

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 08:13:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708608.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_SRR1708608 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708608.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 08:13:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708608.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,105,243
Mapped reads	5,012,696 / 98.19%
Unmapped reads	92,547 / 1.81%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	145 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	49,748 / 0.97%
Duplication rate	0.99%
Clipped reads	68,115 / 1.33%

2.2. ACGT Content

Number/percentage of A's	77,381,772 / 30.95%
Number/percentage of C's	47,463,674 / 18.99%
Number/percentage of T's	77,081,627 / 30.83%
Number/percentage of G's	48,049,406 / 19.22%
Number/percentage of N's	9,499 / 0%
GC Percentage	38.21%

2.3. Coverage

Mean	0.0808

Standard Deviation	0.2963
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2.4. Mapping Quality

Mean Mapping Quality	46.75
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2.5. Mismatches and indels

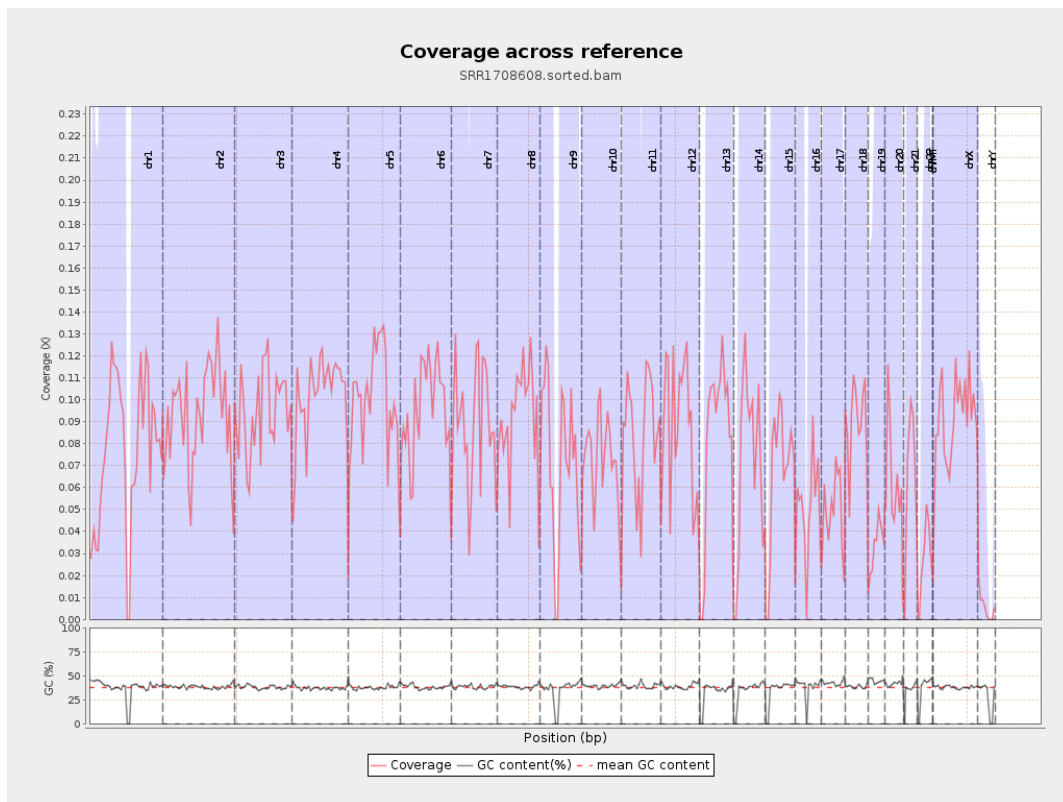
General error rate	0.16%
Mismatches	369,196
Insertions	15,428
Mapped reads with at least one insertion	0.31%
Deletions	12,715
Mapped reads with at least one deletion	0.25%
Homopolymer indels	48.62%

