

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/13 23:44:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004068.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_SRR6004068 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004068.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 13 23:44:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004068.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,519,148
Mapped reads	3,016,425 / 85.71%
Unmapped reads	502,723 / 14.29%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	34,225 / 0.97%
Read min/max/mean length	30 / 76 / 76.34
Duplicated reads (estimated)	262,966 / 7.47%
Duplication rate	6.76%
Clipped reads	1,563,928 / 44.44%

2.2. ACGT Content

Number/percentage of A's	55,108,358 / 28.12%
Number/percentage of C's	35,529,492 / 18.13%
Number/percentage of T's	62,617,212 / 31.95%
Number/percentage of G's	42,590,401 / 21.73%
Number/percentage of N's	113,999 / 0.06%
GC Percentage	39.87%

2.3. Coverage

Mean	0.0633

Standard Deviation	0.6358
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2.4. Mapping Quality

Mean Mapping Quality	41.94
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2.5. Mismatches and indels

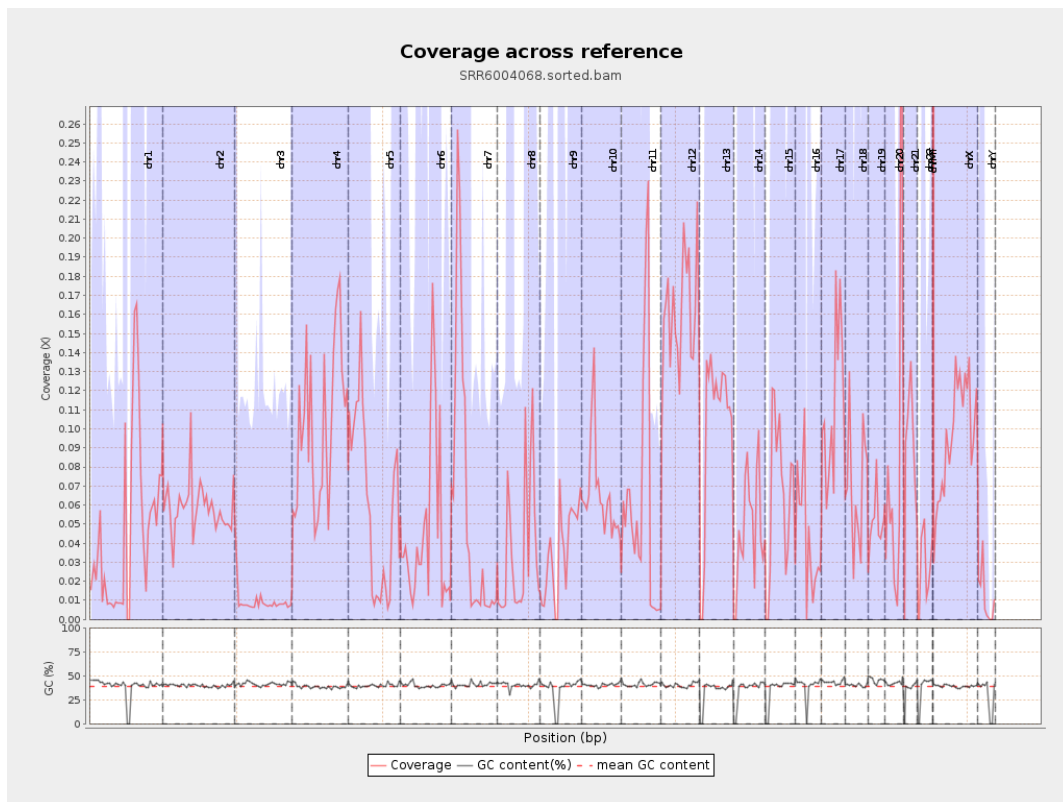
General error rate	0.96%
Mismatches	1,852,270
Insertions	15,781
Mapped reads with at least one insertion	0.52%
Deletions	70,404
Mapped reads with at least one deletion	2.3%
Homopolymer indels	43.55%

