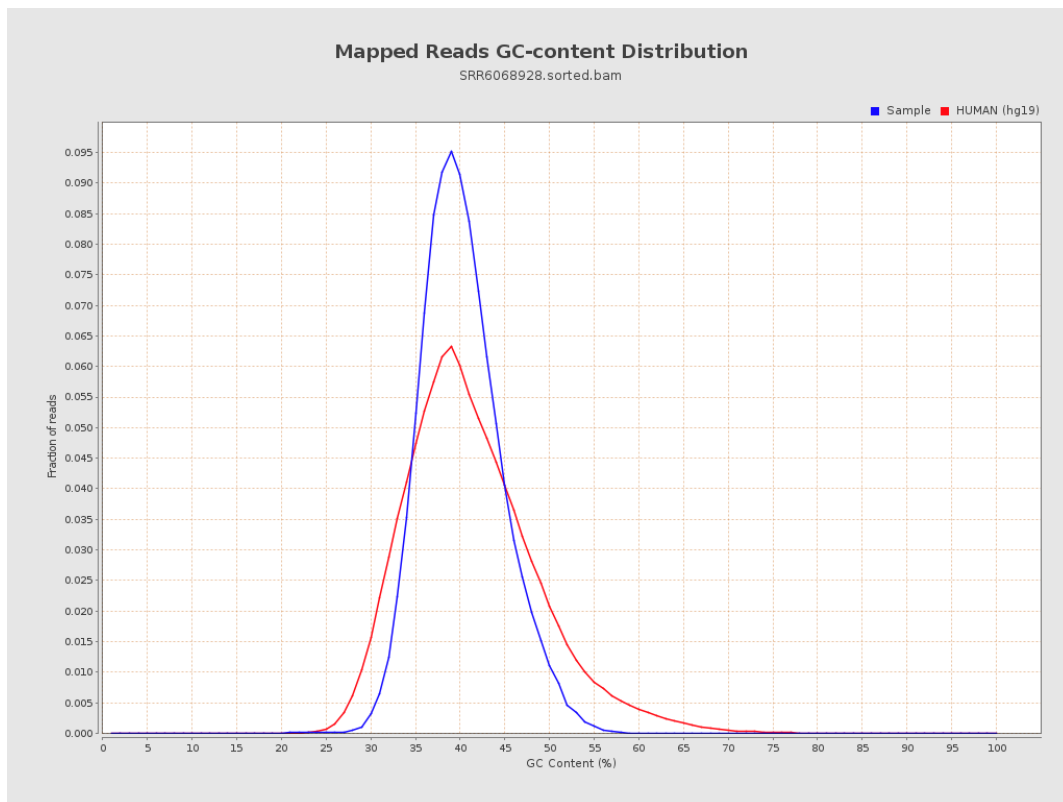
7. Results : Duplication Rate Histogram



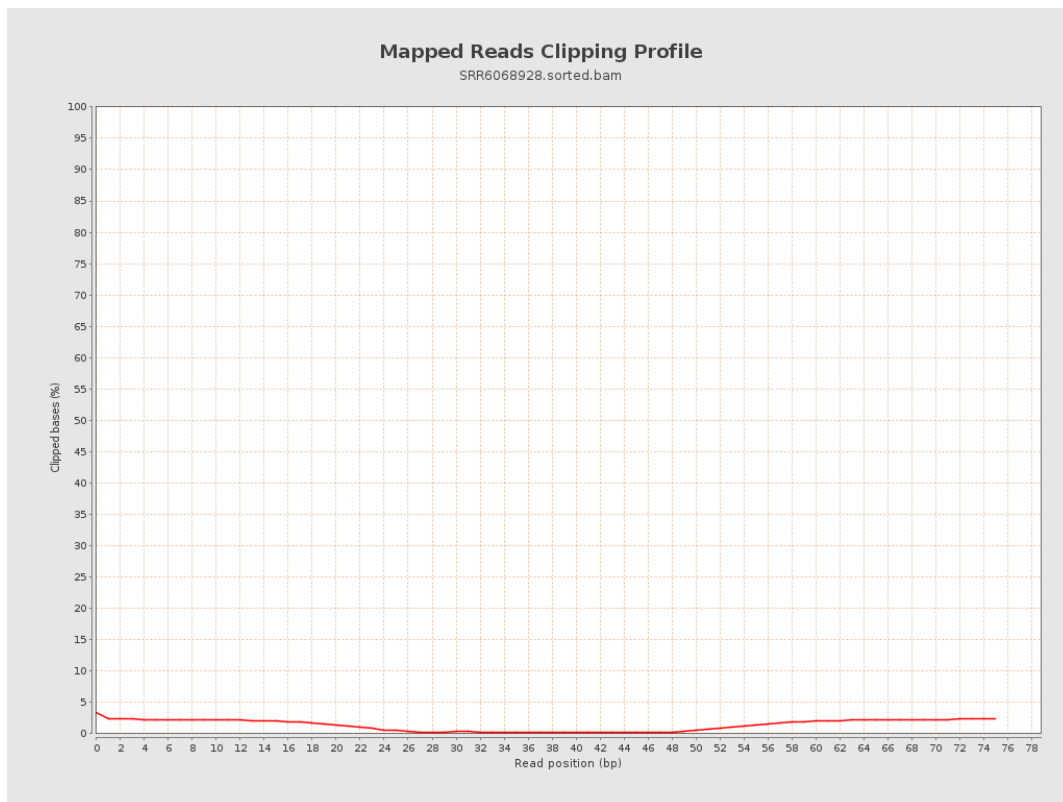
8. Results : Mapped Reads Nucleotide Content