2.6. Chromosome stats

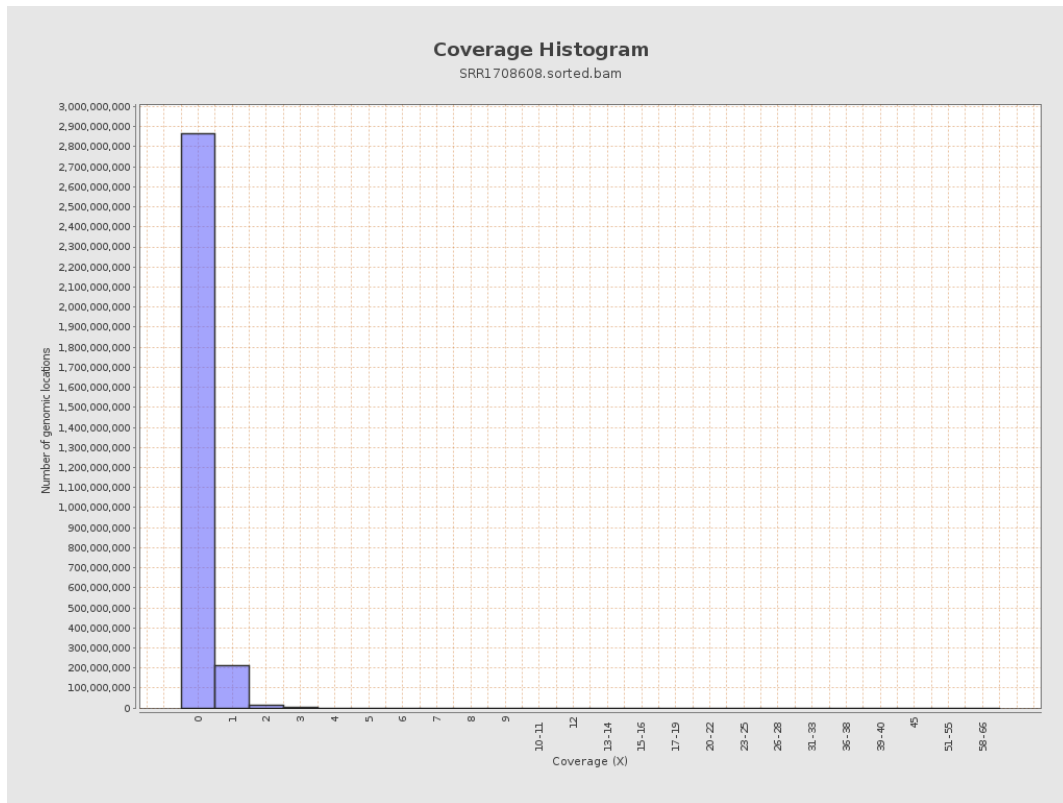
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	19228972	0.0771	0.2927
chr2	243199373	22641151	0.0931	0.3204
chr3	198022430	18800415	0.0949	0.3188
chr4	191154276	19572553	0.1024	0.331
chr5	180915260	17921029	0.0991	0.3257
chr6	171115067	16565420	0.0968	0.3225
chr7	159138663	13985101	0.0879	0.3084

chr8	146364022	13589051	0.0928	0.3155
chr9	141213431	10125657	0.0717	0.279
chr10	135534747	10013008	0.0739	0.2813
chr11	135006516	11381517	0.0843	0.3025
chr12	133851895	11649496	0.087	0.3066
chr13	115169878	9470017	0.0822	0.2986
chr14	107349540	7793911	0.0726	0.2813
chr15	102531392	6721286	0.0656	0.268
chr16	90354753	4448690	0.0492	0.2305
chr17	81195210	4061457	0.05	0.2328
chr18	78077248	7016809	0.0899	0.3097
chr19	59128983	2035937	0.0344	0.1914
chr20	63025520	4005624	0.0636	0.2625
chr21	48129895	2987524	0.0621	0.2617
chr22	51304566	1428677	0.0278	0.1732
chrMT	16571	281	0.017	0.1291
chrX	155270560	14230627	0.0917	0.3143
chrY	59373566	333532	0.0056	0.0788