2.6. Chromosome stats

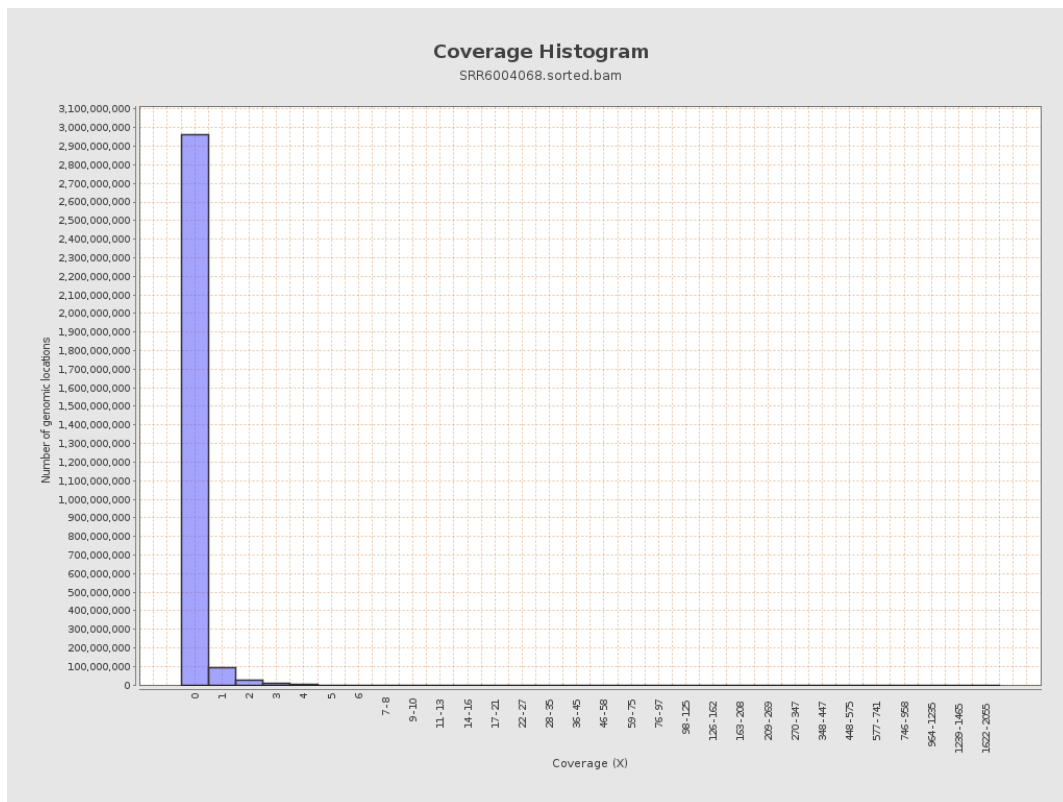
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	11518116	0.0462	1.1818
chr2	243199373	14188903	0.0583	0.5867
chr3	198022430	1980687	0.01	0.1484
chr4	191154276	19774246	0.1034	0.4806
chr5	180915260	10851745	0.06	0.3398
chr6	171115067	7747593	0.0453	0.3097
chr7	159138663	8953337	0.0563	0.4117

chr8	146364022	5320402	0.0364	1.2151
chr9	141213431	5153285	0.0365	0.4708
chr10	135534747	8807454	0.065	0.7047
chr11	135006516	8110469	0.0601	0.437
chr12	133851895	21416945	0.16	0.5521
chr13	115169878	11661207	0.1013	0.4335
chr14	107349540	5211658	0.0485	0.3506
chr15	102531392	6577070	0.0641	0.3588
chr16	90354753	3815965	0.0422	0.387
chr17	81195210	9234259	0.1137	0.5012
chr18	78077248	5430721	0.0696	1.2554
chr19	59128983	3068771	0.0519	0.9143
chr20	63025520	6155089	0.0977	0.4955
chr21	48129895	4157416	0.0864	0.4356
chr22	51304566	1291111	0.0252	0.2122
chrMT	16571	62219	3.7547	3.4923
chrX	155270560	14889501	0.0959	0.4729
chrY	59373566	701917	0.0118	0.3022