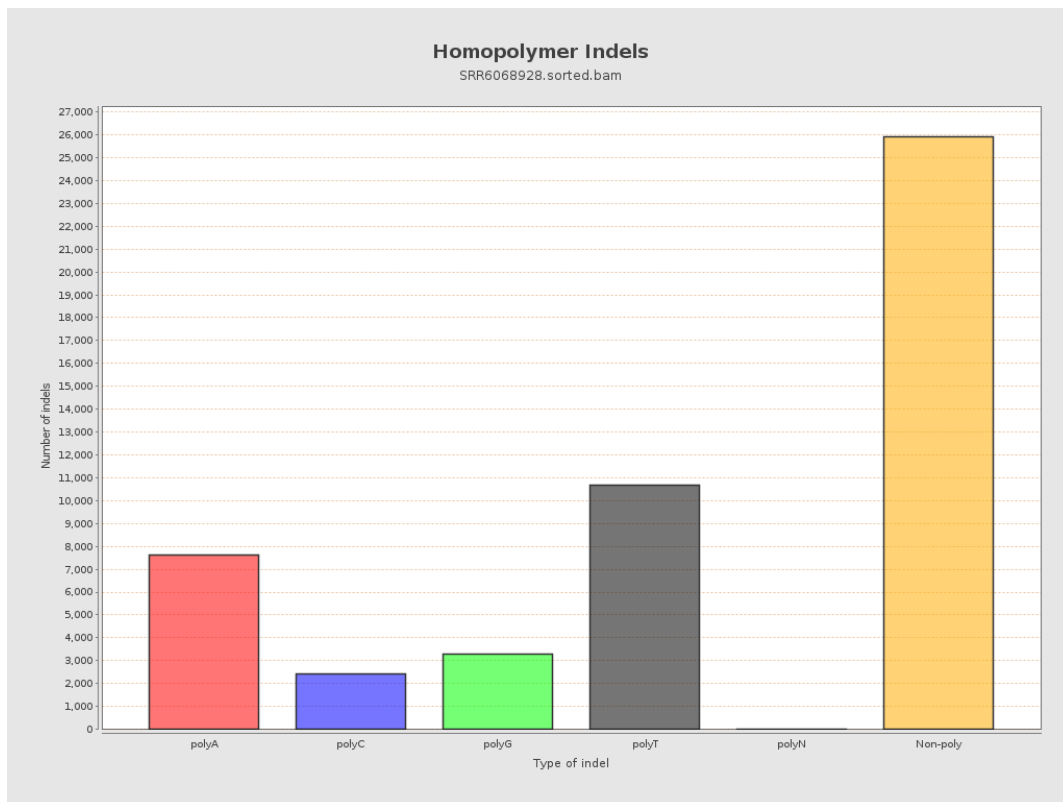
9. Results : Mapped Reads GC-content Distribution



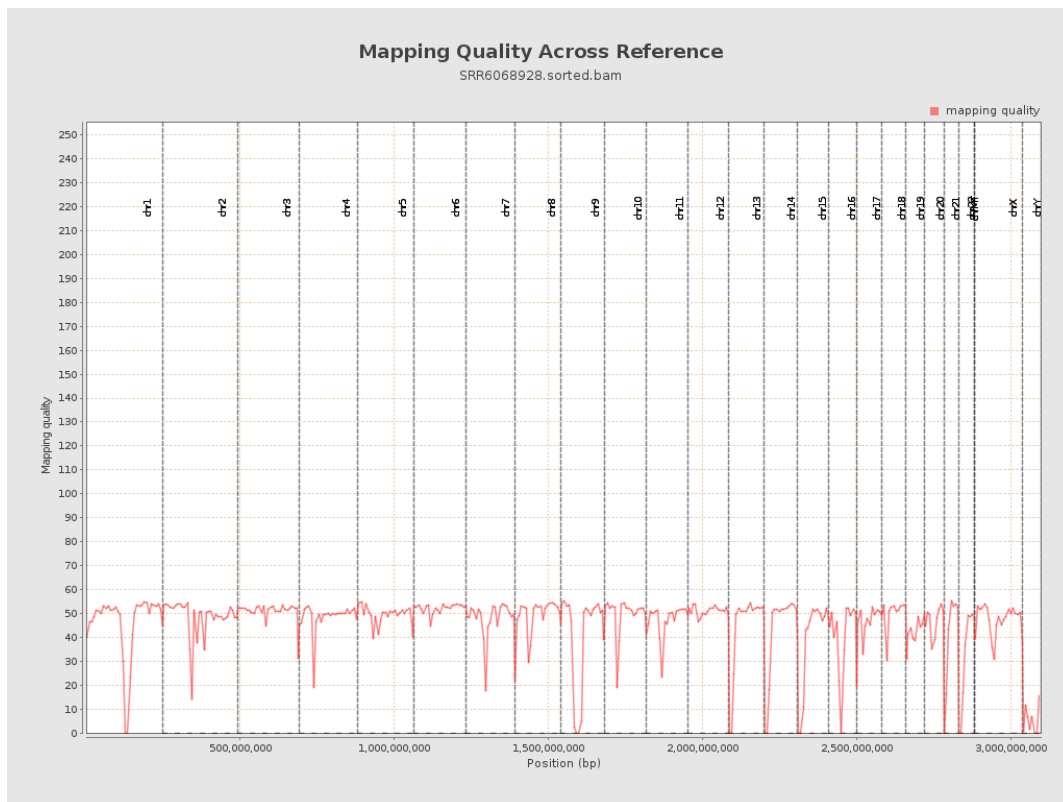
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