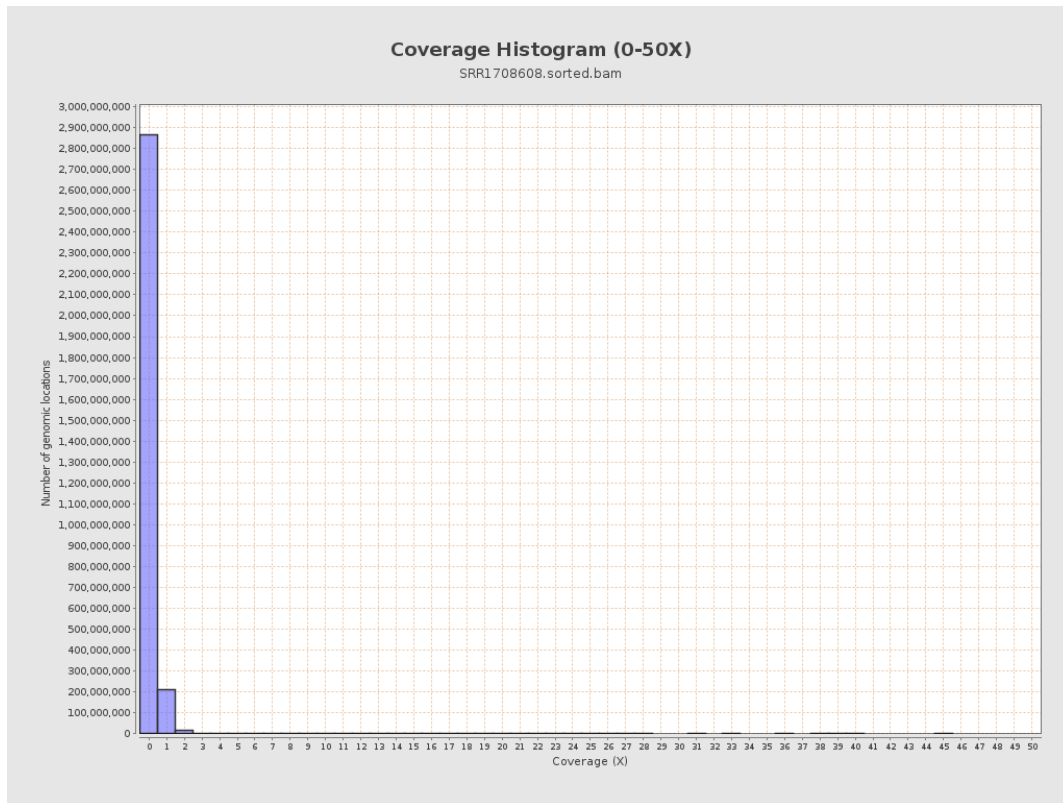
3. Results : Coverage across reference



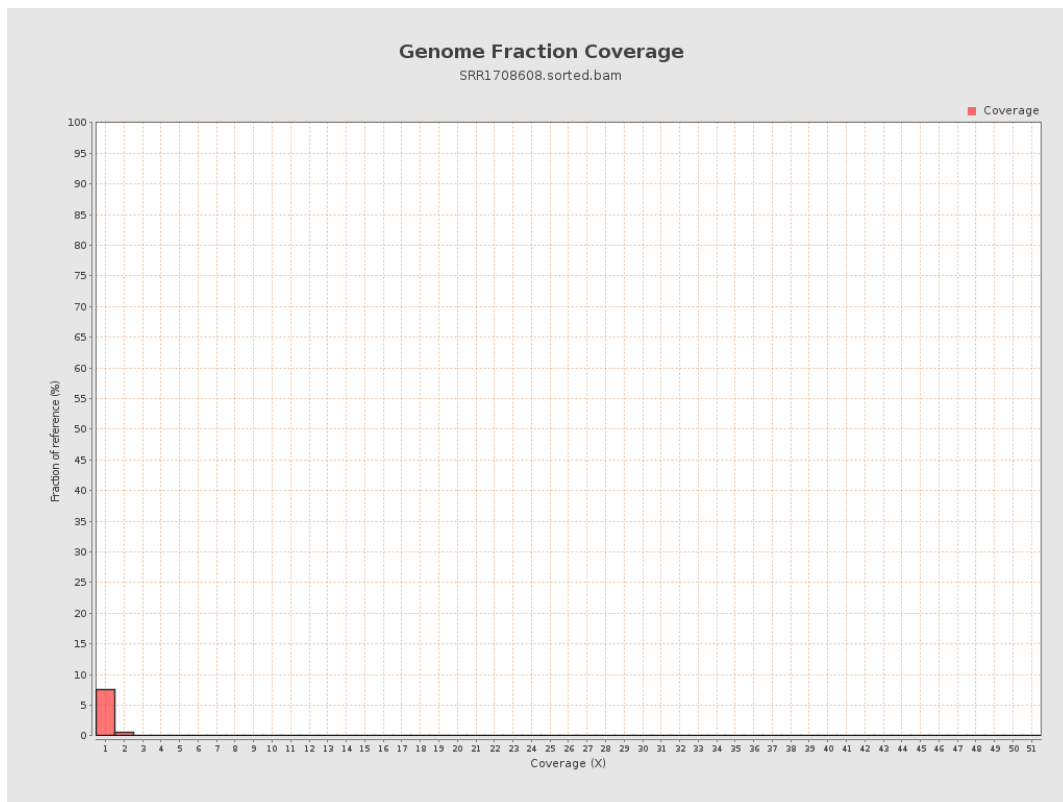