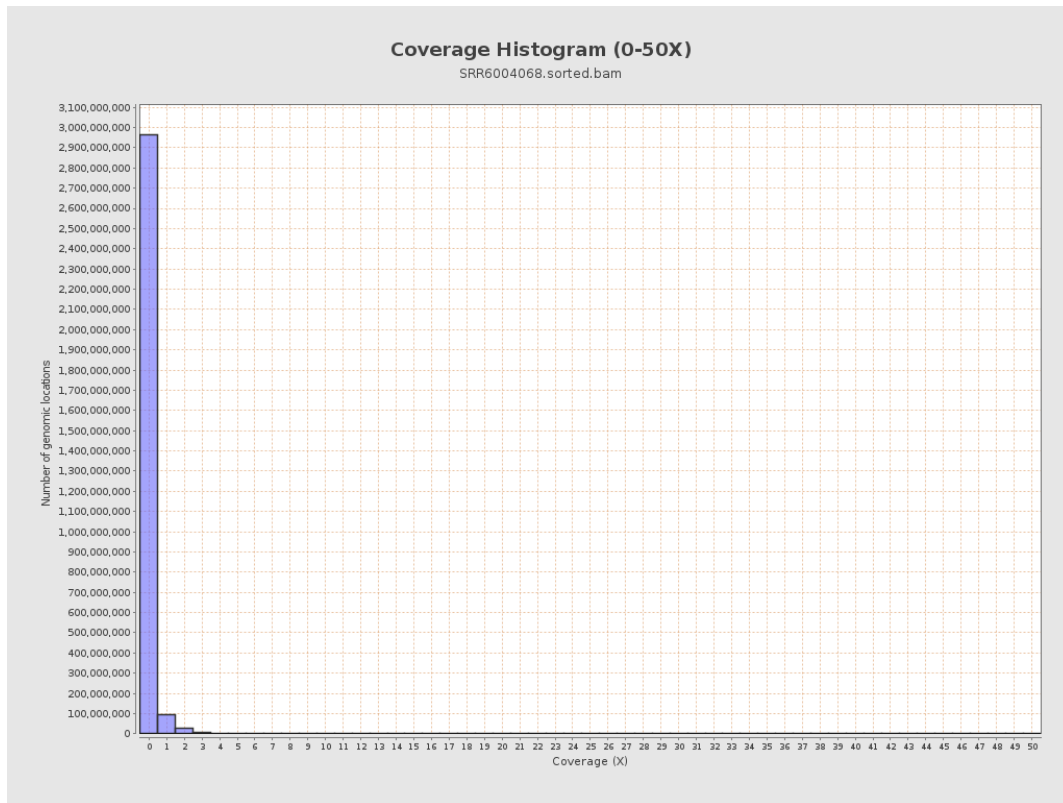
3. Results : Coverage across reference



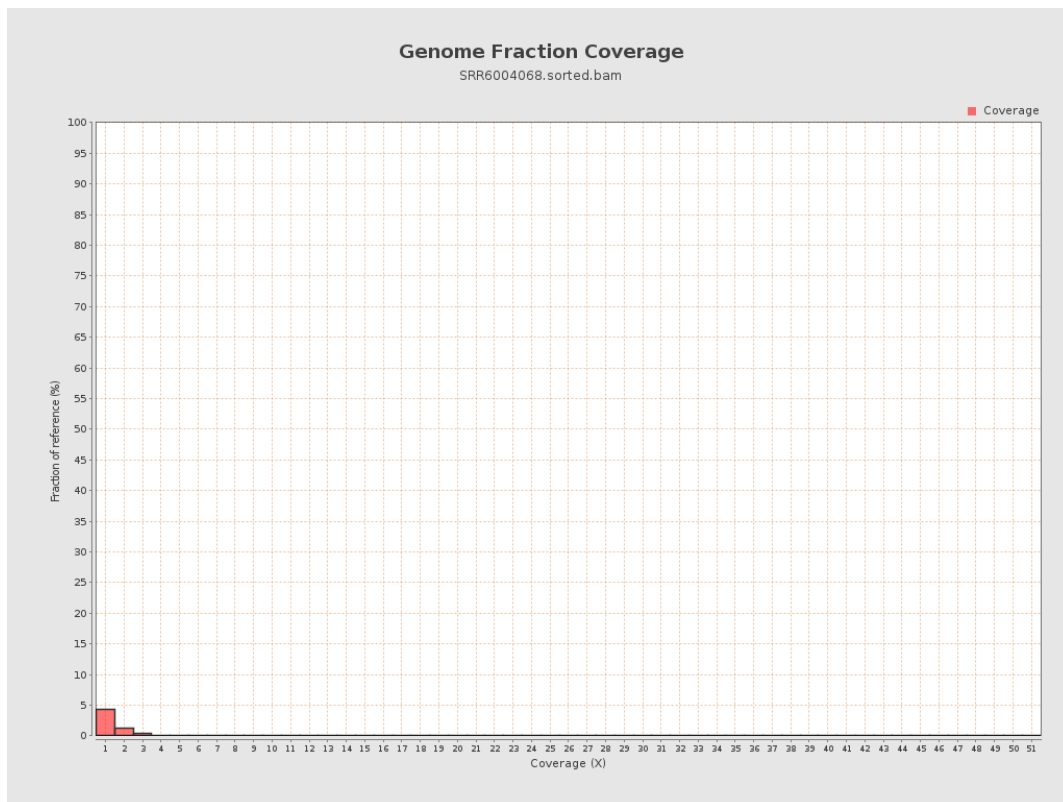
4. Results : Coverage Histogram



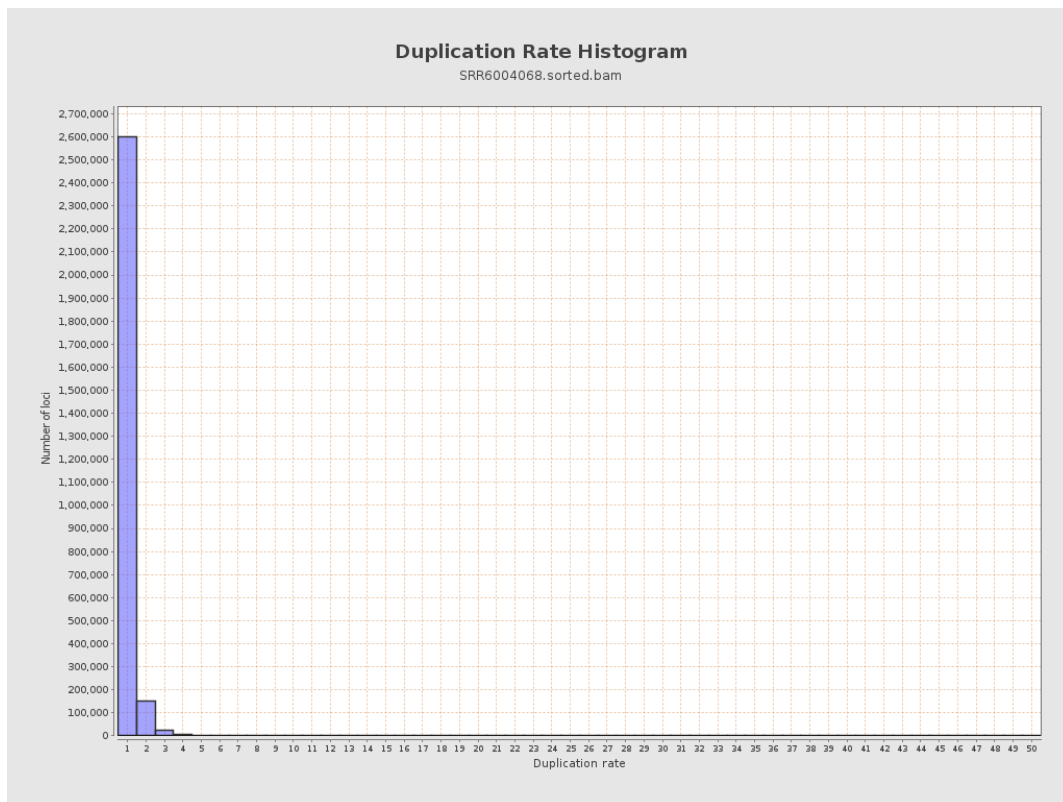
5. Results : Coverage Histogram (0-50X)