4. Results : Coverage Histogram



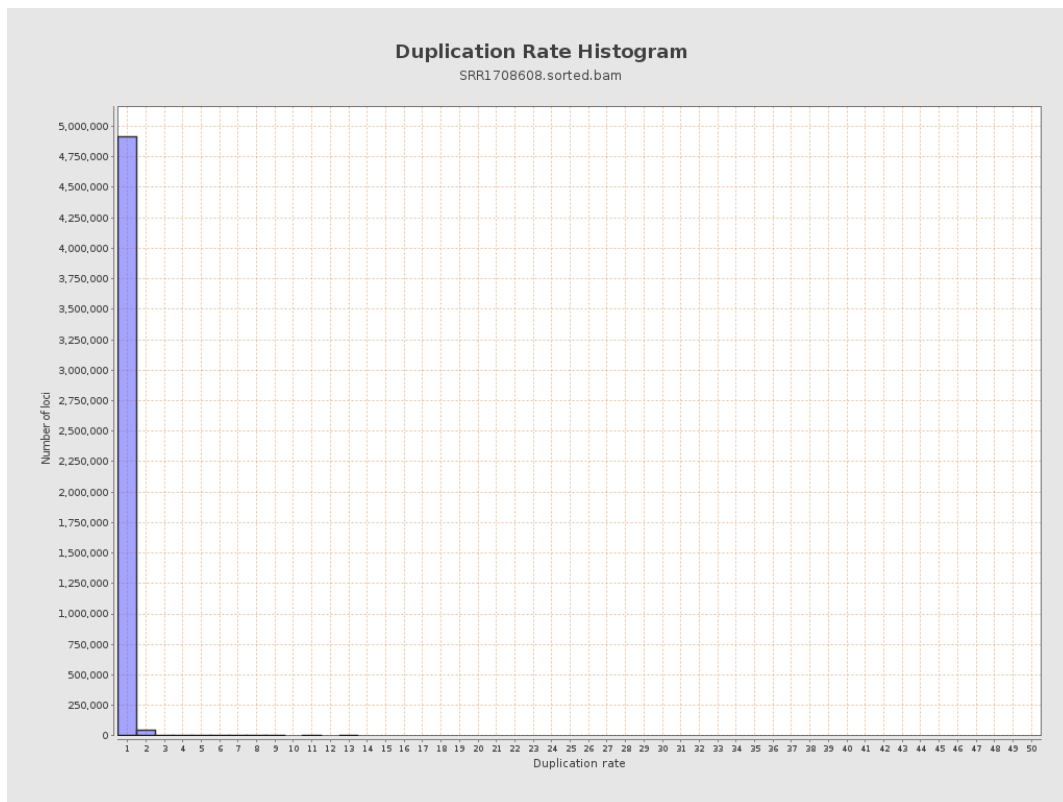
5. Results : Coverage Histogram (0-50X)