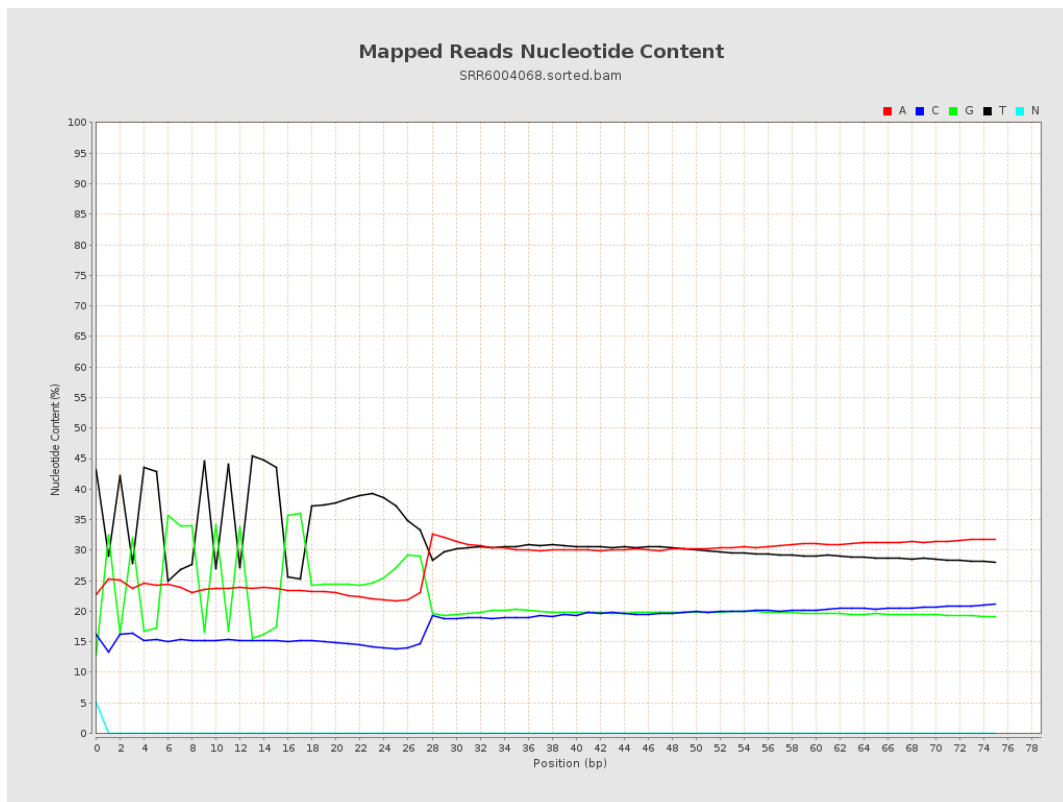
6. Results : Genome Fraction Coverage



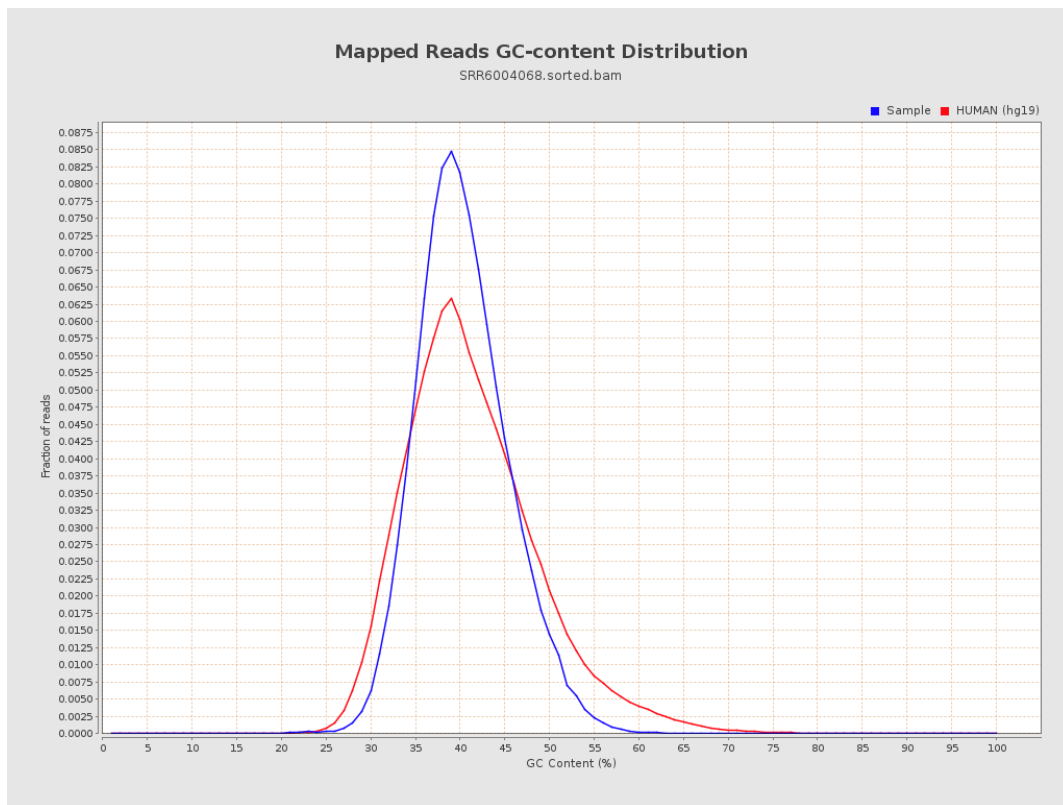
7. Results : Duplication Rate Histogram



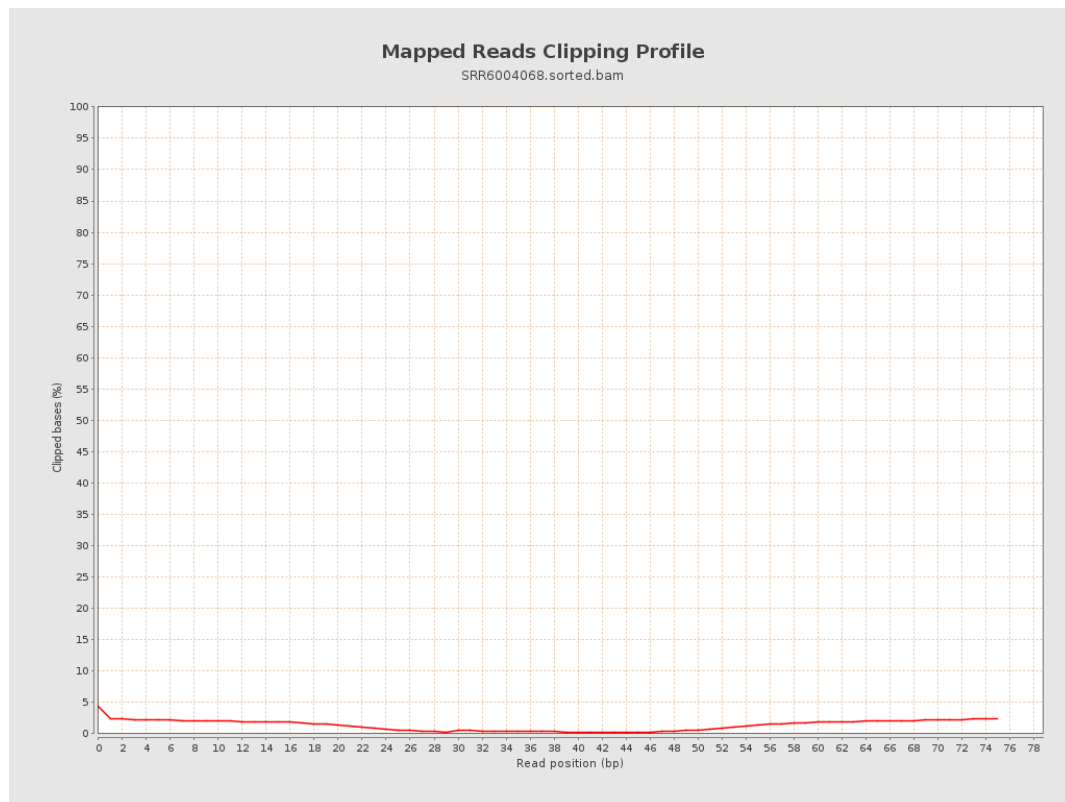
8. Results : Mapped Reads Nucleotide Content