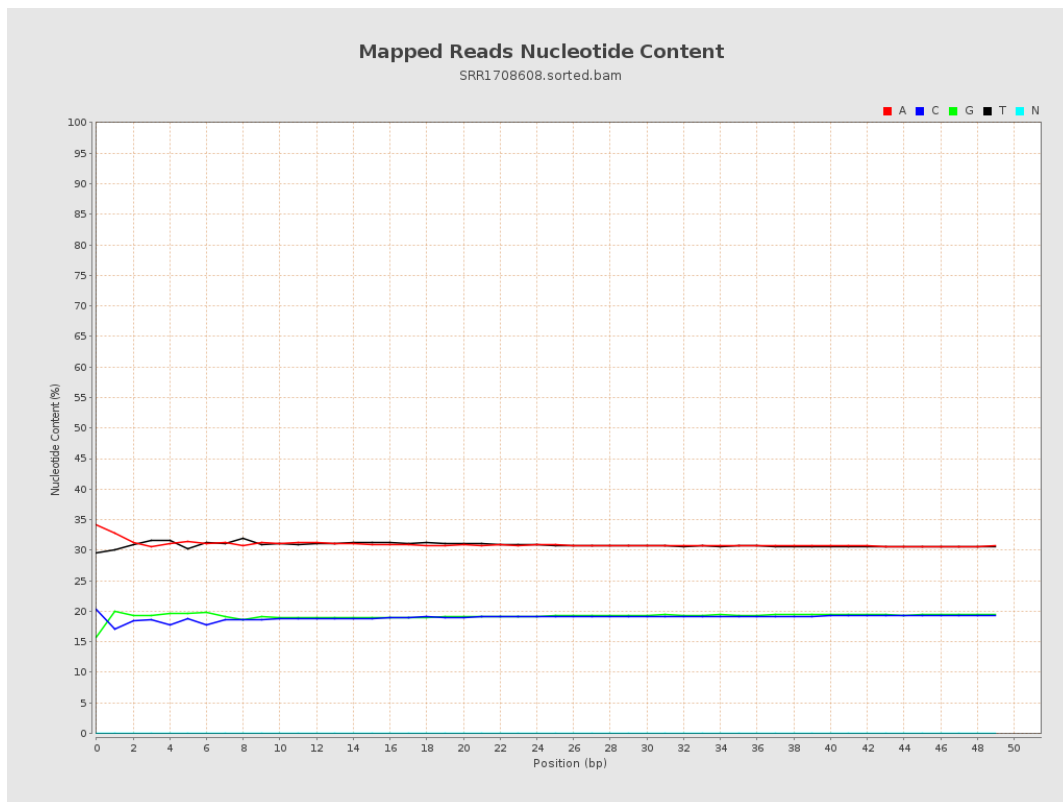
6. Results : Genome Fraction Coverage



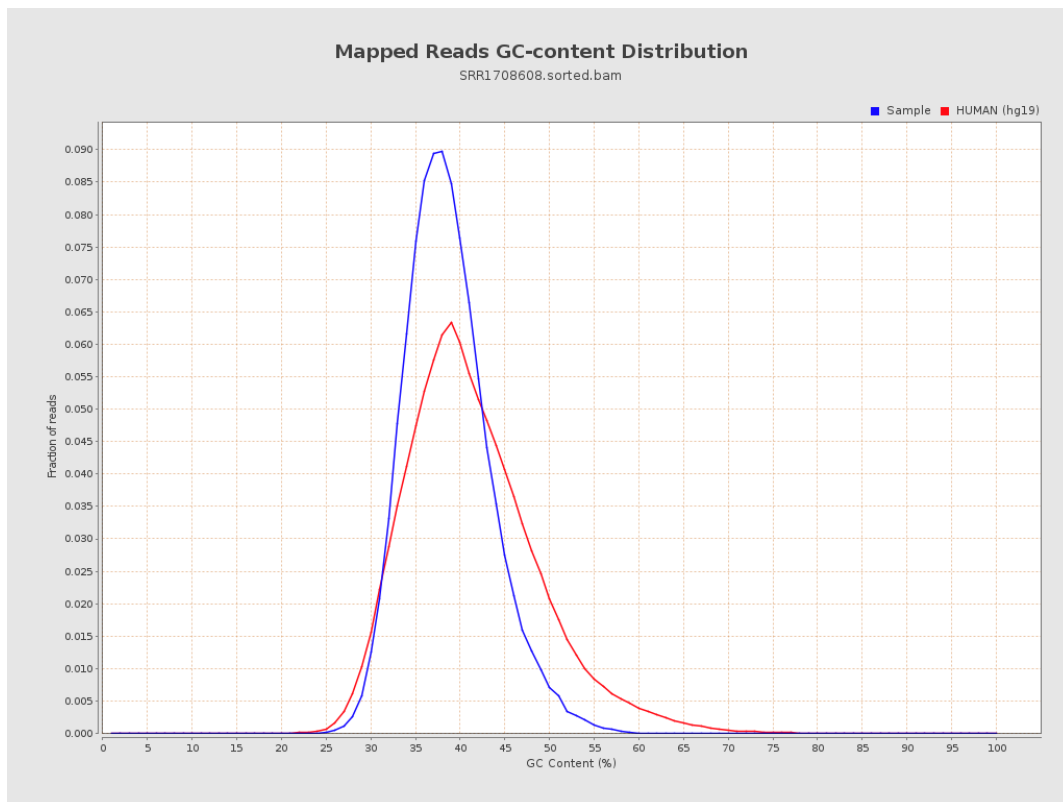
7. Results : Duplication Rate Histogram



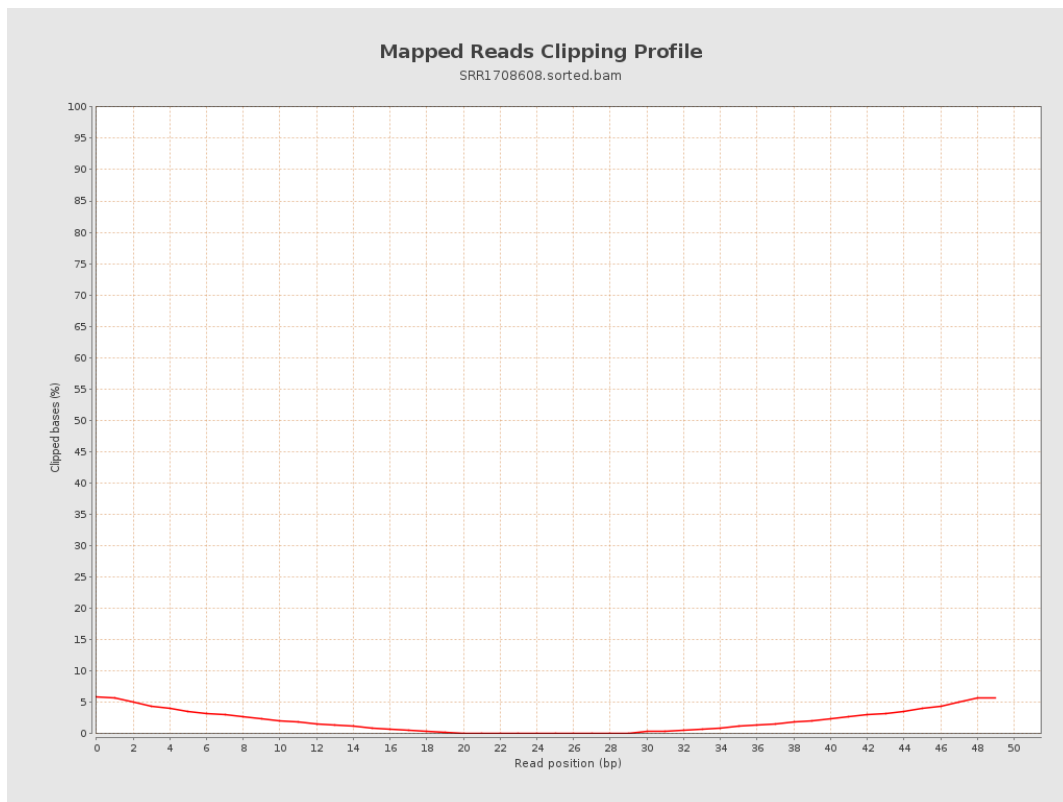
8. Results : Mapped Reads Nucleotide Content