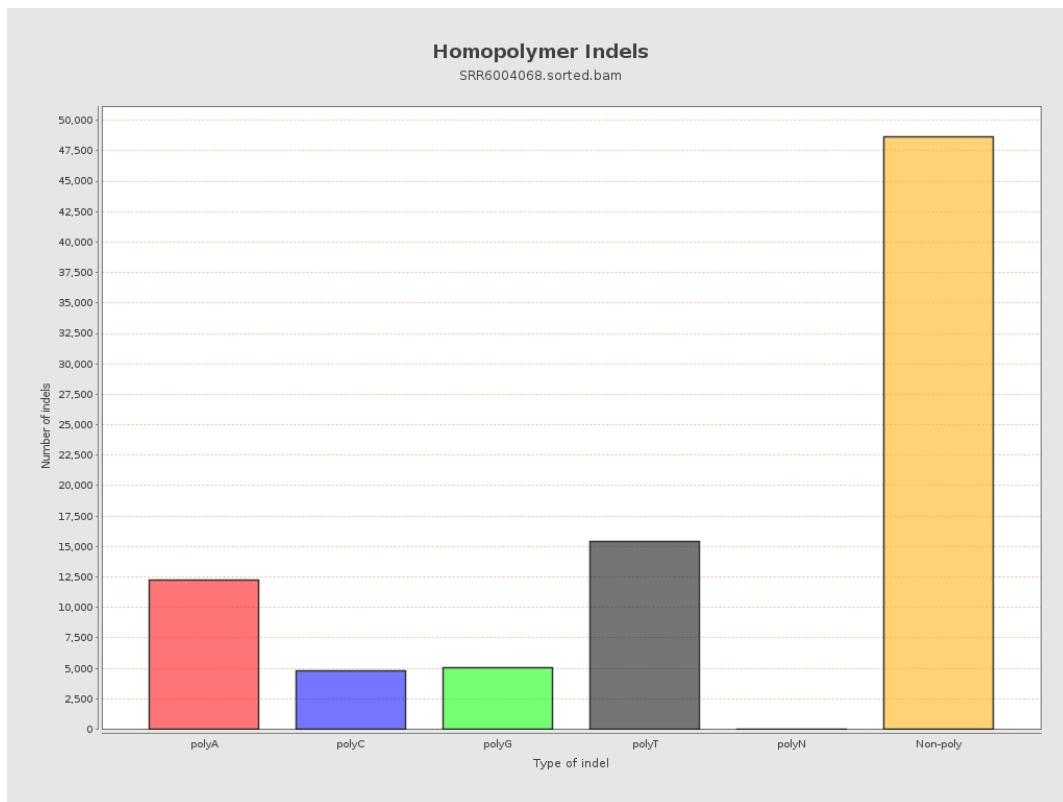
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