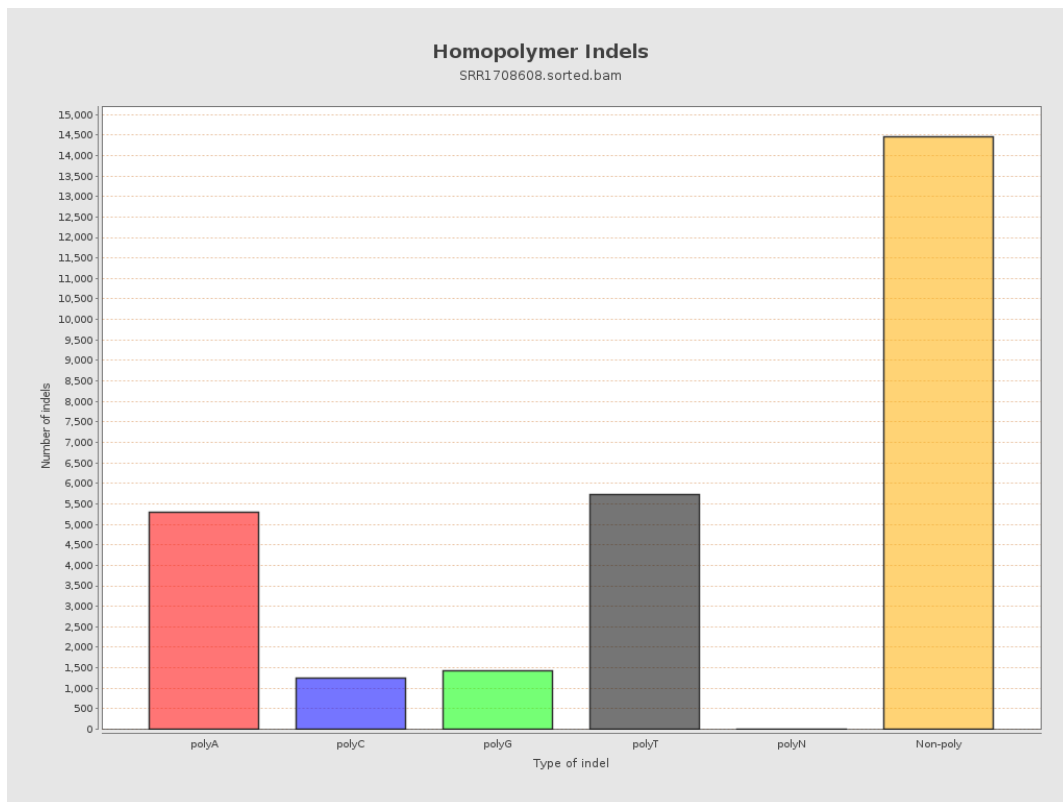
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

